"Studies on genetical parameters for grain yield and its contributing traits in barley (*Hordeum vulgare* L.)"

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IN

Genetics and Plant Breeding

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SUBMITTED BY
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Dedicated to

My

Venerable Parents and Grandmother (Smt. Manaraji Devi)

Rajan Verma….

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Certificate

We, the undersigned members of the advisory committee of **Mr. Rajan Verma, Id. No. CA-11924/2021,** a candidate for the degree of **Master of Science** in **Agriculture** with major in **Genetics and Plant breeding,** agree that the thesis entitled **"Studies on genetical parameters for grain yield and its contributing traits in barley (*Hordeum vulgare* L.)"** is submitted by him in partial fulfillment of the requirements for the degree.

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This is to certify that the thesis entitled **"Studies on genetical parameters for grain yield and its contributing traits in barley (*Hordeum vulgare* L.)"** submitted in partial fulfilment of the requirements for the degree of **Master of Science** in **Agriculture** with major in **Genetics and Plant Breeding** of College of Agriculture, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur is the record of bonafide research work carried out by **Rajan Verma,** Id. No. **CA-11924/2021** under my guidance and supervision. The thesis embodies the work of candidate himself.

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Place: Kanpur

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Date: / 2023

Place: Kanpur (Rajan Verma)

" **Studies on genetical parameters for grain yield and its contributing traits in barley (*Hordeum vulgare* L.)**"

Title **:** Studies on genetical parameters for grain yield and its contributing traits in barley (*Hordeum vulgare* L.)

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ABSTRACT

The present experiment entitled " Studies on genetical parameters for grain yield and its contributing traits in barley (*Hordeum vulgare* L.)" was carried out during the *Rabi* 2022-23 at the Crop Research Farm Nawabganj of C.S. Azad University of Agriculture and Technology, Kanpur-208002 (U.P.). The experimental materials consist of 8 genotypes of barley (RD 2907, KB 1425, KB 1506, KB 1762, KB 1634, HUB 113, K 603, DWRB 137,) were crossed in diallel fashion (excluding reciprocals) to generated 28 F_1 crosses. In a Randomized Block Design with three replications, the F_1 and its parents were assessed. Observation were made on eleven quantitative character namely days to 75% heading, days to maturity, plant height (cm), number of effective tillers per plant, spike length (cm), number of grains per spike, grain weight per spike (g), grain yield per plant (g), 100-grain weight (g), biological yield per plant and harvesting index (%) during the course of investigation.

The analysis of variance revealed highly significant difference among the treatment for all the eleven attributes.

Based on genetic components and combining ability analysis, both additive and non additive gene action were observed for the expression of almost major of the traits, average degree of dominance also supported the gene action through both analysis, keeping in view of the gene action, diallel selective mating recurrent selection followed by inter matting would be helpful for further crop improvement

Combining ability effects indicated that parent KB 1425 was good general combining ability on the basis of GCA effects and *per se* performance for plant height, number of grains per spike, grain weight per spike, 100 grain weight per spike, harvest index and grain yield per plant.

On the basis of SCA effect and *per se* performance cross combination HUB 113 X K 603, KB 1425 X K 603 and KB 1425 X KB 1634 were observed as superior mainly specific combiner for grain yield per plant. The cross combinations namely, KB 1506 X K 603 and KB 1425 X KB 1634 were exhibited desirable heterosis for grain yield per plant.

Low heritability coupled with high genetic advance were observed for grains per spike and grain weight per spike, selection for improvement of such character may be rewarding. Moderate heritability coupled with moderate genetic advance were recorded for plant height, grain yield per plant, and spike length Therefore, consideration should be given for these traits at the time of simple selection.

Phenotypic coefficient of variation (PCV) estimates were found to be slightly higher than their corresponding genotypic coefficient of variation (GCV) estimates for all the characters which indicated the presence of very negligible environmental influence on these characters. Correlation study revealed that grain yield per plant was positive and significantly correlation of phenotypic level with days to 75% heading, days to maturity, plant height, number of effective tillers per plant, spike length, grain weight per spike, number of grains per spike, biological yield per plant, harvesting index were major yield contributing traits in this investigation.

At the phenotypic level, the path coefficient analysis revealed that the positive direct effect on grain yield per plant was observed for 75% heading, days to maturity, plant height, number of effective tillers per plant, spike length, 100 grain weight, harvest index and number of grains per spike Therefore, direct selection for these characters would be rewarding for improvement of grain yield per plant in barley.

Key Word: Diallel, Combining ability, Heterosis, Heritability, Genetic advance, Correlation and Path coefficient.

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CHAPTER - I

INTRODUCTION

Barley, a versatile cereal grain, has been under cultivation for millennia year ago. It belongs to the grass family and is scientifically known as *Hordeum vulgare* (chromosome 2n=14, x=7). Barley is extensively cultivated in diverse regions across the globe and is recognized as one of the earliest cultivated grains.

The exact origin of barley (*Hordeum vulgare*) is believed to be in the Fertile Crescent of the Middle East, specifically in the regions of present-day Iraq and Syria. It is one of the oldest cultivated grains and has a history of cultivation dating back over 10,000 years. Cultivated barley is believed to have originated from wild barley, scientifically referred to as *Hordeum spontaneum*. Over time, humans selected and cultivated specific traits, leading to the development of domesticated barley varieties with improved characteristics such as larger grains and better adaptability to different environments. Historically, barley has played a crucial role in human civilization, serving as a staple food source, a key ingredient in alcoholic beverages such as beer and whiskey, and even as animal feed. It has been an important crop in many ancient civilizations, including those of Mesopotamia, Egypt, and Greece. (**Badr *et al*. 2012)**

Barley is known for its resilience and ability to grow in diverse climates, making it adaptable to different agricultural environments. It is particularly suited for cooler regions and can tolerate harsh conditions such as drought and poor soil quality. Barley's shorter growth period in comparison to other grains is appealing to farmers, making it a desirable crop.

In recent years, there has been growing interest in barley as a sustainable and environment friendly crop. Its ability to thrive in marginal lands and its relatively low water requirements make it an attractive option for farmers aiming to reduce their environmental impact.

The plant has a unique appearance with long, slender leaves and distinctive spikes that contain the grain kernels. These kernels, known as barley grains or seeds, are used in various forms for human consumption. They can be hulled to remove the outer husk, resulting in what is known as "hulled barley," or they can be further processed to remove the bran and polished, resulting in "pearled barley." Barley produces flowers in a spike-like inflorescence called a spike or an ear. The spikes are composed of multiple spikelets, which contain the individual flowers. Each spikelet typically has two florets, one fertile and one reduced or sterile. The spikelets are arranged in pairs along the central axis of the spike. Each spikelet consists of two glumes (modified leaves) that protect the florets. The lower glume is usually smaller and narrower than the upper glume (**Feldman *et al.* 2012)**

Nutritionally, barley is a nutritious grain that offers several health benefits. It is a good source of dietary fibre, vitamins (such as B vitamins) and minerals (such as selenium, manganese and phosphorus). Barley also contains antioxidants and phytochemicals, which have been linked to potential health benefits, including reduced risk of heart disease and improved digestion (**Shen *et al.* 2010**).

In addition to its culinary uses, it is also used as a primary ingredient in the production of malt for brewing as well as in the manufacturing of various food products, such as soups, stews, bread and breakfast cereals. Barley straw has been used historically as animal bedding and for thatching roofs. barley is utilized almost 60% as animal feed, around 30% for malt production, 7% for seed production, 3% as human consumption **(Baik *et al.* 2008)**.

Overall, barley is a versatile grain with a rich history and a wide range of applications. Its nutritional value, adaptability and various uses make it an important crop both in traditional agriculture and in modern food and beverage industries.

Barley cultivation is widespread across different continents, with various regions around the world being involved in its production. Significant barley-producing countries are Russia, Germany, France, Canada, Australia, Ukraine, Turkey, Kazakhstan and the United States. In India, barley is primarily cultivated in states such as Rajasthan, Uttar Pradesh, Bihar, Haryana, Punjab, Madhya Pradesh, and Kashmir, etc. The production volume of barley across India during financial year 2021 was about 1.67 million metric tons, slightly down from about 1.72 million metric tons in the previous year. The production volume of barley was the highest of about 1.83 million tons in 2014 over the past decade in the country **(Statista, 2022).**

The presence of genetic variation is crucial for crop improvement programs, and the selection process is fundamental in plant breeding as it relies on the existing variability. When a population exhibits higher variability, selection tends to yield better results. Therefore, understanding the genetic variability of a crop becomes essential for successful crop improvement efforts. So far, the availability of desirable genotypes with improved yield has not been entirely satisfactory. As a result, various endeavours are underway to develop genotypes that possess desirable traits and can be widely adopted. This involves combining favourable characteristics through breeding methods, such as hybridization and selection, to create genotypes that exhibit superior performance in terms of yield and other desired traits. in order to enhance barley production, it is crucial to develop high-yielding varieties that can adapt to various conditions. These varieties are essential to unlock the crop's full potential in addressing malnutrition, particularly among the vegetarian population in our country. To achieve this, it is necessary to have a comprehensive understanding of the existing genetic variation related to grain yield and its associated traits. This knowledge is vital for improving crop cultivars with high yield potential, as it allows breeders to focus on specific traits that contribute to increased productivity (**Raikwar *et al.* 2014).** Understanding the method of inheritance, the size of gene effects, and their interactions are essential for developing an effective breeding program for the improvement of superior genotypes that are the best general and specific combiners (**Madakemohekar *et al.* 2015).** Various genetic models, specifically second degree statistical models such as the covariance of half-sib and full-sib families **(Comstock and Robinson, 1952)**, combining ability analysis **(Griffing, 1966b)**, and partial diallel **(Kempthorne and Curnow, 1961)**, have been recommended to characterize the nature and extent of gene effects on yield and its components. Among various mating designs, later modified by many others, provides a precise test for epistatic variance as well as unambiguous estimates of additive ($\widehat{D}$) and dominant ($\hat{H}$) components of genetic variance along with directional element '$\hat{F}$'. This particular mating design remains unaffected by gene correlation, allele frequencies and inbreeding levels. Moreover, it demands less experimental effort compared to many other multiple mating designs. Heterosis has been commonly utilized to develop and identify promising hybrids that can be further utilized in both traditional breeding programs and focused on exploiting heterosis. F_1 hybrids in both cross fertilized and self fertilized crops are recognized for displaying hybrid vigour. However, effectively exploiting this phenomenon for commercial cultivation, especially in self-pollinated crops and a select few crops, presents challenges. In the case of autogamous crops such as barley, the complete utilization of heterosis through the creation of hybrid varieties has been made feasible due to the presence of cytoplasmic male sterility and fertility restoration systems, along with the availability of genetic male sterility.

The successful utilization of heterosis in barley has been well established. Knowledge regarding heterosis and the combining ability of yield and its component traits in barley will be highly valuable in selecting suitable parental lines for the development of superior hybrid varieties. The diallel analysis is a method employed to examine the genetic variability, heritability, and genetic advancement of yield attributes. It is also utilized to estimate the general combining ability (GCA) of the parent lines, as well as the specific combining ability (SCA) of the hybrids and their respective effects. In several crops, the use of heterosis over better parent and standard varieties is regarded as one of the outstanding works. Many cross-pollinated and self-pollinated crops have also used it. Therefore, the present investigation, " **Studies on genetical parameters for grain yield and its contributing traits in barley (*Hordeum vulgare* L.)**" was undertaken with the following objective:

1. To determine the extent of variability among the parents and their F_1 hybrids.
2. To estimate genetic components and related parameters based on component analysis.
3. To know the performance of 8 parents and their 28 crosses for their combining ability effects in F_1 generation.
4. To estimate the heterosis of F_1s over economic parent.
5. To determine heritability and genetic advance.
6. To study genetic association between yield contributing traits

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CHAPTER – II

REVIEW OF LITERATURE

The available literature on different aspects of the current study has been thoroughly examined as follows:

(i) Biometrical approaches, for genetic analysis of breeding value for related traits and

(ii) Work done on barley crop

(i) BIOMETRICAL APPROACHES FOR GENETIC ANALYSIS

Galton (1989) first introduced statistical and biometrical approaches, which were later advanced by **Pearson and Lee (1903). Johanson (1909), Nilson Ehle (1909), and East (1916)** pioneered the investigation of quantitative trait inheritance in plants.

Johannsen (1909) stated that somatic variation in segregating plant populations is influenced by both heritable and non-heritable factors. Genes influencing indistinguishable qualitative traits segregate and their expression is influenced by non-genetic factors. New methods were devised for studying quantitative traits. **Fisher (1918)** laid the groundwork for quantitative genetics, partitioning hereditary variances for metric traits into additive, dominance, and epistatic components. **Wright (1935)** similarly described these components as (i) additive genetic variance, (ii) variance due to dominance and (iii) variance due deviations from additive scheme resulting from the interactions of non-allelic genes.

Cockerham (1954) and Kempthorne (1955) extended the partitioning of epistatic variance by introducing factorial components like dysgenic interactions and higher-order interactions, including additive x additive and additive x dominance interactions and dominance x dominance for two loci situations and additive x additive x additive etc. for three loci and so on.

Gardner (1963) proposed essential components for plant breeders, including additive genetic variance, dominance, and epistatic variance. Additionally, he introduced related statistics such as the average degree of dominance, genotypic x environmental interaction, and genetic correlation. These concepts have proved valuable in plant breeding and genetic research.

METHODS OF ESTIMATION OF GENETIC PARAMETERS

Various breeders have commonly used the following methods to estimate genetic parameters in segregating populations. These methods were established by several scientists, including **Mather (1949), Hayman and Mather (1955), Hayman (1958b), Jones (1958), Mather and Jinks (1982), Comstock and Robinson (1948, 1952), Anderson and Kempthorne (1954), and Kempthorne (1957).** Diallel cross-analysis has been established by **Jinks and Hayman (1953), Hayman (1954 a), Griffing (1956 a, b), Gardner and Eberhart (1966).**

Sprague and Tatum (1942), Rajas and Sprague (1952), and Griffing (1956b) have provided the method for analyzing gene action through combining abilities.

In this study, genetic parameters were derived using a diallel mating design, which included various genetic components, combining ability, and heterosis as direct selection criteria. The relevant literature on these aspects has been reviewed below.

DIALLEL CROSS ANALYSIS

Hull (1945) was the pioneer in applying regression techniques to analyse diallel crosses of homozygous lines. **Yates (1947)** defined diallel analysis as the "set of all possible combinations among 'n' genotypes."

Griffing (1956 b) has given four methods of the diallel mating design i.e., MI (P parent, P (P-1)/2 crosses and P (P-l) reciprocals. MII (P parents and P (P-1)/2 crosses), Mg crosses and reciprocals) and M, crosses).

Clearly, the number of crosses significantly rises with a minor increase in the number of parents. As a solution, researchers typically employ Method II and Model I techniques in diallel cross experiments to overcome these challenges.

Arunachalam (1976) provided an examination of diallel crosses and their advantages in plant breeding. **Baker (1978)** explored the application of diallel analysis and the range of validity for various assumptions. Typically, two methods are utilized for diallel analysis:

(a) Graphical approach

(b) Component approach.

in this study, a component approach has been employed.

COMPONENT APPROACH

The variance component analysis, developed by **Jinks and Hayman (1954a)** and based on **Mather's concept (1949),** has been utilized in this study to estimate genetic components and their associated parameters using second-degree statistics**.**

The estimation of various gene effects, including additive, dominance, and epistasis, is commonly done based on genetic models proposed by **Anderson and Kempthorne (1954), Cockerham (1954), and Hayman and Mather (1955).** Additionally, **Cockerham (1954),**

Kempthorne (1954), and Horner *et al*. (1955) have further subdivided epistasis effects into components such as additive x additive, additive x dominance, and dominance x dominance for practical purposes.

According to **Hayman (1958b),** in the presence of significant epistasis, it becomes difficult to measure the additive and dominance gene effects accurately. Furthermore, the partitioning method may not allow for the clear separation of the relative contributions of different gene actions to genetic phenomena, such as heterosis.

Dickinson and Jinks (1956) expanded the previously mentioned diallel analysis method to estimate both the level of parental heterozygosity and comparable genetic components of homozygous analysis. **Gilbert (1958)** expressed criticisms regarding the fundamental genetic assumptions of the diallel technique. On the other hand, **Allard (1956)** examined the stability of specific genetic parameters under various environmental conditions.

Epistasis showed a direct correlation with yield among all the gene effects. Several researchers (**Jinks, 1955; Gamble, 1962; Johnson, 1963; and Eberhart, 1964**) emphasized the significance of epistasis in specific combining ability.

Jinks *et al*. (1969) introduced a novel approach to detect additive, dominance, and epistatic variations, using only 2 x n crosses from a diallel set of n2 crosses. They applied this method to analysed data on final height and flowering. The conclusions drawn from this analysis aligned well with the findings of the comprehensive diallel analysis.

COMBINING ABILITY APPROACH

Sprague and Tatum (1942) introduced the concept of general and specific combining abilities as a means to measure gene action. Combining ability is the genotype's capacity to pass on superior performance to its offspring. They defined general combining ability (GCA) as the average performance of a genotype in a series of hybrid combinations, while specific combining ability (SCA) represented cases where certain combinations performed relatively better or worse than expected based on average performance. Their findings led to the conclusion that the general combining ability (GCA) is mainly attributed to the additive effects of genes, whereas the specific combining ability (SCA) results from interactions within alleles, such as dominance, and interactions between alleles, known as epistasis.

Sprague and Frederer (1951) recommended conducting testing across multiple seasons and various locations when the primary focus is on specific combining ability rather than general combining ability. This approach ensures a more comprehensive evaluation of the specific interactions and their performance across different environmental conditions.

Kempthorne (1957) provided a precise definition of general combining ability (GCA) and specific combining ability (SCA) in terms of the covariance of half-siblings and full-siblings, respectively, analogous to design II.

Comstock and Robinson (1948, 1952) introduced the concept of estimating general combining ability (GCA) effects and their variances from a diallel set of variable populations. This methodology was later developed by **Griffing (1956b), Sprague *et al*. (1959), Sprague (1966), and Gilbert (1967).**

Hayman (1957) observed that without epistasis, GCA represents additive effects, while SCA involves dominance. However, both combining abilities can include epistasis components. In unselected materials, SCA mainly measures dominance and epistasis, while in selected materials, it primarily reflects dominance effects.

Wessely (1973) examined the effects of general combining ability (GCA) and specific combining ability (SCA) concerning the means and variance of the breeding population. On the other hand, **Sneep (1977), Stam (1977), and Bos (1977)** discovered that inter-mating in the early generations of self-pollinated crops resulted in genetic drift, leading them to conclude that there was no advantage in utilizing recombination background.

DEGREE OF DOMINANCE

The impact of individual genes is typically indistinguishable from each other in polygenic inheritance. As a result, it becomes challenging to identify the specific actions of single genes. However, in a segregating population, their collective influence offers some understanding of their behaviour and allows for inferences about the average level of dominance.

In **1949, Mather** introduced the concept of "degree of dominance," which helps us assess the extent of gene action. When the degree of dominance is above zero, it indicates the presence of some degree of dominance in gene action. A value greater than one suggests either no dominance or partial dominance. Conversely, if the degree of dominance is precisely zero, it signifies the absence of dominance.

Comstock and Robinson (1948), Robinson *et al.* (1949), and Gardner (1963) acknowledged the existence of a wide range of over-dominance in yield estimates, particularly observable during the repulsion phase. Additionally, Gardner and Lonnquist (1959), **Robinson and Moll**

(1963), and Moll *et al.* (1964) presented experimental evidence supporting the presence of linkage bias in the outcomes.

HETEROSIS

Heterosis, a term introduced by **Shull (1914)**, denotes the phenomenon where the F_1 generation resulting from the crossing of two genetically dissimilar gametes or individuals often exhibits increased or decreased vigour compared to the better parent or the mid-parent. According to **Jinks (1955),** heterosis may arise from non-allelic interactions instead of being solely dependent on specific gene relationships within the same lines. On the other hand, **Mather (1955)** proposed that heterosis could result from a combination of additive, dominance, and interaction effects between homozygous and heterozygous components, as well as the distribution of genes in the parental lines. **Mather and Jinks (1971)** provided a definition of heterosis, describing it as the degree of superiority displayed by F_1 hybrids over their better parent or mid-parent. However, in the context of plant breeding, heterosis holds little practical significance unless the hybrid's performance surpasses that of a well-established and widely adopted variety in the region. The form of heterosis observed beyond that of the commercial cultivar is commonly referred to as economic heterosis **(Sharma and Ahmad, 1978**). As described by **Jinks and Jones (1958)**, heterosis is a complex genetic phenomenon influenced by a delicate balance of additive, dominance, and interaction effects between homozygous/homozygous and homozygous /heterozygous components, as well as the distribution of genes in the parental line. **Robinson (1963) and Moll *et al*. (1964**) suggested that genetic diversity in parental stocks and the presence of partial to complete gene dominance could be significant factors contributing to heterosis in yield. **Williams (1959), Durate and Adams (1963), Grafius (1964), and**

Coyne (1965) further elaborated that examining individual components in studies could reveal how heterosis is effectively utilized and expressed.

The genetic foundation of heterosis for complex traits could be elucidated through multiplicative interactions at the phenotypic level of the component traits. Some suggestions propose that heterosis can be better understood by considering dominance effects rather than overdominance effects.

SELECTION PARAMETERS

The concept of heritability and genetic advance plays a crucial role in assessing the phenotypic variations observed among different individuals, which arise from genetic changes or environmental influences. Heritability provides insights into the potential and magnitude of improvement achievable through selection processes.

Dudley and Moll (1969) proposed that a plant breeding program can be divided into three distinct stages:

1. Creation of a diverse pool of germplasm with genetic variability.
2. Selecting superior individuals from this pool.
3. Utilizing the selected individuals to develop a superior variety.

In all these stages, estimating genetic variance and heritability becomes essential for making informed decisions and achieving successful outcomes in the breeding process.

According to **Lush (1940),** heritability in the narrow sense refers to the ratio of additive genetic variance to phenotypic variance. On the other hand, heritability in the broad sense is the ratio of total genetic variance to phenotypic variance.

Various scientists have proposed several methods for estimating heritability. These methods include: (i) Parent-offspring regression, which was described by **Fisher (1918), Lush (1940), and Robinson *et al.* (1949)**, (ii) Methods based on variance components of single crosses involving six generations, as suggested by **Fisher (1918) and Mather (1949),** (iii) The use of genetically uniform populations, as outlined by **Lush (1948),** (iv) Utilizing F_2 and backcross progenies, a method introduced by **Warner (1952),** (v) Modified parent-offspring regression, as presented by **Frey and Horner** (**1957**), (vi) Constant parent regression, a method introduced by **Griffing (1950),** (vii) Analytical approaches based on estimates of combining ability variance, described by **Crumpacker and Allard (1962) and Verhalen and Murray (1969)** and relying on the work of **Kempthorne and Curnow (1961)**.

Genetic advance is a measure that evaluates the enhancement in the genotypic value of the new population compared to the previous population. The extent of genetic gain is influenced by several factors:

(i) The level of genetic variability, which signifies the degree of variation among individuals within the base population.

(ii) The strength of the environmental and interaction components of variability, which may mask the underlying genetic diversity.

(iii) The intensity of selection applied, as highlighted by **Comstock and Robinson (1952).**

In summary, the genetic advance is dependent on the amount of genetic variability, the impact of environmental and interaction components, and the level of selection pressure employed in the breeding program.

The improvement achieved in traits through breeding is determined by the genetic gain, which is the result of the product of heritability and selection differential. This value is usually expressed in terms of the phenotypic standard deviation of the trait. However, the heritability value alone lacks full significance as it doesn't consider the estimates of absolute variability within the trait. In other words, heritability provides insight into the proportion of phenotypic variation attributable to genetic factors, but it doesn't reveal the magnitude of the overall variation in the trait. To obtain a more comprehensive understanding of the genetic gain, one must also consider the selection differential that accounts for the absolute variability observed in the trait.

CORRELATION AND PATH COEFFICIENT

The correlation coefficient is a statistical measure used to determine the degree and direction of the relationship between multiple variables. It helps express the correlated response to directional selection of certain characters, which may not have individual value but serve as indicators for consideration (**Johnson *et al*., 1955; Robinson *et al*., 1951)**. Studying the genotypic, phenotypic, and environmental interrelationships among agronomic traits is crucial from a practical standpoint. Phenotypic correlation indicates the direct association observed between two characters. However, for selection purposes, phenotypic correlation holds limited practical value unless genetic and environmental correlations between character pairs are estimated separately and show similar directions. Genetic correlation, on the other hand, measures the genetic association between characters and aids in selecting one character for improving another, providing valuable information on their own (**Miller *et al*. 1958).** According to **Adams (1967) and Stebbins (1950),** genotypic correlation results from the combined impact of segregating genes that influence different characters, leading to both positive and negative correlations. The main factors contributing to genetic correlation include pleiotropy, linkage, and developmentally induced relationships.

(ii) REVIEW OF WORK DONE ON BARLEY

The recent literature covering researches on barley of the last two decades have been made to review on the following aspects:

1. Coefficient of variability
2. Genetic Variance Components (Gene Action)
3. Combining Ability
4. Heterosis
5. Heritability and Genetic Advance
6. Correlation and path coefficient

1. Coefficient of variability

Germplasm is the heart of our crop improvement program. The speed of improvement in any self-pollinated crop depends upon the amount and types of genetic diversity exhibited in the population. Though Genetic variation is heritable and hence significant in any selection program.

Jalata *et al.* (2011) reported that genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) was relatively higher for grain yield per plot, number of kernels per spike and spike weight, across location.

A**l-Tabbal *et al.* (2012)** observed genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield per plant, biological yield and number of kernels per main spike.

Akanksha *et al*. (2012) found significant differences among the genotypes for all the traits viz. plant height, tiller/m^3, spikelets/spike, grains per spike, 1000 grain weight, leaf arca index, chlorophyll content, canopy temperature, spike length, grain per ear and harvest index Justifying the presence of adequate variability with regard to the important traits.

Kumar *et al.* (2013) reported high PCV and GCV for grain/ main spike and number of grains/ ears.

Singh *et al*. (2014) reported the phenotypic coefficient of variation was higher than genotypic coefficient of variation. maximum phenotypic and genotypic coefficient of variation was recorded for grain yield/plant (27.51 and 27.31, respectively).

Singh *et al.* (2015) observed high GCV and PCV for peduncle length followed by number of grains per ear and grain yield per plant.

Akgün (2016) reported close resemblance between genotypic correlation coefficient (GCV) and phenotypic correlation coefficient (PCV) for grain yield.

Ahmadi *et al*. (2016) found highest values of phenotypic and genotypic coefficient of variation for the number of grains per spike followed by peduncle length, early vigour and grain yield.

Hailu *et al.* (2016) recorded high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation for number of productive tillers/m² and number of kernels per spike across locations.

Ram and Shekhawat (2017) revealed significant differences for all the studied traits and indicated the influence of environment on the expression of these characters. The GXE interaction was also found significant for most of the characters except tillers per plant, flag leaf area, spike length.

Dinsa *et al*. (2018) observed genotypic coefficient of variation (GCV) ranged from 3.94% to 22.90% while phenotypic coefficient of variation (PCV) ranged 4.98% to 30.34%.

Gupta *et al*. (2018) evaluated 70 genotypes of barley in Randomized Block Design with 3 replications for 15 traits during Rabi 2014-2015 at Kanpur. The analysis of variance showed significant differences among genotypes for all the traits. high estimates of genotypic coefficient of variability were observed for biological yield per plant, plant height, number of productive tillers per plant, grain yield per plant and shoot length.

Mareiy *et al*. (2018) reported significant differences among the 15 barley cultivars for most of the traits. high phenotypic coefficient of variability (PCV) and genetic coefficient of variability (GCV) were found for most of the studied traits.

Matin *et al*. (2019) recorded the high genotypic coefficient of variation (GCV) for grain/ spike (29.89 %), yield/ plant (28.72%) and effective tiller/plant (21.86 %) and spike length (13.56 %). The characters with high GCV indicated high potential for selection.

Nagash *et al*. (2019) revealed highly significant (p 0.01) to low significant ($p \leq 0.05$) difference for all the characters. sixteen parameters were evaluated to assess the inter relationship among yield and yield-related agronomic characters and their effect on grain yield.

Yadav *et al.* (2019) reported moderate to high level of genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV). The magnitude of phenotypic coefficient of variation (PCV) was higher than their genotypic coefficient of variation (GCV) for all the characters but the extent was quite small, indicating very less environmental influence on the expression of the characters. Higher estimates of (GCV) was recorded for productive tillers per plant (16.62) followed by peduncle length (14.83).

Devi *et al*. (2020) reported the genotypes significantly differed for all the characters under both the environments indicating enough variability in the experimental material among all the traits under both conditions, number of grains per spike had highest phenotypic and genotypic coefficient of variability followed by grains yield per plant.

Dido *et al*. (2020) recorded genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for yield and yield associated characters. Results revealed significant variation for all characters among the tested barley accession.

Sootrakar *et al.* (2020) reported phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for all ten characters. Among the traits, spike weight (20.14), number of grain/spike (21.60), grain weight/spike (21.92), and grain yield per plant (20.29) exhibited the highest magnitude of PCV. On the other hand, days to 50% flowering (7.88) and biological yield per plant (7.55) had the lowest PCV values. Regarding GCV, the traits with the highest values were the number of grains/spike (20.93) and grain weight/spike (20.28).

Angassa (2021) reported phenotypic and genetic coefficients of variations ranged between 11.19 to 38.84% and 3.77 to 33.87%, respectively. Both coefficients of variations had high values for the number of spikelets per spike, number of kernels per spike and grain yield.

Kumar *et al.* (2021) find out, the coefficient of variation attributed to genotypic diversity was recorded highest for grain yield (26.16 %) followed by inclination angle (20.0 %), internode length (13.11 %), and tillers per meter (13.07 %). However, days to maturity (2.69 %) contributed less to diversity with lower coefficient of variation.

Thakur *et al.* (2022) reported genetic diversity and yield performance in barley (*Hordeum vulgare* L.) under rainfed condition, ten barley genotypes were taken for investigation viz., Azad, IBOH 9025, IBOH 9026, IBCB-83, Jyoti, K 409, K 909, Jagrati, IB4T 920 and K 560. The most desirable genotypes for other characters coupled with superior grain yield were IBOH 9025 for high 100 grain weight and plant height, Jagrati for days to flowering, Azad for maximum ear length, IBOH-9025 for maximum ear bearing tillers plant-1, Azad for number of tillers plant-1 and maximum number of seeds ear-1.

Naresh and Kumar (2023) observed significant differences among experimental material for all traits. High PCV along with high GCV were observed for the characters such as peroxidase, grain yield per plot, biological yield per plot.

2. Genetic Variance Components (Gene Action):

Fisher (1918) was the first to categorize genetic variance into three components: additive, dominance, and epistatic variance. Additive variance results from the average effects of alleles at different gene loci. dominance variance arises from deviations in gene action caused by interactions between alleles of the same gene. Epistatic variance arises from interactions between alleles of different genes. Later, **Wright (1935)** defined these three components as: (i) additive genetic variance, (ii) variance due to dominance, and (iii) non-additive variances, which include both dominance and epistatic variance.

Varzaru *et al*. (2012) reported additive gene effects which are higher in magnitude, breeding methods involving reciprocal recurrent selection or biparental mating were suggested for further improvement in grain yield per spike.

Jain *et al.* (2013) reported that the non-additive gene action was predominant for most of the characters including grain yield.

Raikwar *et al.* (2014) observed magnitude of dominance effect (h) has a greater value than additive effect (d) in all the traits.

Assefa and Labuschagne (2015) observed additive gene action for days to heading and maturity while both additive and non-additive gene effects were important in conditioning spike length under both drained and waterlogged conditions. Under drained conditions, only additive gene action was important for seeds spike-1 and grain yield spike, while both additive and non- additive gene effects were important in conditioning grain yield.

Maurer *et al*. (2015) reported additives effects are involved in the determinism of test weight only in the case of "Orizont" and "Plaisant" varieties. The dominant alleles which control the phenotypic expression of this trait have a higher frequency than the recessive ones and also an asymmetry of positive and negative effects of genes due to dominance was highlighted. The dominance effects have a preponderant and significant contribution to the inheritance of test weight, while the contribution of additive effects was much lower.

Mansour *et al*. (2016) observed components of genetic variance more contribution of the dominance effects in the inheritance of the studied traits compared to additive ones. The low values due to excess of dominance effect as well as great effect of the environmental factors in the genetic control of the studied traits. Wr-Vr graphs showed high degree of genetic diversity for parents with different degrees of dominance and different distribution of dominant and recessive alleles in the parental material.

Patial *et al*. (2016) found that significant differences among parents, crosses and parent vs. cross for all the 7 traits studied indicated the presence of sufficient variability that can be exploited for the development of high yielding barley hybrids. Variance of specific combining ability (SCA) were higher than the general combining ability (GCA) for all the traits which indicated the predominance of non-additive (dominant, overdominance and epistasis) type of gene action in the inheritance of the traits

Elakhdar *et al.* (2017) reported dominance effect [dd] was more important and greater than the additive effect [aa] and [ad] for most traits.

Mansour (2017) observed highly significant difference for all traits, in all crosses. dominance × dominance was greater in magnitude than other components in most studied traits, indicating that these traits were greatly affected by dominance and its non-allelic interactions.

Mustafa (2018) find out the value of σ^2A was greater than its $\sigma^2 D$ for grains spike, thousand grain weight and plant height, which pointed out the predominance of additive gene action as the ratio of $\sigma^2A/\sigma^2 D$ was more than unity, whereas the rest of the traits *viz*., spike plant, spike length, harvest index biological yield plant and grain yield plant appeared overbalance of non-additive gene action. The average degree of dominance values for spike length and 1000- grain weight indicated partial dominance while rest of the traits showed over-dominance.

Madhukar *et al.* (2018) studied confirmed that yield related traits like number of grains per spike, grain weight per spike, 100 grain weight and grain yield per plant along with stress related traits like stomatal conductance and proline content were predominantly influenced by dominance (h) and dominance × dominance (l) gene action. Therefore, selection of these traits will be difficult in the early generations.

Patial *et al*. (2018) find out portion of additive and dominance variances showed, importance of both additive and non-additive gene effects for grain yield. The non-significant ratio of GCA to SCA mean square highlighted that non-additive gene effects were more important than additive effects. Distribution of dominant and recessive alleles in parents were asymmetrical and parents possess majority of recessive alleles. Since average degree of dominance has values greater than, which indicated over-dominance type of gene action in the inheritance of the grain yield.

Raikwar and Mishra (2018) observed magnitude of dominance (h) effects which was higher than additive (d) effects, indicating the preponderance of dominance (h) effects over the additive effects. It is obvious that non-fixable gene effects (h), (j) and (l) were higher than the fixable (d) (i) in all the crosses in all the characters, indicating greater role of non-additive effects in the inheritance of all the characters

Swati *et al* (2018) showed that significant differences for most of the traits in both GCA and SCA components revealed the importance of both additive and non-additive gene actions with the predominant effect of nonadditive gene action.

Bouchetat *et al.* (2019) reported existence of a great genetic variability between the hybrids and between their parents; additive and non-additive genetic effects are involved in the control of the variables evaluated. The variance ratio of general combining ability (GCA) and the specific combining ability (SCA) is less than one unit which explains the preponderance of the dominant genes, with a super dominance involved in the expression of the length of the spike, the number of grains per spike and the productivity per plant; on the other hand, complete and partial dominance.

Bocianowski *et al.* (2019) reported additive effect of all genes controlling the trait and the total epistasis effect of 1000 kernel weight were estimated. additive gene action effects based on DH lines were always larger that this parameter estimated on the basis of parental lines. estimates of additive gene action effects based on the all DH lines were significantly larger than zero in each year of study. epistasis effects based on all DH lines were statistically significant in 2011 and 2013.

Habouh (2019) observed significant different for most studied traits in the three crosses. Also, significant estimates for one or more epistatic gene interactions were displayed for all studied traits in the three crosses except, 1000 kernel weight in the second cross, no. of spikes and grain yield per plant in the third cross.

Jalata *et al.* (2020) reported predominance of non-additive gene effects including epistasis gene effects than additive gene effects for all parameters. In general, the results suggest greater influence of non-additive genes including epistasis in the control of both disease parameters studied making early selection ineffective.

Bocianowski, *et al.* (2021) found additive effect of all genes controlling the trait and the total epistasis effect of 1000 kernel weight were estimated. Additive gene action effects based on DH lines were always larger that this parameter estimated on the basis of parental lines. Estimates of additive gene action effects based on the all DH lines were significantly larger than zero in each year of study. Epistasis effects based on all DH lines were statistically significant.

Hudzenko *et al.* (2022) showed that significant differences in gene action for productive tillering between crossing Schemes. The present study contributes to further development of studies devoted to evaluation of gene action for yield-related traits in spring barley, as well as identification of new genetic sources for plant improvement.

Mansour *et al.* (2023) reported highly significant defferent in all evaluated crosses for all traits. The relative importance of additive and dominance effects differed from trait to another in each cross. For epistatic components, dominance × dominance interaction effects were more effective than other components in most studied traits.

Sharma *et al*. (2023) showed that high frequency of dominant genes expression of grain yield per plant, relatively maximum dominant genes. these parents may be used in crossing programme for the improvement of different yield components for tangible advancement of barley.

3. Combing ability

The concept of combining ability was proposed by Sprague and Tatum in 1942 working on maize. combining ability pertains to the inherent capability or aptitude of a genetic makeup to pass on enhanced performance to its offspring through mating. The value of an inbred line depends on its ability to produce superior hybrids in combination with other inbred Combing ability are generally two types one is general combing ability (GCA), the average performance of strain in series of hybrid combination, and second is specific combing ability (SCA), the performance of a parent in a specific cross. GCA mostly associated additive gene action while SCA are associated with non-additive gene action. GCA are positively associated with narrow sense heritability, but SCA are positively associated with broad sense heritability. Combining ability are mostly use for assessment of genetic value of crop, superior hybrid combination and gene action. the combining ability concept is the most important and efficient tool for choosing the desirable parents capable of providing crosses of high genetic worth. the extent of hybrid vigour depends upon the combining ability of genotypes/varieties used in crosses. The varieties which are capable for transmitting desirable characters or hybrid vigour in their offspring or cross are said to be having good combining ability.

Singh *et al*. (2011) observed that GCA and SCA variances were significant for all the traits except number of spikes per plant at SCA level in barley. The GCA variances were higher than SCA variances in respect of all the traits except grain yield per plant where both GCA and SCA were of same in order.

Jain and Sastry (2012) observed the mean square due to GCA and SCA were significant for most of the traits.

Pawar and Singh (2013) reported that GCA and SCA variance highly significant for all the traits. Four parents JB 1, PL 751, JB 58 and RD 2787 were found to be good combiners for most of the characters and can be used in the future breeding program. Cross combinations JB 1 x HUB 208, JB 58 x HUB 208, JB 1 x BH 933 and JB 1 x JB 55 highly significant positive SCA effect for most of the traits, and identified as superior crosses.

Brahim *et al.* (2014*)* revealed the analysis of variance for GCA, SCA and reciprocal effects according to the method of Griffing and showed a preponderance of additive effect for length of the spike, 1000 kernel weight and the number of grains per spike.

Madakemohekar *et al*. (2015) reported combining ability (GCA) and specific combining ability (SCA) effects were highly significant for all the traits studied. among the parents, testers namely, BH 902 and RD 2508 and lines Priestige, Athoulpa, Marriya and Kheel were good general combiners for grain yield and its component traits. on the basis of SCA effects, Marriya X BH 902, Athoulpa X RD 2508, Himani X RD 2508, Yardu X Lakhan, Morac 9-75 X RD 2508 and Prestige X Lakhan for grain yield were observed as most promising crosses.

Ram (2017) reported parents RD 2786, RD 2715 and RD 2035 in E_1, E_2 and E_3; emerged as good general combiners for grains yield. Based on the SCA effects and per se performance, some crosses *viz*., RD 2786 x RD 2715 for F_1, RD 2786 x BH 946 for F_2 in E; RD 2786 x RD 2715 and RD 2786 x BH 946 for F_1 and F_2 in E_2 and in E_3 appeared as good specific cross combinations for grain yield.

Rathore and Chauhan (2017) find out the experimental data recorded for two consecutive years, showed that the Ritambhara, Gitanjali, Jagrati and Lakhan were good general combiners for grain yield per plant. In all 14 crosses out of 45 [F.sub.1] crosses Narmada X Haritima, Narmada X Jagrati, Gitanjali X Azad, Ritambhara X Lakhan, Jyoti X Ritambhara, Azad X Gitanjali, Gitanjali X Lakhan, Prajapati X Azad, Ritambhara X Prajapati, Azad X Jagrati and Haritima X Manjula have expressed positive and highly significant desirable SCA effect for seed yield per plant.

Lal *et al.* (2018) reported that parents BH 959 and RD 2786 emerged as good general combiners for yield and its attributing traits, while among the crosses BHS 400 x BH959, BH 959 x RD 2786 and PL 426 x RD 2552 were emerged as good crosses for grain yield per plant as well as for other yield contributing characters. parents, BH 902, BH 946 and BH 959 has high yield coupled with high malt quality hence can be used for malting purpose.

Mustafa *et al.* (2018) showed that highly significant differences for all of the quantitative traits studied among the genotypes. two crosses were found to be well enough specific combiners, for grain yield plant-1 with maximum SCA effect in cross GOB x MSEL.

Patial *et al*. (2018) studied general combining ability (GCA) and specific combining ability (SCA), the ratio of GCA to SCA mean squares and portion of additive and dominance variances showed, importance of both additive and non-additive gene effects for grain yield. the non-significant ratio of GCA to SCA mean square highlighted that non-additive gene effects were more important than additive effects.

Shekhawat *et al.* (2018) reported five parents each in early sowing (E_1) for both the generations while one parent for F_1 generation and four parents for F_2 generation in normal sowing (E_2) showed positive significant GCA effects. Whereas, eight and twelve crosses for F_1 generation while eleven and eighteen crosses for F_2 generation in early and normal sown conditions, respectively showed positive significant SCA effects. Over all appraisal of present investigation manifested that the parent BH 959 and RD 2786 emerged as good general combiners.

Swati *et al*. (2018) found that line BH 902 emerged as good general combiner for maximum number of yields contributing traits. out of thirty crosses, seven displayed significant and positive specific combining ability (SCA) effects for grain yield. Out of these seven crosses, four hybrids viz., BH 976 × RD 2849, DWRB 134 × DWRUB 52, BH 965 × DWRUB 52, BH 902 ×DWRB 101, were identified as the best promising combinations having good specific combining ability effects.

Khatab *et al.* (2019) found highly significantly positive results for specific combining ability effects. While that, the parents number (1, 2 and 3) exhibited significant and highly significant positively results for GCA effects.

Jalata *et al.* (2019) find out general combining ability (GCA) and specific combining ability (SCA) was highly significant ($P \leq 0.01$) for initial. HB1307 and HB 42 parents were general combiner for scald and net blotch resistance.

Panwar and Sharma (2019) found that the parent BH 393 has been excellent general combiner for majority of traits viz., days to 50 per cent heading, days to 75 per cent maturity. another parent BH 959 has good general combiner for plant height, flag leaf area, number of effective tillers per plant, spike length, number of grains per spike, number of spikelets per plant, 1000grain weight, and grain yield per plant. followed by Parent RD 2786 has been good general combiner for protein content. a perusal of specific combining ability effects revealed that positive significant SCA effects for grain yield per plant was observed in eleven crosses viz., DWRB 91 × BH 959, RD 2552 × DWRB 64, RD 2035 × RD 2786, RD 2035 × BH 393, DWRB 92 × BH 393 RD 2715 × DWRB 64, RD 2715 × DWRB 91, BH 959 × DWRB 64, RD 2552 × RD 2715, RD 2035 × DWRB 92 and DWRB 91 × DWRB 64 expressed higher positive significant sca effects

Yang *et al*. (2019) reported highest general combining ability of catechin content was Clipper barley, the higest general combining ability (GCA) of myricetin content were Schooner barley and Huangchangguang barley, the highest general combining ability of quercetin content were Ziguangmang barley and Kuanying barley, the highest general combining ability of kaempferol content were Ziguangmang barley and Schooner barley, the highest general combining ability of flavonoids are Schooner barley and Huangchangguang barley. The hybrid combination of a good matching were Clipper barley, Schooner barley, Ziguangmang barley and Kuanying barley, as a comprehensive general combining ability, specific combining ability.

Katiyar *et al.* (2020) reported high significant heterobeltiosis for most of the traits. positive heterobeltiosis for grain yield per plant was noticed among the cross combinations *viz*., EC 667365 × NDB-3, EC 667498 × Azad. only one cross combination EC 667365×NDB 3 exhibited positive standard heterosis over standard check (RD-2552) for grain yield per plant.

Kumari *et al.* (2020) showed among the parents, tester NDB 1173 and lines RD 2909, RD 2899 and RD 2768 were good general combiners for grain yield and its component traits. on the basis of SCA effects, RD 2909 x NDB 943, NDB 1618 x NDB 1173, RD 2768 x NDB 3, HUB 240 x NDB 1173 and RD 2899 x NDB 943 for grain yield were observed as most promising crosses.

Medimagh and Mansouri (2020) reported a set of six diverse genotypes of spring barley (*Hordeum vulgare* L.), namely Martin, Taj, Ardhaoui, Sahli, Rihane and Salmas crossed in a complete diallel design and their thirty F_1 crosses. Highly significant genotypic variation for all traits studied was partitioned into variation due to GCA, and SCA effects. Rihane is a good combiner to improve spike lenght.

Akashdeep *et al*. (2021) find out among testers, only a single tester i.e. BH 902 was observed to be best general combiner for number of effective tillers, spike length, 1000 grain weight, harvest index and grain yield per plant. K 745 found to be good combiner for awn length, whereas K 603 found to be good combiner for number of effective tillers. SCA effects of crosses showed significant results for many characters. Crosses, KR 521 x K 603, Azad x K 745, HUB 113 x BH 902, RD 2508 x K 603 were recorded as outstanding specific combiners for grain yield per plant.

Katiyar *et al.* (2021) showed that two lines EC 667509 and EC 667365 and one tester, NDB 3 recorded the high GCA effect for three traits. Non-significant SCA effect for all the traits was observed in 12 out of 21 crosses. In respect to the SCA effect, cross EC 667498 x Azad performed better than the remaining cross combinations.

Abdulhamed *et al*. (2022) observed BKL88-38 x Buhooth-244 hybrid was distinguished by giving a highest mean of heterosis of the 1000 grain weight, grain yield and biological yield (25.50, 28.88 and 14.84%)

Gocheva *et al.* (2022) reported that the variety Scarlett has good combining ability and can be used in crosses to obtain hybrids of high grain weight per spike. The SCA variances were high for parents Zernogradskij 73, Fink and Barke.

Tokhetova *et al.* (2022) found significant differences in general combining ability (GCA) and specific combining ability (SCA) among the parental cultivars and their hybrids in barley.

Callej *et al. (*2023) observed lines with high general combining ability, which could produce promising two-way hybrids.

4. Heterosis

The term heterosis was first used by G.H. Shull (1914) and may be defined as the superiority of the F_1 hybrid of two genetically dissimilar individuals over mid-parent value (relative heterosis) or better-parent value (heterobeltiosis) or standard check variety (standard heterosis). The exploitation of heterosis in cultivated plants is one of the most important accomplishments of the science of grenetic in agriculture practices **(Dobzhansky, 1965).**

The literature pertaining to heterosis for different characters in barley is presented in the following paragraphs: the possibility of commercial exploitation of heterosis in barley have been discussed since the description of the first genetic male sterile by Suneson (1940). The only commercial production of hybrid barley used a genetic recessive gene for male sterility in a balance tertiary trisomic system (BTT) (**Ramage, 1965).** The first barley hybrid "Hember" produced 15 to 27% more grain over better parent under high yield conditions **(Ramage, 1975; Ramage, 1968).** The first assessment of yield heterosis in the barley crop was reported 27% yield increase. the heterosis ranged from 0.0% in 17 hybrids (Hagberg, A.; 1953) to over 100% (**Fejer and Fdak, 1976**) in the cross of spring × winter barley lines.

Vishwakarma *et al*. (2011) studied that the heterosis for yield and chlorophyll content in barley. Best crosses having highest heterobeltiosis for particular traits were NDB 1173 x K 792, NDB 1173 x Narendra Jau 3 for days to heading and days to maturity, NDB 1173 x NDB1245 for number of grains per spike and NDB 1173 x NDB 1245 for grain yield per plant.

Varzaru *et al*. (2012) reported most of the hybrids exhibited remarkable heterosis over mid and better parents for the spike length with average values of 17.94 and 12.03.

Potla *et al*. (2013) studied that cross IBON 65 x RD 2508 showed highest magnitude of economic Heterosis over the best standard check K 603 for grain yield per plant in barley.

Madakemohekar *et al*. (2015) repoted that Marriya X BH 902, V Morles X BH 902, Prestige X Lakhan and Yardu X Lakhanwere recorded highest magnitude of economic heterosis over standard check K 603 for grain yield, which might be of practical use in barley improvement programme under rainfed environment.

Pesaraklu *et al.* (2016) find out highest values of heterosis for grain number per spike, grain weight per spike and 1000 grain weight, respectively

Ram and Shekhawat (2017) reported an experiment in barley to analyse heterosis for yield and its attributing traits using Half diallel analysis. The sufficient degree of heterosis and heterobeltiosis was observed for all the characters. Among top three crosses for grain yield per plant in all the environments, the crosses RD 2786 x RD 2035 and RD 2786 x RD 2715 showed desirable heterosis and heterobeltiosis for one or more characters in all the environments.

Singh *et al*. (2017) observed that out of 15 F_1's studied, twelve crosses expressed desirable heterosis over BP (Better Parent) and one desirable heterosis over SV (Standard Variety). Among the genotypes, HUBL 09-17, IBYT 04-177, IBYT 04-09 and Moroc 09-75 showed significant negative GCA effects. The cross Moroc 09-95 × IBYT(LRA)12 had highest SCA.

Lal (2018) showed heterosis for grain yield per plant ranged from -20.75 (RD 2715 × RD 2552) to 41.86 per cent (BHS 400 × BH 959) and -21.95 (BHS 400 × BH 902) to 39.65 per cent (BHS 400 × BHS 380) under early and timely sown conditions, respectively. out of 45 crosses, nine and fifteen crosses exhibited positive significant heterosis in early and timely sown conditions, respectively; while, seven and nine crosses exhibited positive significant heterobeltiosis in early and timely sown conditions, respectively. In both the early and timely sown conditions, the crosses BG 105 x PL 426, PL 426 × RD 2552 and BH 959 x RD 2786 exhibited positive significant heterosis and heterobeltiosis.

Madakemohekar *et al*. (2018) showed that cross Pristage x BH 902, Himani x RD 2508 and Atahualpa x Lakhan were recorded as desirable for the maximum per cent heterosis over standard check (K 603).

Madhukar *et al*. (2018) observed heterosis over standard check was observed in Lakhan×K-551, Lakhan×Geetanjali and Lakhan×Harmal while the crosses RD-2552×K-551 followed by Lakhan×K-551 and Lakhan×Geetanjali showed positive significant heterosis over better parent. Heterobeltiosis were, HUB-113×Harmal, HUB-113×Moroc-9-75 and HUB113×K-551. high heterosis was also reported for days to 50% flowering, days to maturity, plant height, number of effective.

Habouh (2019) found highly significant positive heterosis over the mid-parent values were obtained for plant height and no. of kernels per spike in the three crosses, no. of spikes per plant; spike length and grain yield per plant in the first and second crosses. Highly significant positive heterosis over the better parent was obtained for plant height in the second and third crosses, grain yield per plant in the first cross and spike length in the second cross.

Khatab *et al.* (2019) found highly significantly positively results for heterosis over better-parent and specific combining ability effects under the same treatments.

Raikwr (2020) showed the heterosis over standard parent for grain yield per plant with ranged between -9.65 to 45.45 (%) and -14.78 to 12.05 (%) under normal and late sown conditions, respectively and heterosis over better-parent for grain yield per plant ranged from -26.43 to 70.77 (%) and -32.16 to 12.05 (%), respectively.

Katiyar *et al.* (2020) found significant high heterobeltiosis for most of the traits. Positive heterobeltiosis for grain yield per plant was noticed among the cross combinations *viz.*, EC 667365×NDB 3, EC 667498×Azad. only one cross combination EC 667365×NDB 3 exhibited positive standard heterosis over standard check (RD 2552) for grain yield per plant.

Yadav *et al.* (2021) observed heterosis ranged between 3.51 (DWRUB 64 x RD 103) to 81.83 (DWRB 137 x RD 2508) for grain yield per plant. out of 45 crosses, twenty -three crosses exhibited positive significant heterosis. cross DWRB 137 x RD 2508, DWRB 137 x RD 2052 and PL 426 x RD 2052 for heterosis; and PL 419 x RD 2052, PL 419 x RD 2508 and PL 426 x RD 2035 for heterobeltiosis were found.

Akashdeep *et al.* (2021) showed that the maximum per cent heterosis over standard check were observed in HUB 113 x BH 902, Azad x K 745, Azad x BH 902, Dolma 6 x K745, RD 2508 x K 745 revealed greatest value of positive significant heterosis over standard check, while the crosses Azad x K 603 followed by Dolma 6 x K 745, RD 2508 x K745, Azad x BH 902 and Azad x K745 showed positive and significant heterosis over better parent.

Abdulhamed *et al*. (2022) find out the BKL88-38 x Buhooth-244 hybrid was distinguished by giving a highest mean of heterosis of the 1000 grain weight, grain yield and biological yield (25.50, 28.88 and 14.84%).

Meena *et al*. (2022) observed that crosses IBON HI 19-94 x RD 2899 followed by IBON HI 19-110 x RD 2786 and IBON HI 19-82 x RD 2035 exhibited desirable positive significant heterosis, therefore, above crosses may be observed as promising types for tangible advancement for yield potential and bold grain. IBON HI 19-82 x RD 2035 revealed significant economic heterosis.

Sharma *et al.* (2022) observed the heterosis for grain yield and its contributing characters under three different environmental conditions using eight diverse barley parents along with their 28 F_1. The crosses BH902 × RD2904, BH902 × DWR143, RD2904 × RD2909, and DWR143 × DWR137 in all the environments exhibited positive significant heterosis.

Panwar *et al.* (2022) found that cross RD 2786 × BH 959 depicted positive significant economic heterosis (8.82%) over the best check BH 946 and also exhibited positive economic heterosis for flag leaf area, spike length, 1000-grain weight. Heterobeltiosis for grain yield per plant was exhibited by cross RD 2035 × DWRB 92 and maximum relative heterosis exhibited by the cross DWRB 91 × BH 959. Parents RD 2786, RD 2715 and BH 959 could be recommended for utilizing in varietal development.

5. Genetic advance and heritability

The heritability expresses proportion of genetic variance to total variance and determines the degree of resemblances between relatives. **Lush (1947**) defined heritability in broad as well as in narrow sense. In broad sense, heritability is the ratio of total genetic variance to the total phenotypic variance, while narrow sense heritability is the ratio of only additive genetic variance to the total phenotypic variance. the selection, natural or artificial, provides improved or fit genotype only by acting on genetic variance of genotypic differences, which are inherited to the next generation. thus, heritability estimates, which provides the assessment of amount or ratio of transmissible genetic variation to total variation, happens to be the most important basic factor that determines genetic improvement or response to selection. The two other important factors, which play important role in determining the response to selection, are the genetic variability existing in the breeding materials and the intensity of the selection.

The estimate of genetic advance in per cent of mean provides more reliable information regarding the effectiveness of selection in improving a trait because involvement of heritability, phenotypic standard deviation and selection intensity derives its estimate. thus, the estimates of heritability and genetic advance are of great significance to plant breeders for developing suitable selection strategy.

Jalata *et al*. (2011) reported that high heritability for spike length (0.87) followed by 1000-kernel weight (0.86), number of kernels per spike

(0.76), grain yield per plant (0.71) across locations showing better condition for effective selection in these characters. Besides this, high genetic advance was observed for spike length, number of kernels per spike and 1000-kernel weight.

Akanksha *et al.* (2012) recorded high heritability for grain yield per plant (99.97%), followed by canopy temperature (99.95%), leaf area index (99.93%), chlorophyll content (99.89%), harvest index (99.86%), days to heading (99.72%), number of spikelet per spike (98.79%), plant height (97.63%), number of grains per spike (97.05%), spike length (95.11%) and 1000-grain weight (87.29%).

Abdel-Ghani (2013) find out higher heritability values to be associated with high predicted genetic advance from selection for grain yield, biological yield and yield component in well watered environment.

Fotokian *et al*. (2013) reported highest and lowest broad sense heritability belonged to grains per spike and grain yield respectively.

Raikwar *et al*. (2014) reported high heritability for number of productive tillers per plant, grain weight per spike, grain yield per plant and lysine content under saline sodic soil.

Shoaib *et al.* (2014) observed highest heritability was associated with G/P (0.98) and T/P (0.89). Greater magnitude of broad sense heritability coupled with higher genetic advance in characters under provided the evidence that these plant characters were under the control of additive genetic effects.

Yadav *et al.* (2014) showed that high heritability estimates coupled with moderate genetic advance as percentage of mean were recorded for biological yield per plant, grains per spike, plant height and days to 50% flowering.

Addisu and Shumet (2015) found that heritability coupled with high genetic advance was observed for characters biomass per plant, grain yield and number of tillers per plant.

Porumb *et al*. (2016) studied heritability coefficient in narrow sense for plant height (0.57), indicating a major involvement in controlling plant height, which would suggest that the selection work for this trait could start from early generations.

Mansour (2017) reported most promising crosses were the two crosses 1 and 5 for earliness and crosses no. 2, 3 and 4 for grain yield found to be higher in magnitude, which had high genetic advance associated with high heritability and would be of interest in breeding programs for improving barley.

Sunil *et al*. (2017) find out all the traits showed high heritability i.e. more than 90 per cent for majority of traits. Genetic advance as percent of mean was highest for peduncle extrusion length followed by number of tillers per plant.

Shrimali *et al.* (2017) found significant differences among entries for all the characters. High heritability along with high genetic advance (% of mean) was observed for plant height, number of effective tillers per plant, spike length, biological yield per plant, relative water content and seed yield per plant in both the environments.

Dinsa *et al.* (2018) reported that broad sense heritability varied from 22.26% to 70.50%. The expected genetic advance as percentage of mean of traits ranged from 6.43% to 35.61%. Moderate high heritability complemented with moderate genetic advance was observed for days to first heading, days tobeading and 1000-kernel weight suggesting. Selection of genotypes to top 5% intensity under one cycle of selection for these traits could result in genetic advance of more than 10% over the and the possibility of increasing grain yield by more than 10% by exerting 5% selection intensity to improve yield in the study area.

Gupta *et al.* (2018) reported high heritability (>60%) and low genetic advance (<10%) for days to 50% flowering and high heritability but moderate genetic advance (10-20%) were observed for days to maturity and plant height. Medium heritability (40-60%) and low genetic advance were recorded for grain weight/spike and 1000-grain weight. Other traits showed low heritability values (<40%) and low genetic advance as percent of mean and indicated non-additive gene effects, therefore selection would not be effective for these traits.

Hashash *et al. (*2018) reported that the high heritability coupled with high genetic advance as percent of the mean was observed for most studied traits under non-stress conditions.

Kumar *et al.* (2018) found high heritability coupled with high genetic advance was recorded for number of grains per spike, biological yield per plant and seed yield per plant.

M**alik *et al*. (2018)** reported that high heritability coupled with high genetic advance was observed for biological yield/plant in F_1 generations. Moderate heritability with moderate genetic advance was found for 1000-grain weight in both generation and leaf area index, grain yield/plant in F_2 generation, indicating that the selection in later generations would be much rewarding. low heritability with low genetic advance was found for days to 50% flowering and days to maturity in F_2 generation.

Sravani *et al*. (2018) find out moderate heritability was showed for grain yield per plant followed by harvest index, 1000 grain weight and grains per spike. were observed high genetic variation between the all characters were moderately (30 to 60%) or low (<20) heritability which indicates that the environmental influence is high on characters. moderate heritability associated with low GA (genetic advance) showed for these traits i.e. effective tillers per plant, plant height, biological yield, spike length, days to maturity, awn length, days to 50% flowering, biological yield, and awn length, which indicates were traits showed were highly environmental effects and genetic improvement through selected characters would be ineffective.

Kumar *et al.* (2018) observed the heritability ranged from 61.2 per cent for harvest index to 95.5 per cent for number of grains coupled with high genetic advance was observed for number of grains per spike, number of tillers per meter row, grain yield, 1000 grain weight and biological yield, indicates the per spike, while grain yield showed 79 per cent heritability. High heritability importance of these traits in selection and crop improvement.

Habouh (2019) find out high heritability values, in broad sense for plant height and 1000 kernel weight. moderate values were obtained for no. of spikes per plant, spike length and grain yield/plant. on the other hand, low to moderate heritability values in narrow sense were detected for all traits studied. It could be concluded that, the best crosses showing advanced values of the mid-parent heterosis and predicted genetic advance from selection for grain yield and some of its components in this study were crosses 1and 2.

Hitaishi *et al.* (2019) reported high heritability in broad sense for 1000 grain weight and number of grains per spike followed by biological yield per plant and grain yield per plant. the characters which showed higher estimates of genetic advance coupled with higher estimates of heritability reflecting additive gene action.

Kumari *et al* (2019) found that the high value of heritability in narrow sense (>30 %) for grains/spike, days to maturity, biological yield/plant, grain yield/plant (g) and harvest index while remaining traits showed moderate estimate. high heritability with high genetic advance in percent of means was recorded for grains/spike and grain yield/plant (g). high heritability coupled with low genetic advance in percent of mean was recorded for days to maturity, ear length(cm), biological yield/plant(g) and harvest index (%), while, low heritability coupled with low genetic advance in percent of mean was recorded for days to ear emergence and low heritability coupled with high genetic advance.

Tripathi *et al*. (2019) observed highly heritability in broad sense for 1000 grain weight and number of grains per spike followed by biological yield per plant and grain yield per plant. the characters which showed higher estimates of genetic advance coupled with higher estimates of heritability reflecting additive gene action.

Devi *et al*. (2020) find out the moderate to high heritability in broad sense observed under timely sown for all the traits except of plant height, harvest index and number of tillers per meter which exhibited low heritability. however, under late sown conditions, all the traits showed moderate to high heritability except plant height. highest genetic advance as per cent of mean was recorded for number of grains per spike followed by grain yield under both environments. moderate to high heritability coupled with high genetic advance under timely sown was observed for number of grains per spike, grain yield, 1000-grain weight, biological yield and spike length likewise, for number of grains per spike, grain yield, number of tillers per meter, biological yield and 1000 grain weight under late sown indicating the importance of these traits in selection and crop improvement.

Dido *et al*. (2020) reposed the high heritability with high genetic for plant height, number of fertile tillers/plant, spike length, number of seeds/spike, and 1000 seed weight, while moderately high heritability coupled with high genetic advance was noticed for grain yield/plan.

Farag (2020) observed the broad sense heritability ranged from intermediate to high according to selection method and population in all studied traits. while, values of genetic advance and genetic gain were lower in the two methods of selection BM and MBM compared to those of PM and SSDM for all traits under Izraa and Kafrdan conditions.

Shiferaw *et al.* (2020) reported broad sense heritability and genetic advance high for days to heading and maturity and thousand kernels weight. grain yield exhibited positive and highly significant correlations with days to heading and maturity, number kernels per spike, biomass yield, harvest index thousand kernels and hectolitre weights.

Dyulgerov *et al*. (2021) found heritability in broad-sense high for the number of days to heading, grain weight per spike, and 1000-grain weight and very high for plant height and spike length. Whereas low heritability of grain yield was found indicating that the phenotypic selection could be ineffective under these specific conditions. a combination of high heritability and high direct on grain yield in 1000-grain weight and days to heading shows that those traits may be used in early-generation selection in breeding of high-yielding facultative lines.

Iannucci *et al.* (2021) reported high heritability and selection response for most of the biochemical compounds. The grain yield showed high significant positive genetic and phenotypic correlations ($p < 0.05$) with phenols and antioxidant activity.

Yadav *et al.* (2021) reported high heritability along with high genetic advance was recorded for all the characters studied

Verma *et al.* (2022) reported the high heritability coupled with high genetic advance as per cent of mean was observed for number of grains/spike, biological yield/plant and grain, yield/plant, indicated their importance for grain yield improvement in barley.

Tehulie (2022) evaluate the days to heading showed the highest heritability at both locations, that is, (86.70%) at Legambo and (80.00%) at Mekdela. Moderate to high heritability was observed for plant height (66.90%), spike length (56.90%), number of kernel/spike (53.20%), and days to maturity (51.20%), number of spikelet (48.50%) and thousand kernel weight (24.30%) at Legambo, and spikelet/spike (45.30%), days to maturity (43.90%) and hectoliter weight (41.80%) at Mekdela. Estimated genetic advance as percent of the mean was generally low for the 13 characters. Among the characters, number of kernel/spike had higher genetic advance as percent of the mean value at both locations.

Mansour *et al*. (2023) reported broad-sense heritability showed high values for studied traits and crosses, while narrow-sense heritability and genetic advance from selection ranged from low to medium in most crosses for the agronomic traits where it had high genetic advance associated with high heritability.

Naresh and Kumar (2023) observed the high heritability coupled with high genetic advance was recorded for the traits namely peroxidase, dehydrogenase, number of grains per spike, spike length, number of effective tillers per meter, harvest index and grain yield per plot.

6. Correlation and path coefficient

Plant breeders should evaluate character association studies between different agronomic traits not only from a theoretical perspective of character quantitative inheritance, but also from a practical perspective.

usually, selection is concerned with simultaneous change in two or more characters. This information may be used to predict the correlated response to directional selection, in the direction selection for the construction of selection indices, and in the detection of some characters that may not have any value on their own but are helpful indicators of the more significant ones under consideration **(Johnson *et al* .1995).** The grain yield or economic yield has a very complex nature in majority of cases because its expression depends upon several other plant characters, referred to as yield components. Yield does not have an independent and isolation existence of its own, as it happens to be the end product of multiplicative interactions between the various yield component characters. The genetic architecture of seed yield can be better resolved through components rather than yield *per se*. therefore, yield is also designated as super character.

Path coefficient is simply a standardized partial regression coefficient and as such measures the direct influence of one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effects. The utility of path coefficient analysis in plant breeding was demonstrated by **Dewey and Lu (1959**).

Sharief *et al.* (2011) found the positive and significant correlation with grain yield/ha. In general, over locations plant height, number of grains/spike and number of spikes/m^2 were positively and significantly correlated with grain yield/ha and revealed high positive and direct influence of 1000 grain weight towards grain yield per plant followed by spikes per plant and tillers per plant.

Singh *et al.* (2014) observed significant positive association of grain yield per plant with 1000 grain weight, peduncle length, number of effective tillers per plant and plant height. Hence by exercising selection for these characters, it may be possible to isolate superior, high yielding genotypes. Path coefficient analysis revealed high positive direct effect of 1000 grain weight followed by number of effective tillers per plant, number of grains per ear and plant height.

Lodhi *et al.* (2015) reported positive significant correlation of seed yield per plant with grains per car, effective tillers per plant, 1000 grain weight and plant height hence by exercising selection for these characters, it may be possible to isolate superior, high yielding genotypes. Grain yield per plant exhibited strong positive association with biological yield/plant. Number of grains/spike, number of tillers/plant and 1000 seed weight for both two rowed as well as six rowed barley genotypes. Path coefficient analysis revealed that all the characters had direct and positive association with grain yield/plant except peduncle length which had negative direct effect in case of two rowed barley.

Hailu *et al.* (2016) observed grain yield had positive and highly significant phenotypic and genotypic correlation with 1000-kernel weight and biological yield in all environments except harvest index at Ofla. Grain yield had positive and highly significant phenotypic and genotypic correlation with 1000 kernel weight and biological yield in all environments except harvest index at Ofla. On the other hand, grain yield had negative and highly significant correlation at genotypic level with days to heading and days to maturity only at Ofla.

Aklilu *et al*. (2017) found that phenotypic and genotypic correlation was positive and highly significant for grain yield with plant height, number of seeds per spike, biological yield and harvest index. Path coefficient analysis revealed maximum positive direct effect of biological yield on grain yield followed by harvest index, showing that these traits can be used for selection to improve the grain yield. In contrast, days to maturity and plant height had negative direct effects on grain yield.

Saroei *et al.* (2017) observed high significant correlations between grain yield with biological yield (0.92), straw yield (0.77), and number of spike per square meter (0.67). In path analysis, biological yield had the greatest effect on grain yield (0.906).

Sunil *et al*. (2017) reported that biological yield/plant, harvest index, number of tillers/plant, days to 75% flowering and peduncle length had positive direct effects on grain yield/plant for the six rowed barley. This suggested that selection will be quite efficient in enhancing yield and its contributing traits in context of germplasm evaluated.

Shrimali *et al*. (2017) showed the seed yield per plant has positively and significantly associated with plant height, biological yield per plant, test weight, number of spikelets per spike and spike length in both the environments. Path coefficient analysis indicated that biological yield per plant and harvest index in both the environments, were the important characters for selection of high yielding genotype as this exerted high positive direct effect as well as showed high and positive correlation with seed yield.

Gupta *et al.* (2018) found the grain yield/plant had a highly significant and positive correlation with biological yield/plant, plant height, and the number of productive tillers/plant, while it showed a non-significant positive correlation with the number of grains/spike, shoot length and main spike length at phenotypic level but significant negative correlation with days to 50% flowering.

Kumar *et al.* (2018) obseved significant positive association of grain yield with harvest index, biological yield and number of grains per spike while the characters *viz.*, days to heading and maturity, plant height and ear length exhibited significant negative correlation with grain yield. harvest index and biological yield exerted the highest positive and significant direct effect on grain yield. Therefore, these characters could be considered as main components for selection in a breeding program for higher grain yield.

Malik *et al*. (2018) observed grain yield per plant exhibited positive and highly significant correlation with plant height, number of productive tillers/plant, length of spike, 1000 grain weight, biological yield per plant and harvest index. While, it showed positive and non-significant correlation with days to maturity, canopy temperature depression, leaf area index and number of grains/spike and showed negative and non-significant correlation with days to 50% flowering and grain weight/spike at phenotypic levels.

Vinesh *et al. (*2018) reported that grains per ear, plant height, 1000 grain weight, days to maturity, stomatal conductivity and spike length showed highly significant and positive correlation with grain yield which indicated strong association of these traits with the yield. path coefficient analysis suggested that spike length, plant height, grains per ear, 1000 grain weight had positive direct effects on grain yield per plant.

Negash *et al*. (2019) studied analysis of variance revealed highly significant ($p \leq 0.01$) to low significant ($p \leq 0.05$) difference for all the characters. grain yield showed positive and significant genotypic correlations with grain weight per spike (rg = 0.36), spike weight per plant (rg = 0.38), 1000seed weight (rg = 0.66), biological yield (rg = 0.83), awn length (rg = 0.34) and plant height (rg = 0.23). The result revealed that biological yield, 1000-seed weight, productive tillers per plant and grain weight per spike were the most important yield components as they exerted positive direct effect on grain yield as well as positive genetic association with each other explaining the existence of significant correlation.

Matin *et al.* (2019) observed the grain/ spike had the highest positive direct effect (5.65) on yield followed by 1000 seed weight (4.65), spike length (1.26), yield/ plant (0.66), days to heading (0.55) and days to maturity (0.34). these parameters were identified as direct selection. direct negative effect on yield was shown by plant height (-0.32) and effective tiller/plant (-0.74). This was an indication of indirect selection.

Dido *et al*. (2020) reported correlation analysis, grain yield/plant was found to be significantly and positively correlated with days to 50% heading, days to 95% physiological maturity, number of fertile tillers, seeds per spike, plant height, 1000 seed weight and biological yield. analysis of path coefficient indicated number of tillers /plant, biological yield, 1000-seed weight and number of seeds/spike had higher positive direct effect on grain yield/plant. Those quantitative characters with significant and positive direct effect on grain yield/plant can be considered as an effective selection criterion

Baye *et al.* (2020) observed the grain yield had significant positive correlation with days to maturity, grain-filling period, plant height, kernels spike−1, hectoliter weight, thousand seed weight, biomass yield, and harvest index at both genotypic and phenotypic levels including spike length at phenotypic levels at Adet and with plant height, thousand seed weight, biomass yield and harvest index at Debre Tabor both at genotypic and phenotypic levels

Dyulgerov *et al.* (2021) reported that the grain yield of facultative barley accessions showed a significant positive correlation with spike length, spikelet number per spike, grain number per spike, and grain weight per spike. The traits with the highest positive direct effect on grain yield were grain number per spike and 1000 grain weight while days to heading had a highly negative direct effect on grain yield. the accession TX01D236 had a significantly higher grain yield compared to check varieties.

Yadav *et al*. (2021) observed biological yield per plant, harvest index, number of tillers per plant, number of grains per spike, 100-seed weight are the most important yield contributing characters as they recorded higher positive direct and indirect effects along with positive significant correlation toward seed yield per plant.

Gupta *et al.* (2022) reported the seed yield per plant had significant and positive association with biological yield, spike length, number of tillers per plant, number of grains per spike, 1000 grain weight, plant height, days to maturity and harvest index. path analysis indicated that traits such as biological yield per plant, harvest index, 1000 grain weight, number of grains per spike and peduncle length directly or indirectly influenced seed yield.

Kumari and Vishwakarma (2022) reported grain yield per plant was found to be positively and significantly associated with number of grains per spike, biological yield per plant, number of tillers per plant, ear length and harvest index, whereas significantly and negatively associated with days to maturity.

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CHAPTER- III

MATERIALS AND METHODS

The present experiment entitled " **Studies on genetical parameters for grain yield and its contributing traits in barley (*Hordeum vulgare* L.)**" was carried out during the *Rabi* 2022-23 at the Crop Research Farm, Nawabganj of C.S. Azad University of Agriculture and Technology, Kanpur 208002 (U.P.).

3.1 EXPERIMENTAL SITE

Geographically Kanpur place is located at a height of 125.9 meters above sea level, between 25.28°N and 26.58°N latitude, and 79.31°E to 80.34°E longitude. This region has a subtropical climate. With only sporadic rains throughout the winter, the monsoon season from July to September accounts for over 80% of all rainfall. the studies were carried out on typical nutrient rich soil with pH 8.1. Meteorological data during the crop season are given in Table 3.1

Table 3.1: Meteorological data recorded at Nawabganj during crop season 2022-23.

Month	Metrological week No.	Temperature (0C)		Mean R.H. (%)	Rainfall (mm)	Wind (Km/hr.)	E.T. (mm /day)
		Min.	Max.				
Nov.	47	10.2	26.7	95	0	1.2	18.8
	48	10.1	27.2	92	0	2.4	16.8
Dec.	49	9.9	25	95	0	1.7	16.2
	50	10.4	25.5	97	0	4.1	15.4
	51	6.8	22.8	96	0	1.7	16.4
	52	7.3	22.9	94	0	3	11.2
Jan.	1	6.8	16.7	93	0	4.1	10
	2	4.6	13.8	95	0	3.5	9.8
	3	5.3	20.2	91	0	4.8	8.6
	4	9.4	22.4	93	96	5.9	8.4

Feb.	5	8.3	21.7	93	0	4.3	9.4
	6	10.5	25.6	87	0	3.9	11
	7	11	26.6	90	0	6.2	13.4
	8	12	30	87	0	3.5	14.6
Mar.	9	12.5	31.1	83	3.3	4.8	15.4
	10	14	30.6	79	0	4.4	38.4
	11	15.1	31.4	72	0	3.7	18.2
	12	15.5	26.3	68	18	5	19
	13	16.6	32.3	64	0	3.5	23.8
April	14	16.5	31.6	62	18.2	4.2	26
	15	17.6	36.1	41	0	3.2	15.2
	16	21.8	39.7	65	0	4.7	3.8
	17	19.5	35.1	68	14.6	7.3	3.8

Source: Department of Agro-meteorology, C.S. Azad University of Agriculture and Technology, Kanpur.

3.2 EXPERIMENTAL MATERIALS

The experimental material for the present investigation consisted of twenty-eight F_1s developed by crossing 8 lines namely, RD 2907, KB 1425, KB 1506, KB 1762, KB 1634, HUB 113, K 603 and DWRB 137 following half diallel mating design. A total of 36 treatments including 8 parents and 28 F_1s were evaluated for the assessment of eleven different characters in barley

3.3 SELECTION OF PARENTS:

The material for the investigation consisted of 8 strains/varieties of barley (*Hordeum vulgare* L.) selected on the basis of significant variability of various characters. The details of the parent lines are given in the Table 3.2.

Table 3.2 Details of the parent lines used in the study.

S.N.	Name of the parents	Place of origin /Institution	Pedigree
1	RD2907	RARI, Durgapur	RD 103 X RD 2518

2	KB1425	CSAU & T, Kanpur	KB551 X NDB1295
3	KB1506	CSAU & T, Kanpur	BH 910 X K 871
4	KB1762	CSAU & T, Kanpur	EIGN1617 X T-13
5	KB1634	CSAU & T, Kanpur	Lakhan X JB137
6	HUB113	BHU, Varanasi	Karan 280 x C 138
7	K603	CSAU & T, Kanpur	K 12 X IB 226
8	DWRB 137	IIWBR, Karnal	DWRB28 X DWRU64

3.4 DEVELOPMENT OF EXPERIMENTAL MATERIAL:

Development of F_1 seed: All 8 barley genotypes have been grown during the *Rabi* 2021-22 for making crosses in half diallel fashion. As a result, seeds from twenty-eight hybrid combinations were harvested and procured for further study.

A. PLAN OF LAYOUT The experimental materials consisted of 36 treatments (28 F_1s+8 parents) that were sown in Randomized Block Design with three replications. The entries were sown in a 3 m length with inter and intra-row spacing of 23 cm and 10 cm, respectively. All the recommended cultural practices were applied to raise good crops.

B. OBSERVATIONS TO BE RECORDED:

The individual plant data of the samples were recorded in each treatment of all replications for the following traits.

1. Days to 75% heading

Days to 75 per cent heading were recorded as a number of days taken from the data of sowing to the appearance of heading on 75 per cent plants of the plot a particular genotype.

2. Days to maturity

It was calculated as the number of days taken from date of sowing to physiological maturity (ear turned yellow) of selected plants.

3. Plant height (cm)

It was measured and recorded in cm from the base of the plant at ground level to extending to the base of the spike (excluding the awn) of the main shoot in the selected plant at the maturity

4. Number of productive tillers per plant:

Total number of ears bearing tillers per plant were counted and recorded before harvesting of the crop.

5. Spike length (cm)

The length of spike each randomly selected main spike was recorded in cm, measuring from the base of spike to tip of spike excluding awns of main shoot.

6. Number of grains per spike

The total number of grains of the main spike was counted and averaged at the time of harvesting in each selected plant.

7. Grain weight per spike (g)

Each randomly selected spike was threshed separately, and the grains of each spike were weighed in grams up to two decimal places on an electronic balance.

8. 100-grains weight (g)

The grains of selected plants from each plot were mixed to draw a representative sample of 100-grain which was weighed in grams up to two decimal places on an electronic balance.

9. Harvest index (%)

The harvest index, which was expressed as a percentage, was calculated as the ratio of grain yield (g) to biological yield of plant (g). The formula used to calculate it is as follows.

$$\text{Harvest index (\%)} = \frac{\text{Grain yield/plant(g)}}{\text{Biological yield/plant(g)}} \times 100$$

10. Biological yield per plant (g)

At the time of harvesting randomly selected plants for each treatment were weighed replication wise with the help of an electronic balance before threshing for obtaining their biological yield in gram and their average was calculated

11. Grain yield per plant (g)

The total quantity of grains obtained from each of the three selected plants after threshing was cleaned and dried then weighed in grams up to two decimal places on an electronic balance and averaged to find out the grain yield per plant.

3.5 SATISTICAL AND BIOMETRICAL TECHNIQUES

The experimental data were compiled by taking the mean of sampled plants in each treatment for all three replications. Based on consideration highlighted in the present investigation entitled **"studies on genetical parameter for yield and its contributing traits in barley (*Hordeum vulgare* L.)"** has taken with the following statistical and biometrical procedures separately:

1. To study the analysis of variance (**Panse and Sukhatme, 1967).**
2. To study components of variances of the characters (**Hayman (1954)**.
3. To estimate general and specific combining ability variances and their effects using method II and model I of diallel mating design (**Griffing,1956 b)**.

4. To work out heterosis (%) over economical parents, **(Fonseca and Patterson, 1968)**.

5. To estimate heritability and genetic advance in per cent of mean (**Crumpacker and Allard, 1962)** and **(Robinson *et al*., 1949).**

6. To find out correlation/association and path coefficient among the characters under study **(Al-Jioauri *et al*.,1958)** and (**Dewey and Lu, 1959)**.

The outlines of the methods used in the analysis are given below:

3.5.1 ANALYSIS OF VARIANCE

The analysis of variance for the design of experiment was carried out according to the procedure outlined by **Panse and Sukhatme (1967).** The significance of difference among treatment means was tested by 'F' test.

To test the hypothesis H_0: $t_1 = t_2 =$ ----------- $= t_v$, the fixed effect model for the analysis of variance for Randomized Block Design is given below:

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

Y_{ij} = Yield of i^{th} entry in the j^{th} replication

μ = General mean of population

t_i = Effect of the i^{th} entry (i = 1, 2, ---------, v.)

b_j = Effect of the j^{th} replication (j = 1, 2, ----------, r.)

e_{ij} = Environmental Effect

Skeleton of ANOVA of the experiment:

Source of variation	**d.f.**	**M.S.**	**'F' test**
Replication	(r-1)	M_r	M_r/ M_{el} for r-1, (r-1) (t-1) d.f.
Treatment	(t-1)	M_t	M_t/ M_{el} for t-1, (r-1) (t-1) d.f.
Error	(r-1) (t-1)	M_{e1}	

Since the experiment consisted of parents and F_1s hence separate ANOVA was prepared separately involving parents + F_1s to test the variability among treatments and heterosis:

Skeleton of ANOVA for parents + F_1s

Source of variation	**d.f.**	**M.S**	**'F' test**
Replication	(r-1)	M_r	M_r/ M_{e1} for r-1, (r-1) (t-1) d.f.
Treatment	(t-1)	M_t	M_t/ M_{e1} for t-1, (r-1) (t-1) d.f.
Parents	(p-1)	M_p	M_p/ M_{e1} for p-1, (r-1) (t-1) d.f.
F_1s	(f_1-1)	M_{f1}	M_{f1}/ M_{e1} for f_1-1, (r-1) (t-1) d.f.
Parents vs F_1s	1	M_{ph}	M_{ph}/ M_{e1} for 1, (r-1) (t-1) d.f.
Error	(r-1) (t-1)	M_{e1}	

Where,

r = Number of replications

t = Number of treatments

p = Number of parents

f_1 = Number of F_1 hybrid

M_{e1} = Mean sum of square due to error

M_{ph} = Mean sum of square due to parents vs f_1 hybrid

The standard error, critical difference and coefficient of variation were calculated as follows:

$$\text{S.E. of mean} = \sqrt{\frac{2MSE}{N}}$$

$$\text{Critical difference} = \sqrt{\frac{2MSE}{r}} \times \text{t value}$$

Where,

Table value of t distribution at error d.f. and $P \leq 0.05$

$$\text{Coefficient of variation (C.V.\%)} = \frac{\sqrt{MSE}}{X} \times 100$$

3.5.2 DIALLEL ANALYSIS:

(a) Testing the validity of the hypothesis

To test the validity of the hypothesis, i.e., the assumptions regarding diallel analysis as proposed by **Hayman (1954**), such as (i) diploid segregation (ii) no maternal effect, (iii) no linkage (iv) no multiple allelism, (v) independent action of non-allelic genes and (vi) homozygosity of parents, the t^2 test was applied as suggested by **Hayman (1954a**):

$$\mathbf{t^2 = (n-2)/4\ [(Var\ Vr - Var\ Wr)^2 / Var\ Vr \times Var\ Wr) - Cov^2\ (Vr, Wr)]}$$

which is an F test with 4 and (n-2) degree of freedom.

A significant value of t^2 would indicate the non-uniformity of Wr, Vr and thus, invalidates the hypothesis postulated. The failure of hypothesis is also indicated by non- significant regression coefficient.

$$b = \frac{Cov.(Wr,Vr)}{Var\ (Vr)}$$

Where,

$$Cov.\ (Wr,\ Vr) = [\sum VrWr - \frac{\sum Vr \sum Wr}{n}]\ /\ (n-1)\ \text{and}$$

$$Var\ (Vr) = [\Sigma\ Vr^2 - \frac{(\Sigma\ Vr)2}{n}]\ /\ (n-1)$$

The standard error of regression coefficient (b) was calculated as:

$SE\ (b) = [(Var\ Wr - b\ Cov.\ Wr - Vr)/\ Var\ Vr\ (n-2)]^{0.5}$

Where,

n = number of parents

Now the significance of differences 'b' from zero and unity was tested by using 't' value of (b-0)/SE (b) and (1-b)/SE (b) with (n-2) degree of freedom.

(b) Variance component analysis

The components of variance in diallel cross were computed in F_1 by the use of equation given by **Hayman (1954a).**

Expectation for F_1 diallel crosses is as follows:

$$Vp = \hat{D} + \hat{E}$$

$$Vr = (1/4)\hat{D} + (1/4)\ \hat{H}_1 - (1/4)\ \hat{F} + [(n+1)/2n]\ \hat{E}$$

$$Wr = (1/2)\hat{D} - (1/4)\ \hat{F} + (1/n)\ \hat{E}$$

$$Vm = (1/4)\hat{D} + (1/4)\hat{H}_1 - (1/4)\hat{H}_2 - (1/4)\hat{F} + (1/2n)\hat{E}$$

Where,

$\hat{D}$ = Components of variation due to additive effects of genes.

$= V_0L_0 - \hat{E}$

$\hat{H}_1$ = Components of variation due to dominance effects of genes.

$= V_0L_0 - 4W_0L_{01} + 4V_1L_1 - (3n-2)\hat{E}/n$

$\hat{H}_2 = \hat{H}_1 [1-(u-v)^2] = 4V_1L_1 - 4V_0\hat{L}_1 - 2E$

Where,

u = Proportion of positive genes in the parents.

v = Proportion of negative genes in the parents

$\hat{F}$ = The mean of F_r over the arrays

$F_r = 2(V_0L_0 - W_0L_{01} + V_1L_1 - Wr - Vr) - 2(n-2)\hat{E}/n$

$\hat{h}^2$ = Dominance effects (as the algebraic sum over all loci in heterozygous phase in all crosses)

$4(M_{L1} - M_{L0})^2 - 4(n-1)\hat{E}/n^2$

$\hat{E}$ = The expected environmental component of variation

$$\left[\frac{Error\ s.s + Replication\ s.s.}{error\ d.f. + Replication\ d.f.}\right] / no.\ of\ replication$$

In order to estimate of the accuracy of the components ($\hat{D}, \hat{F}, \hat{H}_1, \hat{H}_2, \hat{h}^2$ and $\hat{E}$) of variance, the term of main diagonal of matrix given **Hayman (1954**) with common multipliers S^2/n^5, was used.

Where,

S^2 = ½ [var. (Wr-Vr)]. The formula being:

$$SE(\hat{D}) = \pm [S^2 (n^5 + n^4)/n^5]^{0.5}$$

$$SE(\hat{F}) = \pm [S^2 (4n^5 + 20n^4 - 16n^3 + 16n^2)/n^5]^{0.5}$$

$$SE(\hat{H}_1) = \pm [S^2 (n^5 + 41n^4 - 12n^3 + 4n^2)/n^5]^{0.5}$$

$$SE(\hat{H}_2) = \pm [S^2 (36n^4)/n^5]^{0.5}$$

$$SE(\hat{h}^2) = \pm [S^2 (16n^2 + 16n^2 - 32n + 16n)/n^5]^{0.5}$$

$$SE(\hat{E}) = \pm [S^2 (n^4/n^5)]^{0.5}$$

After testing the significance of the components of variation, the mean degree of dominance was calculated as $(\hat{H}_1/\hat{D})^{0.5}$ in F_1 generation. The proportion of genes with positive and negative effects was calculated as $\hat{H}_2/4\hat{H}_1$, the proportion of dominant and recessive genes in parents as the ration of $[(4\hat{D}\hat{H}_1)^{0.5} + \hat{F}] / [(4\hat{D}\hat{H}_1)^{0.5} - \hat{F}]$ in F_1 generation, the number of gene groups which control the character and exhibit dominance as $\hat{h}^2 / \hat{H}_2$ and the coefficient of correlation between the parental order of dominance (Wr + Vr) and parental measurement (Yr) as r.

3.5.3 Combining ability analysis

The combining ability analysis was worked out by the procedure suggested by **Griffings (1956b**) Method 2, Model I. The mathematical model for the combining ability analysis is assumed to be:

$$X_{ijkl} = \mu + g_i + g_j + S_{ij} + 1/bc \sum_k \sum_l e_{ijkl}$$

ij = 1,2, 3….., n;

k = 1,2,3…., b;

1 = 1,2, 3…., c.

Where,

X_{ijkl} = The mean of ij^{th} genotype over k and l replication

μ = The population mean

gi = The general combining ability (gca) of the i^{th} parent

gj = The gca of j^{th} parent

S_{ij} = The specific combining ability (sca) for the cross between i^{th} and J^{th} parents such that $S_{ij} = S_{ji}$

$1/bc\Sigma_k \Sigma_i\ e_{ijkl}$ = The environmental effect (mean error effect) associated with the $ijkl^{th}$ observation on i^{th} individual k^{th} block with i^{th} as female parent and j^{th} as male parent

The usual restrictions, as $\sum_i$ gi = 0, and $\sum_j S_{ij} = S_{ij} = 0$ (for each i) are imposed.

The analysis of variance table for combining ability is as follows

ANOVA table for combining ability

Source of variation	**d.f.**	**S.S.**	**M.S.**	**'F' test**
GCA	(n-1)	Sg	Mg	Mg/Me for (n-1) and $n+f_1-1$ d.f.
SCA	n(n-1)/2	Ss	Ms	Ms/Me for n(n-1)/2 and (r-1) $(n+f_1-1)$ d.f.
Error	M	Se	Me	

Where,

S.S due to GCA = $1/n+2 \, [\sum (x_i + x_{ii})^2 - (4/n)\, x^2 \ldots..]$

S.S due to SCA = $\sum\sum x_{ij}^2 - 1/(n+2) \sum (x_1 + x_{ii})^2 + [2/(n+1)\,(n+2)]\, x^2 \ldots.$

$$M_e = M_e/r$$

Where,

r = Number of replications

f_1 = Number of F_1 hybrids

Me = The error M.S. obtained from parents + F_1s

S_g = The sum of squares (S.S) due to gca

S_s = The sum of squares due to sca

n = Number of parents

x... = The grand total

x_i = Total of the array involving i^{th} as a female parent

x_{ii} = The Value of the i^{th} parent of the array

x_{ij} =The value of the cross, with i^{th} as a female parent and j^{th} as a male parent

The components of variance were estimated according to (**Singh, 1990**) as under:

gca expected m.s. = σ^2 e+ (n+2) / (n -2) σ^2_{gi}

sca expected m.s. = σ^2 e +2/(n-1) σ^2_{sij}

Average degree of dominance = $(\sigma^2 s/\sigma^2 g)^{0.5}$

Estimates of various effects

The Various effects were estimated as follows:

gca effect of i^{th} parent (g_i) = 1/(n+2) [(x_i+x_{ii}) – (2/n) x...)

sca effect of ij^{th} cross (S_{ij}) = x_{ij}– 1/(n+2) [x_i+x_{ii}+x_j+x_{jj})+ 2/(n+1) (n+2)x...]

Where,

gi and S_{ij} = the estimates of the general and specific combining ability effect, respectively,

x_i, x_{ii}, x... xij = the same as explained earlier,

x_j = total of the arrays involving j^{th} parents as a male

Estimation of standard errors

SE (gi) = $[(n-1)\ \sigma^2 e/n\ (n+2)]^{0.5}$

SE (gi-gj) = $[2\ \sigma^2 e/\ (n+2)]^{0.5}$

SE (S_{ij}) = $[2(n-1)\ \sigma^2 e/\ (n+1)\ (n+2)]^{0.5}$

SE (S_{ij} –S_{ik}) = $[2(n+1)\ \sigma^2 e/\ (n+2)]^{0.5}$

Where,

$\sigma^2 e$ = Me/r, taken as error M.S. from the combining ability analysis.

3.5.4 ESTIMATION OF HETEROSIS

The nature and magnitude of heterosis was computed as per cent increase or decrease of the mean value of F_1 over economic parents/standard variety/check (check), was estimated with the help of following formula:

Heterosis (%) over Check = $(\bar{F}_1\text{-}\overline{Check}/\overline{Check})$ x 100

Where,

$\bar{F}_1$ = mean of the F_1

$\overline{check}$ = Mean of the check/economic

Parent (KB 1425)

The value of critical difference (C.D.) was used for testing the significance of heterosis.

The critical difference (C.D.) was calculated with the help of following formula:

C.D. = S.Ed. ×t value

Where,

SEd. is standard error of the difference of the treatment means to be compared, and is equal to:

$$S.Ed. = (2\ Mse/r)^{0.5}$$

Where,

MSe = Error mean square obtained from ANOVA table

r = Number of replications

t = Table value of ‘t’ at 5% and 1% level of significance for error degree of freedom.

3.5.5 Heritability

Heritability (in narrow sense) in F_1 generation was calculated by the formula proposed by **Crumpacker and Allard, (1962)**, which is as follows:

$$\text{Heritability}\quad (\hat{h}^2) = (1/4)\,\hat{D} / [(1/4)\,\hat{D} + (1/4)\,\hat{H}_1 - (1/4)\,\hat{F} + \hat{E}]$$

Where,

$\hat{h}^2$ = Estimates of heritability coefficient and $\hat{D}$, $\hat{H}_1$, $\hat{F}$ and $\hat{E}$ are the same as explained earlier.

$\hat{D}$ = Additive genetic variance

The estimates of heritability were arbitrarily categorised in three classes by **Kempthorn and Curnow in 1961** as:

(i) High- above 30%

(ii) Moderate- below (30-10) %

(iii) Low below- 10%

3.5.6 Genetic advance

The genetic advance was calculated by the formula given by **Robinson *et al.* (1949)** as:

Genetic advance (GA) = (k) x ($\hat{h}^2$) x (σph), and

Genetic advance over mean of the character

$$[GA (\%)] = \frac{GA}{\bar{x}} \times 100$$

Where,

GA = Estimate of genetic advance

k = Selection differential at 5% selection intensity, i.e. 2.06

σph = Phenotypic standard deviation

$\hat{h}^2$ = Heritability coefficient in narrow sense

$\bar{X}$ = Mean of the character concerned

Johnson *et al.* (1955) classified genetic advance as percentage of mean (GAM); values from

(i) 0-10% are low,

(ii) 10-20% are moderate,

(iii) 20% and above are high.

3.5.7 Phenotypic, genotypic and environmental variances

Computed from the respective mean squares following the procedures suggested by **Singh and Chaundhary (1979) and Allard (1960),** thus

Genotypic variance

$$\sigma^2_g = \frac{MSg - MSgI}{rl}$$

Genotypic by environment interaction variance

$$\sigma^2_{gl} = \frac{MSgl - MSe}{rl}$$

Phenotypic variance

$$\sigma^2_p = \sigma^2_g + \left(\frac{\sigma^2 e}{rl}\right) + \left(\frac{\sigma^2 gi}{l}\right)$$

where,

MS_g = mean square of genotype;

MS_{gl} = mean square due to genotype by environment interaction;

MS_e = error mean square (mean square of environment);

l = number of locations;

r = number of replications.

Genotypic (GCV), Phenotypic (PCV) and Environment (ECV) coefficients of variation (%) Estimated according to the procedure outlined by **Johnson *et al.* (1955):**

$$\text{GCV (\%)} = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

$$\text{PCV (\%)} = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

$$ECV\ (\%) = \frac{\sqrt{\sigma^2 gl}}{\bar{X}} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

σ^2_{gl} = Genotypic by environment interaction variance

$\bar{X}$ = Mean of the character concerned

The range of GCV, PCV and ECV suggested by **Subramanian & Menon (1973):**

GCV, PCV & ECV variability categorized into three classes:

Low = $<$10 %,

Moderate = 10-20%

High = $>$ 20 %.

3.5.8 Correlation coefficients analysis

The estimates of phenotypic and genotypic correlation were corked out as given under:

(i) Genotypic correlation

$$r_{xy}(g) = Cov._{xy}(g) / [V_x (g).V_y (g)]^{0.5}$$

Where,

$Cov._{xy}(g)$ = Genotypic covariance between character x and y was obtained as follows:

$$Cov._{xy}(g) = [Cov._{Xy}(p) – Cov._{Xy}(e)]/ r$$

V_X (g) and V_y (g) = Genotypic variance for the characters x and y respectively

r = Number of replications.

3.5.9 Phenotypic correlation

$$r_{xy} (p) = Cov._{Xy} (p) / [V_x (p). V_y (p)]^{0.5}$$

Where,

$Cov._{Xy}$ (p) = Phenotypic correlation between the character x and y and this was obtained as follows:

$$Cov._{xy} (p) = Cov._{xy} (g) + Cov._{xy} (e)$$

V_x (p) and V_y (p) = Phenotypic variance for the characters x and y, respectively.

xy (e) = The error variance obtained from the ANNOVA of x and y characters.

Test of significance of correlation coefficients

The significance of phenotypic coefficient was tested against ‘r’ values from ‘r’ Table of **Fisher and Yates (1938**) for (n-2) degree of freedom where ‘n’ is number of treatments.

(F) Path analysis

The concept of path coefficient analysis was originally developed by **Wright in 1921**, but the technique was first used for plant selection by Dewey and Lu 1959 in crested wheat grass.

Path coefficient analysis is simply standardized partial regression coefficient which split the simple correlation into the measures of direct and indirect effects and it measures the direct and indirect contribution of each independent variable on the dependent variable. If "Y" is dependent (causal) characters by X_1, X_2, X_3 ------- independent characters and some undefined factors designated by R, this relation can be represented by

$$\mathbf{Y = X_1 + X_2 + X_3 + ----- + R}$$

Path analysis reveals whether the association is due to their direct effect or is a consequence of their indirect effects *viz.*, other component characters. Correlation between cause (X_1) and effect (Y_1) is partitioned into the direct effects and indirect effects via other characters.

(a) Direct effects

Path coefficient is ratio of standard deviation of the effect due to given cause to the standard deviation of effect i.e. (X_1/y). This gives the direct effect of cause on yield.

$$r\,(x,y) = a + r\,(x_1, x_2)\,b + r\,(x_1, x_3)(---------)$$

Where,

r (x, y) = correlation coefficient between cause (x_1) and yield (effect) a, b, c is path coefficient (direct effects) of causal characters x_1, x_2, x_3 respectively.

r (x_1, x_2) = Correlation coefficient between cause x_1 and x_2

r (x_1, x_3) = Correlation coefficient between cause x_1 and x_3

(b) **Indirect effect**

Indirect effect of x_1 via x_2 on y = r (x_1, x_2) b

Similarly, direct and indirect effects of all possible combinations were calculated for all component characters.

(c) **Residual effect**

The residual effect R was calculated as below

$R = [1- (Px_1y.rx_1y)- (Px_2y.rx_2y) \ldots\ldots (Px_ny.rx_ny)^{1/2}$

Where,

$Px_1y, Px_2y \ldots. Px_ny$ = Direct effects of respective character on seed yield.

$Rx_1y, rx_2y \ldots. rx_ny$ = correlation coefficient between respective characters and yield.

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CHAPTER - IV

EXPERIMENTAL FINDINGS

The data were collected for 11 different characters *viz*., days to 75% heading, days to maturity, plant height (cm), number of effective tillers per plant, spike length (cm), number of grains per spike, 100 grain weight (g), biological yield per plant and harvesting index (%), grain weight per spike (g), grain yield per plant (g) which were subjected for the statistical and biometrical analyses:

4.1 Analysis of variance

4.2 Mean, ranges and coefficient of variability in parents and F_1s

4.3 Genetic components analysis

4.4 Combining ability analysis

- **(A)** Analysis of variance for combining ability
- **(B)** General combining ability (GCA) effects
- **(C)** Specific combining ability (SCA) effects

4.5 Heterosis

4.6 Selection parameter

- **(A)** Heritability and genetic advance
- **(B)** Correlation and path coefficient

4.1 ANALYSIS OF VARIANCE

ANOVA for all characters mentioned above was subjected to the 'F' test (Table 1). Highly significant differences were observed among the treatments for all characters. Since, the treatments consist of parents and F_1s, the analysis of variance further indicated highly significant differences among the parents and F_1s for all the characters except biological yield per plant in parents; number of effective tillers per plant and grain yield per plant in F_1s. It indicated significant variability among the parents and F_1s generated subsequently involving all the possible straight single crosses excluding reciprocal combinations. Parents vs. F_1s showed highly significant differences for all the characters except number of effective tillers per plant and 100 grain weight under study indicating considerable amount of heterotic response in these characters. The variance due to replication was found to be non-significant in the case of all the characters except days to 75% heading and days to maturity.

4.2 MEAN AND RANGES AND COEFFICIENT OF VARIABILITY IN PARENTS AND F_1s

The mean performance of F_1s was higher than parents for all the attributes, *viz*., days to 75% heading, days to maturity, plant height (cm), the number of effective tillers per plant, spike length (cm), the number of grains per spike, grain yield per plant (g), 100 grain weight (g), biological yield per plant, and harvesting index (%), grain weight per spike (g). Similarly, ranges were also higher in F_1, than parents except for number of effective tillers per plant, number of grains per spike, grain weight per spike and grain yield per plant which showed less mean value than parent (Table 2).

A wide range of variability was recorded among parents for the number of grains per spike (30.33 to 53.00), plant height (73.83 to 84.43), biological yield per plant (45.49 to 56.12), harvest index (32.12 to 39.57), days to 75% heading (71.33 to 77.00), grain yield per plant (15.32 to 21.10), number of effective tiller per plant (6.33 to 11.00), spike length (5.93 to 9.13), days to maturity (116.00 to 120.00), grain weight per spike (1.45 to 2.50) and 100 grain weight (4.54 to 5.37). Similarly, in F_1s also recorded wide range variability *viz*., biological yield per plant (47.33 to 69.75), plant height (74.60 to 94.00), number of grains per spike (45.00 to

59.67), harvest index (32.79 to 44.28), days to 75% heading (69.67 to 79.00), grain yield per plant (2.22 to 25.95), spike length (5.93 to 11.80), days to maturity (117.00 to 122.00), number of effective tillers per plant (7.66 to 11.00), 100 grain weight (4.52 to 5.17) and grain weight per spike (2.30 to 2.73).

4.3 GENETIC COMPONENTS ANALYSIS

The variance component analysis in F_1, generation was furnished according to the model suggested by Hayman (1954).

The regression coefficient 'b' deviated significant from zero for days to 75% heading (5.95), grain weight per spike (5.33), grain yield per plant (4.81) and number of grains per spike (4.54) indicating the presence of non allelic gene interaction. Rest of all traits were observed for non-significant values (Table 3).

The regression coefficient 'b' deviated significantly from unity for plant height (5.25). Such significant deviations of 'b' from unity indicated the presence of non-allelic gene interaction while the regression coefficient was not deviate significantly from unity for grain weight per spike (2.90), days to 75% heading (2.50), days to maturity (1.87), biological yield per plant (1.77), spike length (1.66), number of effective tiller per plant (1.51), harvest index (1.48), grain yield per plant (1.44), number of effective tillers per plant (1.36) and 100 grain weight (0.96) indicating the involvement of additive gene action.

Non significant values of "t^2" in 8 out of 11 attributes revealed the validity of the hypothesis. Significant values of "t^2" for days to 75% heading (10.93), plant height (6.0) and grain weight per spike (3.99) revealed the failure of one or more assumptions (Table 3).

The estimates of all the components of variation namely, $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{F}$ and $\hat{E}$ along with their standard errors and related statistics were worked out. The findings on these aspects are presented in Table 4.

The estimates of the ($\hat{D}$) genetic component were significant for most of the characters *viz.*, days to 75% heading (3.74), days to maturity (1.01), number of effective tillers per plant (1.68), spike length (1.05), number of grains per spike (55.41), grain weight per spike (0.15), 100 grain weight (0.06), harvest index (4.42) and grain yield per plant (3.71). Rest of traits were non significant for plant height (7.41) and biological yield per plant (7.84).

The dominance components ($\hat{H}_1$ and $\hat{H}_2$) were observed significant for all characters such as, days to 75% heading, days to maturity, plant height, number of effective tillers per plant, spike length, number of grains per spike, grain weight per spike, 100 grain weight, biological yield per plant, harvest index and grain yield per plant. The values of $\hat{H}_1$ were observed higher than the value of $\hat{H}_2$ for all the characters. The estimates of dominant component $\hat{H}_1$ were higher than additive ($\hat{D}$) genetic component for all characters.

The values of $\hat{F}$ component were found significant and positive for number of grains per spike (90.82), grain yield per plant (6.34), number of effective tillers per plant (2.57), grain weight per spike (0.25) and 100 grain weight (0.09) while all remaining traits were non significant and positive namely biological yield per plant (20.08), plant height (12.09), harvesting index (7.09), days to 75% heading (5.58), spike length (1.65) and days to maturity (1.11).

The estimates of $\hat{h}^2$ were found positive and significant in all the attributes, namely number of grain per spike (392.75), biological yield per plant (197.81), plant height (86.56), grain yield per plant (52.09), days to 75% heading (12.2), harvest index (11.63), spike length (8.21), days to maturity (2.71), number of effective tillers per plant (2.50) and grain weight per spike (0.72), indicating presence of dominance for these characters while positive and non significant 100 grain weight (0.02).

The estimates value of $\hat{E}$ components were found positive and non significant for all attributes except biological yield per plant (7.43), harvest index (2.55), grain yield per plant (1.55), number of effective per plant (0.63) and days to maturity (0.48) with positive and significant values.

The estimates of the mean degree of dominance $(\hat{H}_1/\hat{D})^{0.5}$ were greater than one (more than unity) for all characters. This indicates that for most of the characters, dominance gene played a significant role in their expression.

The proportion of genes with positive and negative effects $(\hat{H}_2/4\hat{H}_1)$ were recorded less than the theoretical value (0.25) for all attributes indicating asymmetrical distribution of positive and negative alleles over all the array.

The ratio of dominant and recessive genes $[(4\hat{D}\hat{H}_1)1/2 + \hat{F} / 4\hat{D}\hat{H}_1) -\hat{F})]$ was observed more than unity for all character like number of effective tillers per plant (3.56), grain weight per spike (3.50), 100-grain weight (3.03), number of grains per spike (2.60), spike length (2.31), grain yield per plant (2.30), biological yield per plant (2.17), harvesting index (1.97), days to75% heading (1.95), and days to maturity (1.74), and days to maturity (1.55), indicating greater role of dominant genes for all these traits.

The estimated values of the $\hat{h}_2$ /$\hat{H}_2$ were found more than unity for all the characters except days to 75% heading (0.72), days to maturity

(0.72), and harvest index (0.62) indicating that one major gene group was responsible for the inheritance of these attributes.

4.4. COMBINING ABILITY ANALYSIS

4.4 (A). Analysis of variance

Analysis of variance for combining ability was under taken for all characters and findings are presented in Table 5. The mean sum of squares due to general combining ability (GCA) were observed highly significant for all the attributes studied except number of effective tillers per plant and biological yield per plant. Similarly, the mean sum of squares due to specific combining ability were observed highly significant for all the characters except number of effective tillers per plant.

The estimates of $\hat{\sigma}^2s$ were higher than the respective to $\hat{\sigma}^2g$ for all characters were recorded in F_1 generation.

The ratio of the average degree of dominance $(\hat{\sigma}^2s/\hat{\sigma}^2g)^{0.5}$ were found to be greater than one for all the characters. Indicates a significant contribution of non-additive genetic variance in the expression of all the attributes.

4.4. (B). GENERAL COMBINING ABILITY (GCA) EFFECTS

The estimates of GCA effects of all the parents for 11 characters were given in Table 6. The positive and significant values of GCA effect were considered desirable for all the characters except days to 75% heading, days to maturity and plant height where negative significant values were considered desirable.

Days to 75% heading

Negative significant and desirable GCA effects were observed for days to 75% heading in KB 1425 (-0.75) and KB 1762 (-0.48) while non significant negative general combining ability effects were observed in HUB 113 (-0.32) and KB 1506 (-0.18).

Positive significant and undesirable GCA effects were observed for days to 75% heading in DWRB 137(1.18) and positive non significant general combining ability effects were observed in K 603(0.25), RD 2907(0.21) and KB 1634(0.08).

Days to maturity

Negative significant and desirable GCA effects were observed for days to maturity in KB 1762 (-0.71) and non-significant negative general combining ability effects were observed in KB 1506 (-0.31) and KB 1634 (-0.08).

The positive non-significant and undesirable GCA effects were observed for days to maturity in K 603(0.31), KB 1425 (0.28), HUB 113 (0.25), RD 2907 (0.18) and DWRB 137(0.08).

Plant height (cm)

Negative significant and desirable GCA effects were observed for plant height in RD 2907 (-1.9), DWRB 137 (-1.89) and HUB 113 (-1.47).

Positive significant and undesirable GCA effects were observed for plant height in KB 1506 (2.57) KB 1634 (1.27) and KB 1425 (1.13) while non-significant positive general combining ability effects were observed in K 603 (0.28) and KB 1762 (0.012).

Number of effective tillers per plant

Positive significant and desirable GCA effects were observed for number of effective tillers per plant in KB 1506 (0.79) and non significant positive general combining ability effects were observed in DWRB 137 (0.03) and KB 1425 (0.02).

Negative non significant and undesirable GCA effects were observed for number of effective tillers per plant in KB 1762 (-0.44), KB 1634 (-0.18), RD 2907 (-0.17), HUB 113 (-0.04), and K 603 (-0.01).

Spike length (cm)

Positive significant and desirable GCA effects were observed for spike length in DWRB 137 (0.44) and non significant positive general combining ability effects were observed in KB 1506 (0.18) and KB 1634 (0.12).

Negative significant and undesirable GCA effects were observed for spike length in KB 1762 (-0.48) and non-significant negative general combining ability effects were observed in K 603 (-.013), KB 1425 (-0.07), RD 2907 (-0.04) and HUB 113 (-0.03).

Number of grains per spike

Positive significant and desirable GCA effects were observed for number of grains per spike in KB 1634 (2.44) and DWRB 137(1.34) while non significant positive general combining ability effects were observed in HUB 113 (0.74) and K 603 (0.51).

Negative significant and undesirable GCA effects were observed for number of grains per spike in KB 1425 (-1.82), KB 1762 (-1.23) and KB 1506 (-1.19) while non-significant negative general combining ability effects were observed in RD 2907 (-0.79).

Grain weight per spike (g)

Positive significant and desirable GCA effects were observed for grain weight per spike in KB 1634 (0.12) and HUB 113 (0.06) and DWRB 137 (0.05) while non-significant positive general combining ability effects were observed in RD 2907 (0.02).

Negative significant and undesirable GCA effects were observed for grain weight per spike in KB 1425 (-0.09), KB 1762 (-0.07) and K 603 (-0.05) while non-significant negative general combining ability effects were observed in KB 1506 (-0.03).

100 grain weight (g)

Positive significant and desirable GCA effects were observed for 100 grain weight in RD 2907 (0.10) and KB 1634 (0.06) and non-significant positive general combining ability effects were observed in DWRB 137 (0.03), KB 1506 (0.01) and KB 1425 (0.01).

Negative significant and undesirable GCA effects were observed for 100 grain weight in K 603 (-0.14) and KB 1762 (-0.07) while non-significant negative general combining ability effects were observed in HUB 113 (-0.003).

Biological yield per plant (g)

Positive non-significant and desirable GCA effects were observed for biological yield per plant in K 603 (1.24), KB 1762 (0.90), KB 1425 (0.32), KB 1634 (0.32) and KB 1506 (0.05).

Negative significant and undesirable GCA effects were observed for biological yield per plant in RD 2907 (-1.69) and non-significant negative general combining ability effects were observed in HUB 113 (-1.16) and DWRB 137 (-0.11).

Harvest index (%)

Positive significant and desirable GCA effects were observed for 100 grain weight in HUB 113 (1.70) and KB 1634 (1.07) while non-significant positive general combining ability effects were observed in KB 1506 (0.17).

Negative significant and undesirable GCA effects were observed for 100 grain weight in KB 1762 (-1.69) and non-significant negative general combining ability effects were observed in RD 2907 (-0.77), K 603 (-0.28), DWRB 137 (-0.17) and KB 1425 (-0.04).

Grain yield per plant (g)

Positive significant and desirable GCA effects were observed for grain yield per plant in KB 1634 (0.78) and non-significant positive general combining ability effects were observed in HUB 113 (0.53), K 603 (0.29), KB 1506 (0.25) and KB 1425 (0.23).

Negative significant and undesirable GCA effects were observed for grain yield per plant in RD 2907 (-1.07) and KB 1762 (-0.75) while non-significant negative general combining ability effects were observed in DWRB 137 (-0.26).

4.4. (C) Specific combining ability effect

The estimates of specific combining ability (SCA) effects along with mean performance of all attributes were given in Table 7. In the previous assessment, character-wise outcomes were obtained regarding specific combining ability effects, showing positive estimates for all the traits investigated, except for days to 75% heading, days to maturity, and plant height, which were demonstrated as desirable in the negative direction.

Days to75% heading

Three highly significant and one significant desirable combiner for SCA effects were observed for days to75% heading, five in order of ranking, were KB 1762 X KB 1634 (-5.21), KB 1425 X K 603 (-3.78), RD 2907 X K 603 (-2.74), KB 1506 X DWRB 137 (-1.28) and KB113 X DWRB 137 (-1.14).

Days to maturity

One highly significant and one significant desirable combiner for SCA effects were observed for days to maturity. Five good combiners, in order of ranking, were KB 1634 X DWRB 137 (-2.09), KB 1762 X K 603 (-1.36), KB 1506 X KB113 (-1.03), and RD 2907 X KB 1634 (-0.86).

Plant height (cm)

Five highly significant and one significant desirable combiner for SCA effects were observed for plant height. Five good combiners, in order of ranking, were RD 2907 X K 603 (-5.83), KB113 X K 603 (-5.78) KB 1506 X KB 1762 (-5.56), KB 1762 X KB113(-5.22) and RD 2907 X KB 1425 (-4.88).

Number of effective tillers per plant

One significant desirable combiner for SCA effects was observed for number of effective tillers per plant. Five good combiners, in order of ranking, were KB 1425 X KB 1634 (1.66), KB 1762 X KB 1634 (1.46) KB 1634 X HUB 113 (1.39), KB 1506 X K 603 (1.39) and RD 2907 X KB113 (1.06).

Spike length (cm)

Eight highly significant and three significant desirable combiners for SCA effects were observed for spike length. Five good combiners, in order of ranking, were KB 1762 X DWRB 137 (2.49), RD 2907 X KB 1634 (1.15) KB 1425 X KB 1762 (1.08), KB 1506 X K 603 (1.08) and KB 1506 X KB 1634 (1.07).

Number of grains per spike

Fourteen highly significant desirable combiners for SCA effects were observed for number of grains per spike. Five good combiners, in order of ranking, were KB 1425 X K 603 (9.62), KB 1762 X DWRB 137 (8.52), RD 2907 X K 603 (7.92), RD 2907X DWRB 137 (7.76) and KB 1762 X KB 1634 (7.42).

Grain weight per spike (g)

Ten highly significant and three significant desirable combiners for SCA effects were observed for grain weight per spike. Five good combiners, in order of ranking, were KB 1425 X K 603 (0.39), KB 1762 X K 603 (0.33), KB 1506 X K 603 (0.32), KB 1425 X KB 1506 (0.29) and KB 1425 X KB 1634 (0.29).

100 grain weight (g)

Four highly significant and four significant desirable combiners for SCA effects were observed for 100 grain weight. Five good combiners, in order of ranking, were KB 1506 X K 603 (0.34), RD 2907 X KB 1762

(0.21), KB 1634 X K 603 (0.20), KB 1634 X HUB 113 (0.19) and KB 1425 X DWRB 137 (0.17).

Biological yield per plant (g)

One highly significant and two significant desirable combiners for SCA effects were observed for biological yield per plant. Five good combiners, in order of ranking, were KB 1506 X K 603 (3.62), KB 1425 X KB 1634 (2.85), KB 1762 X KB 1634 (2.41), RD 2907 X DWRB 137 (2.26) and KB 1762 X DWRB 137 (2.04).

Harvesting index (%)

Two highly significant and four significant desirable combiners for SCA effects were observed for harvest index. Five good combiners, in order of ranking, were KB 1506 X K 603 (10.72), KB 1425 X KB 1762 (8.52), RD 2907 X KB 1762 (6.38), KB 1762 X 1634 (5.96) and KB 1506 X HUB 113 (5.83).

Grain yield per plant (g)

Two highly significant and one significant desirable combiner for SCA effects were observed for grain yield per plant. Five good combiners, in order of ranking, were HUB 113 X K 603 (4.83), KB 1425 X K 603 (4.19), KB 1425 X KB 1634 (3.10), KB1762 X HUB 113 (2.44) and KB 1506 X KB 1634 (2.41).

4.5 HETEROSIS

Heterosis percentages were calculated relative to the economic parent (KB 1425) for all eleven traits. The results concerning these traits are present in Table 8. Negative and significant heterosis values were considered favorable for traits like days to 75% heading, plant height, and days to maturity, while positive and significant heterosis values were also considered favorable. The specific findings for each trait are provided below:

Days to 75% heading

Heterosis over economic parent for days to 75% heading ranged from -9.52 (KB 1762 X KB 1634) to 2.60 (KB 1762 X DWRB 137) per cent. Six cross combination in desirable direction revealed highly significant and three significant responded for this attribute. Out of these, five crosses in order of merit, were KB 1762 X KB 1634 (-9.52), KB 1425 X K 603 (-7.79), RD 2907 X K 603 (-5.19), KB 1425 X KB 1634 (-4.33) and KB 1425 XKB 1506 (-3.90).

Days to maturity

The extent of heterosis over economic parent for days to maturity ranged from -2.50 (KB 1634 X DWRB 137) to 1.67 (HUB113 X DWRB 137) per cent. One cross combination giving significant and three cross combination highly significant desirable heterosis. five out of these, in order of merit, were KB 1634 X DWRB 137 (-2.50), KB 1762 X K 603 (-2.22), KB 1506 X HUB 113 (-1.67), RD 2907 X KB 1634 (-1.39) and KB 1425 X KB 1506 (-1.39).

Plant height (cm)

Heterosis over economic parent for plant height ranged from -11.65 (RD 2907 X K 603) to 11.33 (KB 1425 X KB 1762) per cent. Five cross combination showed highly significant in desirable heterosis for this attribute. Out of these five, in order of merit, were RD 2907 X K 603 (-11.65), HUB 113 X K 603 (-11.09), KB 1762 X KB113 (-10.74), RD 2907 X KB 1425 (-9.51), and KB 1425 X DWRB 137 (-8.37).

Number of effective tillers per plant

Heterosis over economic parent for number of effective tillers per plant ranged from -30.30 (RD 2907 X KB 1762) to 0.00 (KB 1506 X K 603). No cross combination had shown significant and desirable heterosis.

Spike length (cm)

The extent of heterosis over economic parent for spike length ranged from 29.20 (KB 1762 X DWRB 137) to -6.2 (RD 2907 XKB 1425) per cent, seven cross combination highly significant desirable heterosis. five out of these, in order of merit, were KB 1762 X DWRB 137 (29.20), KB 1506 X KB 1634 (17.15), RD 2907 X KB 1634 (15.69), KB 1506 X DWRB 137 (15.33), and KB 1506 X K 603 (14.60).

Number of grains per spike

Heterosis over economic parent for number of grains per spike ranged from 12.58 (KB 1762 X KB 1634) to -15.09 (RD 2907 X KB 1634) per cent, five cross combination showed highly significant desirable heterosis for this attribute. Out of these five, in order of merit, were KB 1762 X KB 1634 (12.58), KB 1762 X DWRB 137 (12.58), RD 2907 X DWRB 137 (11.95), KB 1425 X K 603 (11.95), and RD 2907 X K 603 (10.69).

Grain weight per spike (g)

The extent of heterosis over economic parent for grain weight per spike ranged from 9.07 (KB 1425 X KB 1634) to -9.73 (KB 1762 X KB113) per cent, two cross combination highly significant desirable heterosis. five out of these, in order of merit, were KB 1425 X K 603 (6.67), KB 1506 X K 603 (6), RD 2907 X KB 1406 (4.93), KB 1762 X K 603 (4.67) and KB 1634 X DWRB 137 (4.67).

100-grain weight (g)

Heterosis over economic parent for number of effective tillers per plant ranged from -15.94 (HUB 113 X K 603) to -3.58 (KB 1634 X DWRB 137). But it did not show any cross combination with significant and desirable heterosis.

Biological yield per plant (g)

Heterosis over economic parent for number of biological yields per plant ranged from -6.28 (HUB113 X K 603) to 24.27 (KB 1506 X K 603) per cent. One cross combination showed highly significant desirable heterosis and one significant for this attribute. Out of these five, in order of merit, were KB 1506 X K 603 (24.27), KB 1425 X KB 1762 (20.25), KB 1762 X KB 1634 (15.67), KB 1762 X DWRB 137 (133.78) and RD 2907 X KB 1762 (12.74)

Harvest index (%)

The extent of heterosis over economic parent for harvest index ranged from 11.89 (HUB 113 X K 603) to -17.14 (RD 2907 X KB 1762) per cent, one cross combination significant desirable heterosis. five out of these, in order of merit, were HUB 113 X K 603 (11.89), KB 1425 X KB 1634 (6.55), KB 1425 X K 603 (5.86), KB 1425 X HUB 113 (5.59) and KB 1634 X DWRB 137 (4.33).

Grain yield per plant (g)

Heterosis over economic parent for number of grains yield per plant ranged from -4.4 (RD 2907 X KB 1634) to 23.09 (KB 1506 X K 603) percent. One cross combination showed highly significant desirable heterosis and one significant responded for this attribute. Out of these five, in order of merit, were KB 1506 X K 603 (23.09), KB 1425 X KB 1634 (21.71), KB 1634 X HUB 113 (15.02) and KB 1762 X KB 1634 (14.93).

4.6. SELECTION PARAMETERS

4.6. (A) HERITABILITY AND GENETIC ADVANCE

The success of any plant breeding program depends greatly on the essential knowledge of the genetic variations within a specific crop species that are targeted for improvement (**Sankar *et al*. 2006**). The utilization of parameters like genotypic and phenotypic coefficients of variation (GCV and PCV) plays a significant role in determining the extent of variability in a particular characteristic. The effectiveness of harnessing genotypic variability through selection depends on both the heritability and the genetic advance (GA) of the specific trait. (**Bilgin *et al*. 2010**). To design an efficient breeding program for enhancing quantitative traits in plants, it is crucial to have accurate estimates of heritability. Reliable estimations of heritability are essential for determining the proportion of phenotypic variation attributable to genetic factors. This information helps breeders understand the potential success of selective breeding and enables them to make informed decisions regarding the selection of superior individuals for further breeding efforts (**Akinwale *et al*. 2011**). Heritability offers valuable information regarding the degree to which a specific morphogenetic character can be inherited and passed on to future generations (**Bello *et al*. 2012**).

The combination of high heritability and substantial genetic advance is particularly valuable in predicting the ultimate impact when selecting the best genotypes for yield and its associated traits. (**Singh *et al.* 2011**). The values for narrow-sense heritability, genetic advance, genotypic coefficient of variation, phenotypic coefficient of variation, and environmental coefficient of variation, expressed as a percentage of the mean, were calculated for eleven different traits as shown in Table 9.

HERITABILITY

In 1961, Kempthorne and Curnow classified narrow-sense heritability estimates into three groups based on their magnitude: high (> 30%), medium (10-30%), and low (10%). Moderate heritability was observed for harvesting index (25.8%), 100 grain weight (22.7%), plant height (22.1%), grain yield per plant (12.5%), days to 75% heading (12.2%), and spike length (10.2%) while low heritability was observed for days to maturity (9.8%), grain weight per spike (6.2%), biological yield per plant (6.1%), and the number of grains per spike (5.2%). It's noteworthy that none of the traits showed a high narrow-sense heritability estimate based on the analysis.

GENETIC ADVANCE

Johnson *et al.* (1955) categorized genetic advance estimates into three groups based on their magnitude: high (> 20%), medium (10-20%), and low (10%). The genetic advance was expressed as a percentage of the mean (GA%) and was evaluated at a selection intensity of 5% to compare the traits. In the F_1 generation, the percentage of genetic advance over the mean varied for different traits, ranging from 1.09 for days to maturity to 25.63 for the number of grains per spike

High genetic advance values were observed for the number of grains per spike (25.63) and grain weight per spike (22.55) and moderately high genetic advance were observed for spike length (19.73), grain yield per plant (13.60), biological yield per plant (10.87), and plant height (10.38) while low genetic advance were observed for harvesting index (8.3), number of effective tillers per plant (6.29), 100-grain weight (5.98), days to 75% heading (5.2), and days to maturity (1.09).

4.6. (B) GENOTYPIC AND PHENOTYPIC COEFFICIENT OF VARIATION

Subramanian & Menon (1973), studied the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were classified into three categories for convenience: Low (<10%), Moderate (10-20%), and High (>20%). GCV represents the heritable component of overall phenotypic variation, signifying the variation between different genotypes.

The magnitude of the phenotypic coefficient of variation was, on an average, greater than the genotypic coefficient of variation, which may be due to the interaction between genotype and environment.

Genotypic coefficient of variation (GCV %)

Moderate genetic coefficient of variation (GCV) percentages were observed for the number of grains per spike (13.32), grain weight per spike (11.85), and spike length (10.90) and low GCV percentages were observed for grain yield per plant (9.51), biological yield per plant (7.71), number of effective tillers per plant (7.28), harvesting index (6.18), plant height (6.03), 100-grain weight (3.62), days to 75% heading (2.81), and days to maturity (0.81). However, no traits showed a high genetic coefficient of variation.

Phenotypic coefficient of variation (PCV %)

Moderate phenotypic coefficient of variation (PCV) percentages were observed for the number of effective tillers per plant (17.35), number of grains per spike (14.26), grain yield per plant (13.69), grain weight per spike (12.82), spike length (12.41), and biological yield per plant (11.7) and low PCV percentages were observed for harvesting index (9.47), plant height (7.22), 100-grain weight (4.52), days to 75% heading (3.14), and days to maturity (1.23). However, no traits were associated with high phenotypic coefficient of variation.

4.6. (C). CORRELATION AND PATH COEFFICIENT

(I) CORRELATION COEFFICIENT

The phenotypic and genotypic correlation coefficient of the F_1 generation among the eleven characters under investigation presented in Table 10 (a) and (b). Typically, the phenotypic correlation coefficients for the F_1 generation were found to be higher than their corresponding genotypic correlation coefficients. This finding indicated a significant association between several pairs of traits in the barley genotype. The results of phenotypic and genotypic correlation coefficients are shown as follows:

Highly significant and positive correlation at phenotypic level was observed for grain yield per plant with Grain weight per spike (0.987), number of grains per spike (0.985), biological yield per plant (0.777), spike length (0.770), plant height (0.644), harvesting index (0.554), days to maturity (0.497), number of productive tillers per plant (0.460), and days to 75% heading (0.306) while non significant and positive correlation was observed for grain yield per plant with 100-grain weight (0.087).

Significant and positive correlation at genotypic level was observed for grain yield per plant with biological yield per plant (0.723)number of effective tillers per plant (0.686), number of grains per spike (0.642), grain weight per spike (0.613), spike length (0.543), harvest index (0.520), plant height (0.358), days to maturity (0.317), whereas positive and significant for days to 75% heading (0.214) while positively non significant observed for 100 grain weight (0.054).

Days to 75% heading

At phenotypic level, highly significant and positive correlation was observed for days to 75% heading with spike length (0.413), biological yield per plant (0.300), grain yield per plant (0.306) and grain weight per spike (0.251) whereas positive and significant correlation was observed with days to maturity (0.22); positive non significant correlation was found with plant height (0.135), harvest index (0.056), 100 grain weight (0.009) and number of effective tillers per plant (0.003).

At genotypic level, highly significant and positive correlation was observed for days to 75% heading with spike length (0.324) whereas positive and significant correlation was observed with biological yield per plant (0.233) and grains yield per plant (0.214); rest non significant and positive correlation were exhibited with grain weight per spike (0.183), days to maturity (0.180), number of grains per spike (0.173), plant height (0.109), number of effective tillers per plant (0.039) and 100 grain weight (0.011) while non significant and negative correlation was observed for harvest index (-0.009).

Days to maturity

Highly significant and positive correlation at phenotypic level was observed for days to maturity with grain yield per plant (0.497), spike length (0.466), biological yield per plant (0.464), plant height (0.458), grain weight per spike (0.296), number of grains per spike (0.296) and days 75% heading (0.216) while non significant and positive correlation was observed with number of effective tillers per plant (0.181), harvest index (0.128) and 100 grain weight (0.015).

Highly significant and positive correlation at genotypic level was observed for days to maturity with gains yield per plant (0.317), while positive and significant correlations were observed with biological yield per plant (0.225), plant height (0.209) and spike length (0.200) while non significant and positive correlation was observed with number of effective tillers per plant (0.156),grain weight per spike (0.149), harvest index (0.144), plant height (0.109) and 100 grain weight (0.071).

Plant height (cm)

At phenotypic level highly significant and positive correlation was observed for plant height with biological yield per plant (0.827), grain yield per plant (0.644), spike length (0.607), number of effective tillers per plant (0.515), days to maturity (0.458), grain weight per spike (0.385), and number of grains per spike (0.308) while non-significant positively correlation observed with 100 grains weight (0.174) and days to 75%

heading (0.135). Conversely, the harvesting index (-0.172) showed a non significant negative correlation.

At genotypic level, highly significant and positive correlation was observed for plant height with biological yield per plant (0.562), spike length (0.435), grain yield per plant (0.358), grain weight per spike (0.270), and number of grains per spike (0.204) while non-significant positively correlation observed with number of effective tillers per plant (0.135), 100 grain weights (0.088) and days to 75% heading (0.039). Conversely, the harvesting index (-0.172) showed a non-significant negative correlation.

Number of effective tillers per plant

Highly significant and positive correlation at phenotypic level was observed for number of effective tillers per plant with harvesting index (0.653), grain weight per spike (0.639), number of grains per spike (0.605), spike length (0.552), plant height (0.515) and grain yield per plant (0.460) while non-significant positively correlation observed with biological yield per plant (0.054), days to maturity (0.181) and days to 75% heading (0.003).

Highly significant and positive correlation at genotypic level was observed for number of effective tillers per plant with grain yield per plant (0.686), biological yield per plant (0.545), spike length (0.314), harvesting index (0.291), and number of grains per spike (0.256) while non-significant positively correlation observed with days to maturity (0.135), plant height (0.126), 100 grain weight (0.111) and days to 75% heading (0.039).

Spike length (cm)

Highly significant and positive correlation at phenotypic level was observed for spike length with grain yield per plant (0.770), grain weight per spike (0.715), biological yield per plant (0.705), number of grains per spike (0.699), plant height (0.607), number of effective tillers per plant (0.552), days to maturity (0.466) and days to 75% heading (0.413) while positively significant correlation observed with harvesting index (0.225) and positively non significant correlation observed with 100 grain weight (0.132).

Highly significant and positive correlation at genotypic level was observed for spike length with number of grains per spike (0.616), grain weight per spike (0.612), grain yield per plant (0.543), biological yield per plant (0.533), plant height (0.435) number of effective tillers per plant (0.314) and days to 75% heading (0.324) while positively significant correlation observed with days to maturity (0.200) and positively non significant correlation observed with 100 grain weight (0.0.048) and harvesting index (0.112).

Grain weight per spike (g)

At phenotypic level, highly significant and positive correlation was observed for grain weight per spike with gains yield per plant (0.987), number of grains per spike (0.938), spike length (0.715), biological yield per plant (0.673), harvest index (0.657), number of effective tillers per plant (0.639), plant height (0.385), days to maturity (0.323), 100-grain weight (0.262) and days to 75% heading (0.251).

At phenotypic level, highly significant and genotypic correlation was observed for grain weight per spike with number of grains per spike (0.896), gains yield per plant (0.613), spike length (0.612), biological yield per plant (0.422), harvesting index (0.401) and plant height (0.270) while positively significant correlation observed with 100 grain weight (0.241) number of effective tillers per plant (0.223). Positively non significant correlation observed with days to 75% heading (0.183) and days to maturity (0.149).

100 grain weight (g)

Highly significant and positive correlation at phenotypic level was observed for 100 grain weight with number of effective tillers per plant (0.321) and grain weight per spike (0.262) while non significant and positive correlation was observed for 100 grain weight with plant height (0.174), biological yield (0.137), spike length (0.132), grain yield per plant (0.087), days to maturity (0.015) and days to 75% heading (0.009); significant and negative correlation was observed with harvesting index (-0.067) and number of grains per spike (-0.038).

Significant and positive correlation at genotypic level was observed for 100 grain weight with grain weight per spike (0.241) whereas non significant and positive correlation with number of effective tillers per plant (0.111), plant height (0.088), days to maturity (0.071), harvesting index (0.056), grain yield per plant (0.054), spike length (0.048) and biological yield per plant (0.005); non significant negatively correlation was observed with number of grains per spike (-0.031).

Harvest index (%)

At phenotypic level, highly significant and positive correlation was observed for harvest index with number of grains per spike (0.677), grain weight per spike (0.657), number of effective tillers per plant (0.653) and gains yield per plant (0.554) while significant and positive correlation with spike length (0.225); non-significant and negative correlation was observed with plant height (-o,172), biological yield per plant (-0.102) and 100 grain weight (-0.067).

At phenotypic level, highly significant and genotypic correlation was observed for harvest index with grain yield per plant (0.520) and number of grains per spike (0.415), grain weight per spike (0.401) and number of effective tillers per plant (0.291) whereas non significant and positive correlation with days to maturity (0.144), spike length (0.112) and 100 grain weight (0.056); non significant and negative correlation was exhibited with plant height (-0.186), biological yield per plant (-0.165) and days to maturity (-0.009).

Biological yield per plant

At the phenotypic level, biological yield per plant was highly significant and positively correlated with plant height (0.827), gains yield per plant (0.777), spike length (0.705), number of grains per spike (0.695), grain weight per spike (0.673), days to maturity (0.464) and days to 75% heading (0.300), whereas non significant and positively correlated with 100 grain weight (0.137) and number of effective tillers per plant (0.054); non significant and negatively correlation was observed with harvest index (-0.102).

At the genotypic level, biological yield per plant was highly significant and positively correlation with grain yield per plant (0.723), plant height (0.562), number of effective tillers per plant (0.545), spike length (0.533), grain weight per spike (0.422) number of grains per spike (0.446), Whereas significant and positively correlation with days to 75% heading (0.233); non-significant and negatively correlation was observed with harvest index (-0.165).

Number of grains per spike

At the phenotypic level, number of grains per spike was highly significant and positively correlated with gains yield per plant (0.985), grain weight per spike (0.938), spike length (0.699), biological yield per plant (0.695), harvest index (0.677), number of effective tillers per plant (0.605), plant height (0.308) and days to maturity (0.296) while non significant and negatively correlated with 100 grain weight (-0.038).

At the genotypic level, number of grains per spike was highly significant and positively correlated with gains yield per plant (0.642), grain weight per spike (0.896), spike length (0.616), biological yield per plant (0.446), harvest index (0.415) and number of effective tillers per plant (0.256) whereas non significant and positively correlated with days to 75% heading (0.173) and days to maturity (0.156); non significant and negatively correlated was observed with 100 grain weight (-0.031).

(II) PATH COEFFICIENT ANALYSIS

Simple correlation coefficient values do not make a complete picture of complex situation of association among different characters therefore the assessment of real contribution of each individual character towards grain yield per plant is important to decide about selection indices. Path coefficient analysis provides more realistic picture of the relationship among the characters. The path coefficient analysis reveals whether the association of each individual character with yield is due to its direct effect on yield or is a consequence of indirect effects via other component characters. Thus, path coefficient is essential to know the effectiveness of selection for simultaneous improvement in these characters. The results obtained from path analysis using genotypic and phenotypic correlation are presented in Table-11 (a) and (b). The following estimates are given on the basis of phenotypic path matrix.

Days to 75% heading

Positive and highly significant genotypic correlation was exhibited for days to 75% heading (0.306) on grain yield per plant. Positive direct effect (0.085) was observed for day to 75% heading on grain yield per plant whereas, positive indirect effect was observed with days to maturity (0.089), number of effective tillers per plant (0.003) and grain weight per spike (0.886) while, negative indirect effect was exhibited via plant height

(-0.064), spike length (-0.309), 100 grain weight (-0.009), harvest index (-0.097), biological yield per plant (-0.092) and number of grains per spike (-0.186).

Positive and significant phenotypic correlation was exhibited for days to 75% heading (0.214) on grain yield per plant. Positive direct effect (0.293) was observed for day to 75% heading on grain yield per plant whereas, positive indirect effect was observed with days to maturity (0.0065), plant height (0.0034), number of effective tillers per plant (0.0038), spike length (0.0070), 100 grain weight (0.000), biological yield per plant (0.1672) and number of grains per spike (0.0039). while negative indirect effect was exhibited via grain weight per spike (-0.0012) and harvest index (-0.057).

Days to maturity

There were positive and highly significant genotypic correlation days to maturity (0.497) on grain yield per plant. Path analysis indicated the positive direct effect for days to maturity on grain yield per plant (0.414) while negative indirect effect was exhibited for plant height (-0.216), spike length (-0.349), 100 grain weight (-0.016), harvest index (-0.222), biological yield per plant (-0.142) and number of grains per spike (-.0284). Positive indirect effect was observed for day to 75% heading (0.018), number of effective tillers per plant (0.156) and grain weight per spike (1.138).

There were positive and highly significant phenotypic correlation days to maturity (0.317) on grain yield per plant. Path analysis indicated the positive direct effect for days to maturity on grain yield per plant (0.363) while, negative direct effect was exhibited for grain weight per spike (-0.0010). Positive indirect effect was observed for day to 75% heading (0.0053), plant height (0.0065), number of effective tillers per plant (0.132), spike length (0.0043), 100 grain weight (0.0001), harvest index (0.0870), biological yield per plant (0.1613) and number of grains per spike (0.0035).

Plant height

Positive and highly significant genotypic correlation was observed for plant height (0.358) on grain yield per plant. Positive direct effect (0.0312) was observed for plant height on grain yield per plant whereas, positive indirect effect was observed with day to 75% heading (0.0032), days to maturity (0.0076), number of effective tillers per plant (0.123), spike length (0.0093), 100 grain weight (0.0001), biological yield per plant (0.4033), and number of grains per spike (0.0046) while, negative indirect effect was exhibited via grain weight per spike (-0.0018) and harvest index (-0.1120).

Positive and highly significant phenotypic correlation was observed for plant height (0.644) on grain yield per plant. Negative direct effect (-0.472) was observed for plant height on grain yield per plant whereas, positive indirect effect was observed with day to 75% heading (0.011), days to maturity (0.190), number of effective tillers per plant (0.444), grain weight per spike (1.356), and harvest index (0.299) while, negative indirect effect was exhibited via spike length (-0.454), 100 grain weight (-0.182), biological yield per plant (-0.253) and number of grains per spike (-0.296).

Number of effective tillers per plant

There were positive and highly significant genotypic correlation number of effective tillers per plant (0.460) on grain yield per plant. Path analysis indicated the positive direct effect for number of effective tillers per plant on grain yield per plant (0.863) while, negative indirect effect was exhibited for plant height (-0.243), spike length (-0.413), 100 grain weight

(-0.337), harvest index (-1.139), biological yield per plant (-0.016) and number of grains per spike (-0.580). Positive indirect effect was observed for day to 75% heading (0.000), days to maturity (0.075) and grain weight per spike (2.250).

There were positive and highly significant phenotypic correlation number of effective tillers per plant (0.686) on grain yield per plant. Path analysis indicated the positive direct effect for number of effective tillers per plant on grain yield per plant (0.0979) while, negative indirect effect was exhibited for grain weight per spike (-0.0015). Positive indirect effect was observed for day to 75% heading (0.0012), days to maturity (0.0049), plant height (0.0039), spike length (0.0067), 100 grain weight (0.0002), harvest index (0.1752), biological yield per plant (0.3913) and number of grains per spike (0.0058).

Spike length

Positive and highly significant genotypic correlation was observed for spike length (0.770) on grain yield per plant. Negative direct effect (-0.748) was observed for spike length on grain yield per plant whereas, positive indirect effect was observed with day to 75% heading (0.035), days to maturity (0.193), number of effective tillers per plant (0.477), grain weight per spike (2.518) while, negative indirect effect was exhibited via plant height (-0.287), 100 grain weight (-0.139), harvest index (-0.393), biological yield per plant (-0.215) and number of grains per spike (-0.671).

Positive and highly significant phenotypic correlation was observed for spike length (0.543) on grain yield per plant. positive direct effect (0.241) was observed for day to 75% heading (0.0095), days to maturity (0.0073), plant height (0,0136), number of effective tillers per plant (0.0307), 100 grain weight (0.0001), harvest index (0.0677), biological yield per plant (0.3830) and number of grains per spike (0.0140) while, negative indirect effect was exhibited via grain weight per spike (-0.0040).

Grain weight per spike

There were positive and highly significant genotypic correlation grain weight per spike (0.987) on grain yield per plant. Path analysis indicated the positive direct effect for grain weight per spike on grain yield per plant (3.523) while, negative indirect effect was exhibited for plant height (-0.182), spike length (-0.535), 100 grain weight (-0.275), harvest index (-1.145), biological yield per plant (-0.206) and number of grains per spike (-0.900). Positive indirect effect was observed for day to 75% heading (0.021), days to maturity (0.134) and number of effective tillers per plant (0.551).

There were positive and highly significant phenotypic correlation grain weight per spike (0.613) on grain yield per plant. Path analysis indicated the negative direct effect for grain weight per spike on grain yield per plant (-3.0065) whereas, positive indirect effect was observed for day to 75% heading (0.054), days to maturity (0.0054), plant height (0.0084), number of effective tillers per plant (0.0219), spike length (0.0131), 100 grain weight (0.0004), harvest index (0.2417), biological yield per plant (0.3028) and number of grains per spike (0.0203).

100 grains weight

Positive and non significant genotypic correlation was observed for 100 grain weight (0.087) on grain yield per plant. Negative direct effect (-1.049) was observed for 100 grain weight on grain yield per plant whereas, positive indirect effect was observed with day to 75% heading (0.001), days to maturity (0.006), number of effective tillers per plant (0.277), grain weight per spike (0.922), harvest index (0.117) and number of grains per spike (0.037).

Positive and non significant phenotypic correlation was observed for 100 grain weight (0.054) on grain yield per plant. Positive direct effect (0.0016) was observed for 100 grain weight on grain yield per plant whereas, positive indirect effect was observed with day to 75% heading (0.0003), days to maturity (0.0026), plant height (0.0027), number of effective tillers per plant (0.0109) spike length (0.0010) and harvest index (0.0338) while negative indirect effect was observed for grain weight per spike (-0.0016) and number of effective tillers per plant (-0.0007).

Harvesting index

There were positive and highly significant genotypic correlation harvest index (0.554) on grain yield per plant. Path analysis indicated the negative direct effect for harvest index on grain yield per plant (-1.744) while, negative indirect effect was exhibited for spike length (-0.169) and number of grains per spike (-0.650). Positive indirect effect was observed for day to 75% heading (0.005), days to maturity (0.0053), plant height (0.081), number of effective tillers per plant (0.564), grain weight per spike (2.313) 100 grain weight (0.070) and biological yield per plant (0.031).

There were positive and highly significant phenotypic correlation harvest index (0.520) on grain yield per plant. Path analysis indicated the positive direct effect for harvest index on grain yield per plant (0.6021) while, negative indirect effect was exhibited for day to 75% heading (-0.0003), plant height (-0.0085), grain weight per spike (-0.0026) and biological yield per plant (-0.1187). Positive indirect effect was observed for days to maturity (0.0052), number of effective tillers per plant (0.0285), spike length (0.0024), 100 grain weight (0.0001) and number of grains per spike (0.0094).

Biological yield per plant

Positive and highly significant genotypic correlation was observed for biological yield per plant (0.777) on grain yield per plant. Negative direct effect (-0.306) was observed for biological yield per plant on grain yield per plant whereas, positive indirect effect was observed with day to 75% heading (0.026), days to maturity (0.192), number of effective tillers per plant (0.046), grain weight per spike (2.370) and harvest index (0.177) while, negative indirect effect was exhibited via plant height (-0.391), spike length (-0.527), 100 grain weight (-0.144) and number of grains per spike (-0.667).

Positive and highly significant phenotypic correlation was observed for biological yield per plant (0.723) on grain yield per plant. Positive direct effect (0.7179) was observed for biological yield per plant on grain yield per plant whereas, positive indirect effect was observed with day to 75% heading (0.068), days to maturity (0.0082), number of effective tillers per plant (0.0533), spike length (0.0114), 100 grain weight (0.0000) and number of grains per spike (0.0101) while, negative indirect effect was exhibited via plant height (-0.391), spike length (-0.527), 100 grain weight (-0.144) and number of grains per spike (-0.667).

Number of grains per spike

Positive and highly significant genotypic correlation was observed for number of grains per spike (0.985) on grain yield per plant. Negative direct effect (-0.959) was observed for number of grains per spike on grain yield per plant whereas, positive indirect effect was observed with day to 75% heading (0.017), days to maturity (0.123), number of effective tillers per plant (0.522), grain weight per spike (3.306) and 100 grain weight (0.040) while, negative indirect effect was exhibited via plant height (-0.146), spike length (-0.523), harvest index (-1.182) and biological yield per plant (-0.212).

Positive and highly significant phenotypic correlation was observed for number of grains per spike (0.642) on grain yield per plant. Positive direct effect (0.0227) was observed for number of grains per spike on grain yield per plant whereas, positive indirect effect was observed with day to 75% heading (0.051), days to maturity (0.0057), plant height (0.0064), number of effective tillers per plant (0.0250), spike length (0.0132), 100 grain weight (0.0000), harvest index (0.2497) and biological yield per plant (0.3202) while, negative indirect effect was exhibited via grain weight per spike (-0.0085).

The positive residual effect observed in the path analysis suggests that certain crucial yield-contributing traits, whether genetically (0.1154) or phenotypically (0.2219), were not considered in the study. Therefore, it is recommended to include these traits in future investigations, alongside the attributes that contribute to high yield potential. This will allow for a more comprehensive analysis of the factors influencing yield and enable a better understanding of how to improve and optimize yield outcomes.

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CHAPTER - V

DISCUSSION

To build the groundwork for a successful crop improvement programme, it is crucial to have a thorough understanding of the numerous genetic features of a crop in the ecosystems where it will be cultivated. In order to design a successful breeding program that will result in the development of superior strains or varieties through effective and efficient manipulation of the genetic variability that is currently available, it is necessary to have knowledge about the inheritance of quantitative traits, identification of superior parents and best crosses on the basis of combining ability, nature, and magnitude of heterosis for important characters. Barley, a crop with a rich historical background, has been cultivated in challenging environments characterized by poor soil fertility and limited moisture availability, especially in rainfed conditions. Due to its autogamous nature, where self pollination is common, barley populations have a narrow genetic foundation and are predominantly homozygous.

The effectiveness of plant breeding research to improve existing crops primarily depends on:

1. Creation or assembly of variable genotypes.
2. Selection of superior genotypes from gene pool
3. Utilization of selected genotypes to develop superior varieties over the existing ones

Kempthorne (1956) supported the idea of independent gene distribution, which can be challenging to establish. He also proposed that removing any specific array of genes is undesirable when breeders are primarily interested in a particular group of parents selected for their desired traits. The outcomes obtained in such scenarios are limited to the specific material being studied, as seen in the present case, as discussed by Gilbert (1958) and Hayman (1958). Hence, a study was conducted to investigate the characteristics of genetic variation, combining ability, heterosis, heritability, genetic advance, correlation coefficients, and path analysis in diallel crosses for both yield and yield related traits in barley (*Hordeum vulgare* L.). This research aimed to contribute to crop improvement efforts for barley. Various biometrical approaches have been employed to evaluate the worth of parental material by assessing components of variation and combining ability variances and their effects. One commonly used methodology for studying the genetic aspects of quantitative traits is diallel analysis. This approach allows for a systematic investigation of the genetic study of such characters. It originated from the early work of Schmidt (1919), Yates (1947), and Mather (1949), and developed through the studies made by Griffing (1956a), Jinks and Hayman (1953), Hayman (1954a & 1954b), Jinks (1954), and Hayman (1958a).

The diallel cross analysis technique was initially introduced by Jinks and Hayman (1953) and further expanded upon by Hayman (1954) and Hayman (1956a, 1956b). These researchers highlighted the strength of this method in studying both qualitative and quantitative systems, as it provides valuable genetic information that can be used to develop superior genotypes with a wide range of desirable traits. The diallel cross analysis technique has proven to be a powerful tool in genetic research and crop improvement endeavors.

The diallel cross analysis relies on a set of assumptions established by Hayman (1954b). These assumptions are fundamental to the methodology and encompass the following principles:

1. It is essential that the parents involved are individuals with a homozygous diploid (2n) genotype,

2. Reciprocal differences should not exist,
3. There are no epistasis or non-allelic interactions between genes,
4. The absence of multiple allelism, meaning that each gene under consideration has only two possible alleles,
5. The genes are equally distributed among the parents involved in the cross,
6. There is no genetic linkage between the genes under study.

Since genetic variability management and characterization are essent ial to crop improvement quantitative characterization of crop variability is necessary. The utilization of genetic variation in crop improvement is influenced by the presence of fixable and non fixable variation. Furthermore, the development of desirable traits in crops is influenced by the nature of gene expression and the magnitude of genetic variability. These factors play a significant role in determining the appropriate breeding methodology to be employed

The present experiment was carried out during the *Rabi* 2022-23 at the Crop Research Farm, Nawabganj of C.S. Azad University of Agriculture and Technology, Kanpur-208002 (U.P.). The experiment involved eight genetically diverse parent plants that exhibited a wide range of variation. Total of 28 crosses derived from these parents were selected for further investigation. In the *Rabi* season of 2022-2023, the final experimental material, consisting of the selected crosses, was evaluated using a randomized block design with three replications.

5.1. ANALYSIS OF VARIANCE

The present study primarily focused on understanding the nature of gene action within a carefully selected group of materials. Its implications were significant in formulating appropriate breeding programs and facilitating the development of desired genotypes. This investigation played a major role in utilizing the studied materials and achieving the goal of creating improved crop varieties.

The analysis of variance revealed highly significant values among the treatments and parents for all the characters, indicating appreciable variability (Table 1). Parents and F_1s indicated highly significant differences for all the characters except biological yield per plant in parents; number of effective tillers per plant and grain yield per plant in F_1s. The parents vs F_1s, exhibited highly significant differences for all the characters except number of effective tillers per plant and 100 grain weight indicating much variability in parents as well as in crosses. The variance due to replication was found non significant for all attributes except days to75% heading and days to maturity. The selection of parents based on morphological differences was validated by analysis of variance. Similar findings were also reported by **Akaksh *et al*. (2012), Patial *et al*. (2016), Ram and shekhawat (2017), Gupta *et al*. (2018), Nagesh (2019), Devi *et al.* (2020), Naresh and Kumar (2023).**

5.2. MEAN AND VARIBILITY

The mean performance of F_1s was higher than parents for all the attributes, *viz*., days to 75% heading, days to maturity, plant height (cm), the number of effective tillers per plant, spike length (cm), the number of grains per spike, grain yield per plant (g), 100 grain weight (g), biological yield per plant, and harvesting index (%), grain weight per spike (g). Similarly, ranges were also higher in F_1, than parents except for number of effective tillers per plant, number of grains per spike, grain weight per spike and grain yield per plant which showed less mean value than parent (Table 2).

5.3. GENETIC COMPONENTS ANALYSIS

The regression coefficient of 'b' deviated significantly from unity for plant height. The significant deviation of regression coefficient from unity indicating non-allelic gene action, while the regression coefficient was not deviated significantly from unity indicating additive gene action (Table 3).

The regression coefficient of ‘b’ deviated significantly from zero for days to 75% heading, number of effective tillers per plant, grain weight per spike and grain yield per plant indicating the presence of additive gene action.

The validity of assumptions concerning to diallel cross analysis in the present investigation was tested by "t^2" test (Hayman, 1954). Significant values of "t^2" (Table 3) for eight out of 11 attributes in F_1, generation indicated validity of hypothesis. Significant values of "t^2" of days to 75% heading, plant height and grain weight per spike were indicating the failure of one or more assumptions of diallel analysis which might be due to sampling error.

The genetic components of variance of different attributes of barley were estimated using "diallel" mating design with two approaches, genetic component and combining ability. Analysis of genetic component revealed presence of both additive ($\hat{D}$) as well as dominance ($\hat{H}_1$ and $\hat{H}_2$) genetic components for all the attributes. The highly significant value of additive genetic component ($\hat{D}$) was observed for all characters except plant height and biological yield per plant, indicating additive gene action for the expression of these characters However, dominance genetic variances were highly significant to all the characters. Thus, both the additive and non additive genetic components were responsible for the expression of these quantitative characters Similar findings were also reported by **Varzaru *et al.* (2012), Mishra (2018), Mustafa (2018), Patial *et al* (2018), Bocianowski *et al.* (2019), Assefa and Labuschagne (2022), Sharma *et al*. (2023)**

The values of $\hat{H}_1$ component were observed higher than the values of $\hat{H}_2$ for all the attributes, which indicating unequal distribution of positive and negative alleles were observed for days to 75% heading, days to maturity, plant height, number of effective tillers per plant, spike length, number of grains per spike, grain weight per spike, 100 grain weight, biological yield per plant, harvest index and grain yield per plant, indicating unequal distribution of positive and negative alleles in the parent.

The positive and significant value of $\hat{F}$ component the dominant genes were frequently distributed than the recessive genes for all the attributes.

Positive and highly significant values of $\hat{h}^2$ estimates were observed for all attributes except 100 grain weight. The positive and significant values of $\hat{h}^2$ indicated presence of dominance genes. Similar finding was also reported by **Elkadar *et al.* (2018).**

The values of average degree of dominance $(\hat{H}_1/\hat{D})^{0.5}$ were recorded more than unity for all the attributes indicating over dominance for controlling these characters.

The proportion of genes with positive and negative effects $(\hat{H}_2/4\hat{H}_1)$ was less than the theoretical value (0.25) for all the traits indicating asymmetrical distribution of positive and negative alleles among the parent.

The ratio of dominant and recessive genes $[(4\hat{D}\ \hat{H}_1)^{0.5} + F/ (4\hat{D}\ \hat{H}_1)^{0.5} - F]$ in the parents was observed more than unity for all attributes more than unity indicated distribution of dominant genes for all the attributes.

The Ratio of $\hat{h}^2/\hat{H}_2$ was obtained less than unity for all the attributes except plant height, number of effective tillers per plant, spike length, number of grains per spike, grain weight per spike, grain yield per plant and biological yield per plant which indicates that the frequent involvement of single gene group for inheritance of traits and it may be due to complementary gene interaction causing depression in ratio.

5.4. COMBINING ABILITY

Combining ability analysis was a valuable tool in screening desirable strains and their cross combinations for effective utilization. It provides essential information necessary to develop a systematic breeding program aimed at achieving rapid and sustained improvement. The present study revealed significant contribution of both the additive and non-additive components of genetic variance for all the characters (Table 5).

The mean sum of squares due to general combining ability (GCA) were observed highly significant for all the attributes studied except number of effective tillers per plant and biological yield per plant. Similarly, the mean sum of squares due to specific combining ability were observed highly significant for all the characters except number of effective tillers per plant in F_1 generation indicating that additive as well as non-additive genetic effects in determining the attributes. Genetic components analysis also indicated predominance of non-additive genetic estimate for all the characters. Similar result also was reported by **Jain and sastry (2012), Pawar and Singh (2013), Katiyar *et al.* (2021) and Tokhetova *et al.* (2022)** also reported most of traits significant.

The ratio of the average degree of dominance $(\hat{\sigma}^2 s/\hat{\sigma}^2 g)^{0.5}$ were observed to be greater than one for all the characters. Indicating a significant contribution of non-additive genetic variance in the expression of all the attributes.

The aforesaid analysis involves *per se* performance, GCA and SCA effects to determine the potentiality of parents or crosses for mobilizing them in an efficient hybridization programme (Table 7 and 8). The different standard methods for combining ability estimates (**Griffing, 1956b; Kempthorne, 1957; Kempthorne and Curnow, 1961; Fyfe and Gilbert, 1963; Gardner and Eberhart, 1966)** may or may not be compatible with one another with equal weightage and in the same order of ranking. On the other hand, a plant breeder is mainly concerned with relative ranking coupled with desirable and significant combining abilities rather than absolute values.

General combining ability (GCA) effects

The GCA effects include both additive and additive x additive interaction components of genetic variability (**Griffing, 1956b; Sprague, 1966**) which represents predictable (fixable) genetic variance as also reported by **Gilbert (1967).** The additive parental effects as measured by GCA effects are of practical use, whereas non-allelic interactions are unpredictable and cannot be easily manipulated.

Considering GCA effects, good general combiners were; KB 1425 and KB 1762 for days to 57% flowering; KB 1762 and KB 1506 for days to maturity; RD 2907 and DWRB 137 for plant height; KB 1506 and DWRB 137 for the number of effective tillers per plant; DWRB 137 for spike length; KB 1634 and DWRB 137 for the number of grains per spike; KB 1634, HUB 113 and DWRB 137 for grain weight per spike; RD 2907 and KB 1634 for 100 grain weight; K603 and KB 1762 for biological yield per plant and HUB 113 and KB 1634 for harvesting index; KB 1634 and HUB 113 for grain yield per plant.

Specific combining ability (SCA) effect

Grafius (1959) proposed that the existence of a specific gene system solely responsible for yield might be a misconception. Some researchers found that the genetic basis for high Specific Combining Ability (SCA) in complex traits could be explained by the interaction of different components of directly and indirectly related traits on the phenotypic level. Generally, SCA effects do not significantly contribute to improving self-fertilizing crops unless there is potential for exploiting heterosis commercially. Breeders are usually interested in obtaining transgressive offspring through crosses to produce homozygous lines in self-pollinated crops such as barley. **Jinks and Jones (1958)** highlighted that the superiority of hybrids might be attributed to their ability to generate transgressive offspring through the interaction of heterosis and non-additive gene effects. Based on the analysis of specific combining ability (SCA) effects and the individual performance of the crosses, as presented in Tables 6, the following findings were observed:

Based on *per se* performance and significant SCA effects, the following cross combination emerged as promising combiners: KB 1762 X KB 1634 , KB 1425 X K603, RD 2907 X K 603, KB 1506 X DWRB 137 AND HUB 113 X DWRB 137 for days to75% heading; KB 1634 X DWRB 137 and KB 1762 X K 603 for days to maturity; RD 2907 X K 603, HUB 113 X K 603, KB 1506 X KB 1762 , KB 1762 X HUB 113 and RD 2907 X KB 1425 for plant height; KB 1425 X KB 1634 for number of effective tillers per plant; KB 1762 X DWRB 137 , RD 2907 X KB 1634, KB 1425 X KB 1762, KB 1506 X K603 and KB 1506 X KB 1634 for spike length; KB 1425 X K603 , KB 1762 X DWRB 137, RD 2907 X K 603, RD 2907 X DWRB 137 and KB 1762 X KB 1634 for number of grains per spike; KB 1425 X K603, KB 1762 X K 603, KB 1506 X K 603, KB1425 X KB 1506 and KB1425 X KB 1634 for grain weight per spike; KB 1506 X K603, RD 2907 X KB 1762, KB 1634 X K 603, KB 1634 X HUB 113 and KB 1425 X DWRB 137 for 100-grain weight; KB 1425 X K603, KB 1425 X KB 1762 and KB 1762 X DWRB 137 for biological yield per plant; HUB 113 X K603, KB 1425 X K603 and KB 1425 X KB 1634 for harvesting index; HUB 113

X K 603, KB1425 X K 603 AND KB 1425 X KB 1634 for grain yield per plant.

Based on their individual performance, the top three crosses were KB 1425 X KB 1634, KB 1425 X K603, and KB 1762 X KB 1634. the cross KB 1425 X KB 1634 observed superior performance in traits such as the number of productive tillers per plant, number of grains per spike, grain weight per spike, grain yield per plant, 100-grain weight, and harvesting index. For traits like days to 75% heading, ear length, number of grains per spike, grain weight per spike, and harvesting index, the cross KB 1425 X K603 exhibited remarkable performance. Lastly, the cross KB 1762 X KB 1634 exhibits notable performance in traits including days to 75% heading, ear length, number of grains per spike, grain weight per spike, and biological yield per plant. these top-performing crosses show great potential and can be considered for further breeding and selection in order to enhance the desired traits.

5.5. HETEROSIS

Heterosis breeding play an important role in crop improvement for obtaining high degree of productivity. The primary step in the exploitation of heterosis is to know its magnitude and direction in both directly and indirectly components related to productivity in particular crop of economic value.

The hybrid vigour has not widely been exploited in self-pollinated crops except paddy in China and Japan. In barley, it is due to non-availability of stable male sterile lines on commercial scale.

The estimates of heterosis over F_1 hybrids in real sense decide whether the hybrid is worth exploiting or not, though, the production of hybrid seed is technically feasible (**Briggle, 1963**), yet the practical approach of this concept needs further exploration and perfection.

Heterosis was calculated in per cent over economic parent (KB 1425) in F_1 generation for all eleven characters. Estimates of heterosis are presented in Table 8. Negative and significant values of heterosis were considered desirable for days to 75% heading, days to maturity and plant height, on the other hand positive and significant values were considered desirable for remaining characters.

Significant and desirable heterosis over economic parent were observed in nine crosses for days to 75% heading; four crosses for days to maturity; five crosses for plant height; no any crosses for number of effective tillers per plant; seven crosses for spike length; five crosses for number of grains per spike; two crosses for grain weight per spike; no any crosses for 100-grain weight; two crosses for Biological yield per plant; five crosses for harvesting index; two crosses for grain yield per plant. This conclusion was supported by **Habouh (2019), Panwar *et al.* (2022) and Akashdeep *et al.* (2021).**

In the present investigation, economic heterosis ranged from -4.4 (RD 2907 X KB 1634) to 23.09 (KB 1506 X K 603) per cent for grain yield per plant. The cross combinations, *viz*., KB 1506 X K 603 and KB 1425 X KB 1634 with positive and significant values were in the order of merit for grain yield per plant. Cross combination KB 2907 X K 603 was also exhibited desirable heterosis for days to 75% heading, plant height and number of grains per spike. KB 1425 X KB 1634 was also exhibited desirable heterosis for days to 75% heading, grain weight per spike and grain yield per plant; KB 1506 X K 603 was also exhibited desirable heterosis for spike length, biological yield per plant and grain yield per plant; KB1762 X KB 1634 days to 75% heading, number of grains per spike and biological yield per plant.

In barley, heterosis is a complicated phenomenon that depends on the distribution of genes in the parental lines, the balance of additive and dominance components, and their interactions. The over-dominance effect of the parent in this present investigation was indicated by the positive and significant values.

5.6. SELECTION PARAMETER

(A) HERITABILITY AND GENETIC ADVANCE

Estimates of heritability provide information about the transmissibility of characters from parents to offspring. This facilitates the evaluation of hereditary and environmental influences in phenotypic variation and helps in determining selection intensity. The important function of heritability is its predictive role in expressing the precision of the phenotypic value as a guide to the breeding value. Only the phenotypic values of individuals can be directly measured but it is the breeding value that determines their effect on the next generation. Therefore, if the breeder or experimenter selects individuals to be parents based on their phenotypic values, his success in altering the characteristics of the population can be predicted only from the knowledge of the degree of correspondence between phenotypic values and breeding values. This degree of correspondence is measured by heritability, as the following considerations be display:

According to **Falconer (1986),** The heritability in narrow sense is refers as the proportion of additive variance to phenotypic variance.

The efficiency of selection depends upon the transmissibility of characters from parents to offspring. Though the estimates of heritability in biometrical investigations were affected by the method of estimation, the generation of study, sample size and environments even though it helps the breeders during selection **(Hanson, 1963)**. **Kempthorne and Curnow (1961)** classified narrow sense heritability as low when less than 10 percent, medium when between 10-30 percent, and high when greater than 30 percent.

Moderate heritability was observed for harvesting index, 100 grains weight, plant height, days to 75% heading and spike length while low heritability was recorded for days to maturity, number of effective tillers per plant, grain weight per spike, biological yield per plant, and number of grains per spike (Table 9). On other handed none of the character was showed high heritability. These findings partially supported by the work of **Sravani, *et al*. (2018), Devi *et al.* (2020) and Tehulie (2022).**

High genetic advance in per cent over the mean was observed for grains per spike and grain weight per spike whereas moderate genetic advance in per cent over the mean was exhibited for Spike length, grain yield per plant, biological yield per plant, and plant height. Low genetic advance values in per centage over the mean was observed for harvesting index, number of effective tillers per plant, 100 grain weight, days to 75% heading, and days to maturity. Such reports giving by **Dinsa *et al.* (2018), Gupta *et al.* (2018) and Shiferaw *et al.* (2020).**

4.7. GENOTYPIC AND PHENOTYPIC COEFFICIENT OF VARIANCE

The effectiveness of plant selection in enhancing plant characteristics primarily relies on the existence of significant genetic diversity. Genetic diversity serves as the fundamental foundation of a plant breeding program, enabling the generation of superior genotypes through the process of selection. To assess and compare the nature and extent of variability in breeding materials for various traits, the phenotypic and genotypic coefficients of variation can be utilized.

GCV and PCV were categorized into three classes, viz., low (less than 10%), moderate (10-20%) and high (more than 20%) for 11 characters of 36 genotypes, estimates of direct selection parameters, and coefficients of variation, were computed. The phenotypic and genotypic coefficient of variation for all 11 characters has been given in Table 9.

Moderate values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in per cent were recorded for spike length, grain weight per spike, and number of grains per spike; modarete PCV with low GCV were observed for number of effective tillers per plant, grain yield per plant, and biological yield per plant while low values GCV and PCV were exhibited for harvesting index, plant height, 100-grains weight, days to 75% heading, and days to maturity. Notably, no traits were associated with a high genetic coefficient of variation. Similar findings were documented by **Gupta *et al.* (2018), Yadav *et al.* (2019), Sootrakar *et al.* (2020)**

4.8. CORRELATION COEFFICIENT

Indirect selection is more effective than direct selection procedure when the attribute in question has low heritability and/or is not easily and precisely measured. The aim of correlation studies is primarily to know the suitability of various characters for indirect selection because selection for one or more traits results in correlated response for several other traits (**Searle, 1965**), and the pattern of variation will also be changed (**Waddington and Robertson, 1966**). Therefore, knowledge of genetic correlation existing between yield and its components is essential.

All possible phenotypic and genotypic correlations were worked out for 11 characters (Table 10) in eight parents, 28 F_1s, though, the significance of genotypic correlations could not be tested as no suitable statistical test is available (Nasr et al. 1973) yet their magnitude is considered in relation to the corresponding phenotypic estimates **(Fisher, 1918).** The magnitudes of phenotypic correlation were greater than genotypic correlations coefficients in parents and F_1s for all the traits except in few combinations.

Highly significant and positive phenotypic correlations were observed between grain yield per plant and grain weight per spike, number of grains per spike, biological yield per plant, spike length, plant height, harvesting index, days to maturity, number of productive tillers per plant, and days to 75% heading. On the other hand, non-significant correlation was observed with 100 grain weight, suggesting that it may not play a significant role in determining the overall yield.

Highly significant and positive correlation at the phenotypic level was observed for spike length with grain yield per plant, grain weight per spike, biological yield per plant, number of grains per spike, plant height, number of effective tillers per plant, days to maturity and days to 75% heading.

At the phenotypic level highly significant and positive correlation was observed for grain weight per spike with gains yield per plant, number of grains per spike, spike length, biological yield per plant, harvest index, number of effective tillers per plant, plant heigh, days to maturity, 100-grain weight and days to 75% heading.

Highly significant and positive correlation at phenotypic level was observed for 100 grain weight with number of effective tillers per plant and grain weight per spike

highly significant and positive correlation was observed for harvest index with number of grains per spike, grain weight per spike, number of effective tillers per plant and gains yield per plant.

Number of grains per spike was highly significant and positively correlated with gains yield per plant, grain weight per spike, spike length, biological yield per plant, harvest index, number of effective tillers per plant, plant height and days to maturity. **Kumar *et al.* (2018), Gupta *et al*. (2018) and dido *et al.* (2020)** was observed significant positive association of grain yield with different character**.**

4.9 PATH COEFFICIENT ANALYSIS

Correlation coefficient measures the degree and direction of association between two
characters. However, this may not give true picture under complex situation. Thus, it becomes necessary to perform path coefficient analysis.

Path coefficient analysis is a tool to partition the observed correlation coefficient into direct and indirect effects of yield components on grain yield to provide clear picture of attributes associations for efficient selection strategy.

The direct and indirect effects in F_1 generation of different attributes on grain yield at genotypic level given in Table- 11 (a) and (b).

At phenotypic level, the path coefficient analysis was observed positive direct effects on grain yield per plant for days to 75% heading, days to maturity, plant height, number of effective tillers per plant, spike length, 100 grain weight, harvest index and number of grains per spike.

At genotypic level, the path coefficient analysis was observed positive direct effects on grain yield per plant for days to 75% heading, days to maturity, number of effective tillers per plant and grain weight per spike.

The path coefficient analysis was observed positive direct effects at genotypic and phenotypic level for days to 75% heading, days to maturity, number of effective tillers per plant and grain weight per spike. Similar finding also reported by **Singh *et al*. (2014), lodhi *et al*. (2015), Matin *et al*. (2019), Gupta et al (2022)** for direct effect of all traits on grain yield.

SUGGESTION REGARDING BREEDING METHODOLOGY

Breeding procedure like pedigree method can be utilized to exploit additive genetic variance in improvement of the characters; the presence of non additive gene action necessitates the maintenance of heterozygosity in the population. The breeding methods like bi-parental mating followed by recurrent selection may increase rate of genetic improvement for these characters.

Most of the crosses exhibited a favourable level of significant economic heterosis in nearly all traits, except few. Therefore, employing heterosis breeding techniques can fully exploit the potential of these specific characteristics.

Moderate heritability and high or moderate genetic advance for a character indicates that the character will respond to selection and selection may be profitable. Characters were moderate heritability coupled with moderate genetic advance, so due consideration should be given to these traits at the time of selection.

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CHAPTER - VI

SUMMARY AND CONCLUSION

The present investigation **" Studies on genetical parameters for grain yield and its contributing traits in barley (*Hordeum vulgare* L.)"** was carried out with 36 genotypes involving 8 diverse parents and their 28 F_1s straight crosses which were developed from an 8 x 8 parent diallel cross mating design in barley.

The experiment with 36 genotypes was performed in complete randomized block design with three replications during 2022-2023 at Crop Research Farm, Nawabganj of C. S. Azad University of Agriculture and Technology, Kanpur, 208002 (Uttar Pradesh), India. The observations were recorded on 11 attributes namely, days to 75% heading, days to maturity, plant height, number of effective tillers per plant, spike length, number of grains per spike, grains weight per spike, 100-grain weight, biological yield per plant, harvest index and grain yield per plant.

The data recorded on the characters were subjected to different statistical and biometrical calculations i.e. analysis of genetic variance, genetic component analysis, combining ability analysis, heterotic parameters along with their effects and selection parameters *viz.*, estimates of heritability, expected genetic advance, correlation and path coefficients.

Analysis of variance indicated highly significant differences among the treatments for all the traits like, days to 75% heading, days to maturity, plant height, number of effective tillers per plant, spike length, number of grains per spike, grains weight per spike, 100-grain weight, biological yield per plant, harvest index, and grain yield per plant the orthogonal break up namely, parents and F_1s, revealed highly significant differences for all the characters studied except biological yield per plant in parents; number of effective tillers per plant and grain yield per plant in F_1s. Parents Vs F_1s revealed highly significant differences for all the attributes except number of effective tillers per plant and 100 grain weight showing considerable amount of heterotic response in these traits.

The mean performance of F_1s was higher than parents for all the attributes. Similarly, ranges F_1 were also higher than parents except for number of effective tillers per plant, number of grains per spike, grain weight per spike and grain yield per plant which showed less range value than parent.

The regression coefficient of ‘b’ deviated significantly from zero for days to 75% heading, number of effective tillers per plant, grain weight per spike and grain yield per plant and significantly from unity for plant height indicating the involvement of non allelic gene action interaction.

Significant values of "t^2" for eight out of 11 attributes in F_1, generation indicated validity of hypothesis. Significant values of "t^2" of days to 75% heading, plant height and grain weight per spike were indicating the failure of one or more assumptions of diallel analysis which might be due to sampling error.

Analysis of genetic component revealed presence of both additive ($\hat{D}$) as well as dominance ($\hat{H}_1$ and $\hat{H}_2$) genetic components for all the attributes. The highly significant value of additive genetic component ($\hat{D}$) was observed for all characters except plant height and biological yield per plant, indicating additive gene action for the expression of these characters However, dominance genetic variances were highly significant to all the characters. Thus, both the additive and non-additive genetic components were responsible for the expression of these quantitative characters

The estimates of $\hat{h}^2$ were observed positive and significant in all the attributes except 100 grain weight, indicating presence of dominance for these attributes.

The estimates value of Ê components were found positive and significant for biological yield per plant, harvest index, grain yield per plant number of effective per plant and days to maturity, indicating these attributes were highly effected environment.

The ratio of average degree of dominance $(\hat{H}1/\hat{D})^{0.5}$ reflects presence of over dominance for all the traits. The asymmetrical distribution of positive and negative alleles was observed among the parents for all the traits except spike length.

Dominant gene were more frequently distributed than the recessive ones for all the attributes. One major genes group was responsible for controlling the inheritance for all the traits it may be due to complementary gene interaction.

Combining ability study revealed highly significant variances for general combining ability as well as specific combining ability in respect of all the characters except number of effective tillers per plant; biological yield per plant in only GCA.

On the basis of GCA effect and *per se* parents namely; KB 1762 for days to 57% flowering; KB 1762 for days to maturity; RD 2907 and DWRB 137 for plant height; KB 1506 for the number of effective tillers per plant; DWRB 137 for spike length; KB 1634 and DWRB 137 for the number of grains per spike; KB 1634, HUB 113 and DWRB 137 for grain weight per spike; RD 2907 for 100 grain weight; none cross for biological yield per plant HUB 113 and KB 1634 for harvesting index; KB 1634 for grain yield per plant These parents could be exploited further in breeding programme for simultaneously improved in grain yield and quality attributes.

Based on per se performance and significant SCA effects, the following cross combination emerged as promising combiners: KB 1762 X KB 1634 , KB 1425 X K 603, RD 2907 X K 603, KB 1506 X DWRB 137 AND HUB 113 X DWRB 137 for days to75% heading; KB 1634 X DWRB 137 and KB 1762 X K 603 for days to maturity; RD 2907 X K 603, HUB 113 X K 603, KB 1506 X KB 1762 , KB 1762 X HUB 113 and RD 2907 X KB 1425 for plant height; KB 1425 X KB 1634 for number of effective tillers per plant; KB 1762 X DWRB 137 , RD 2907 X KB 1634, KB 1425 X KB 1762, KB 1506 X K 603 and KB 1506 X KB 1634 for spike length; KB 1425 X K 603 , KB 1762 X DWRB 137, RD 2907 X K 603, RD 2907 X DWRB 137 and KB 1762 X KB 1634 for number of grains per spike; KB 1425 X K 603, KB 1762 X K 603, KB 1506 X K 603, KB 1425 X KB 1506 and KB 1425 X KB 1634 for grain weight per spike; KB 1506 X K 603, RD 2907 X KB 1762, KB 1634 X K 603, KB 1634 X HUB 113 and KB 1425 X DWRB 137 for 100-grain weight; KB 1425 X K 603, KB 1425 X KB 1762 and KB 1762 X DWRB 137 for biological yield per plant; HUB 113 X K 603, KB 1425 X K 603 and KB 1425 X KB 1634 for harvesting index; HUB 113 X K 603, KB 1425 X K 603 and KB 1425 X KB 1634 for grain yield per plant.

Based on heterosis cross combination were observed for highly grain yield per plant KB 1506 X K 603 AND KB 1425 X KB 1634. It was consider as desirable cross combination.

In the F_1 generation, none of the traits was not showed observed high heritability. Moderate heritability was recorded for harvesting index, 100-grain weight, plant height, grain yield per plant, days to 75% heading and spike length indicating these characters largely governed by additive and non additive gene. Rest of traits were exhibited low heritability values indicating that these traits are primarily influenced by non-additive genes.

High genetic advance in per cent over the mean was observed for grains per spike and grain weight per spike indicating these characters largely governed by additive gene; moderate genetic advance in percent of the mean was exhibited for spike length, grain yield per plant, biological yield per plant and plant height indicating characters are largely governed by additive and non additive gene while rest of traits was observed for low genetic advance.

Moderate values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in per cent were recorded for number of grains per spike, grain weight per spike, and spike length; high PCV with low GCV were observed for number of effective tillers per plant, grain yield per plant, and biological yield per plant while rest of traits observed low PCV and GCV.

The grain yield per plant was highly significant and positively associated with grain weight per spike, number of grains per spike, biological yield per plant, spike length, plant height, harvesting index, days to maturity, number of productive tillers per plant, and days to 75% heading. Selection for these characters would be effective in the improvement of grain yield in barley.

At phenotypic and phenotypic level, the path coefficient analysis was exhibited positive direct effects on grain yield per plant for days to 75% heading, days to maturity, plant height, number of effective tillers per plant, spike length, 100 grain weight, harvest index and number of grains per spike. Therefore, direct selection for these characters would be rewarding for improvement in yield of barley.

Conclusion:

In the present investigation, based on genetic components and combining ability analysis, both additive and non additive gene action were observed for the expression of almost major of the traits, average degree of dominance also supported the gene action through both analysis, keeping in view of the gene action, diallel selective mating recurrent selection followed by inter matting would be helpful for further crop improvement. Combining ability effects indicated that parent KB 1425 was good general combining ability on the basis of GCA effects and *per se* performance for plant height, number of grains per spike, grain weight per spike, 100 grain weight per spike, harvest index and grain yield per plant.

On the basis of SCA effect and *per se* performance cross combination HUB 113 X K 603, KB 1425 X K 603 and KB 1425 X KB 1634 were observed as superior mainly specific combiner for grain yield per plant.

The cross combinations namely, KB1506 X K603 and KB1425 X KB1634 were exhibited desirable heterosis for grain yield per plant.

Low heritability coupled with high genetic advance were observed for grains per spike and grain weight per spike, selection for improvement of such character may be rewarding. Moderate heritability coupled with moderate genetic advance were recorded for plant height, grain yield per plant, and spike length Therefore, consideration should be given for these traits at the time of simple selection.

Phenotypic coefficient of variation (PCV) estimates were found to be slightly higher than their corresponding genotypic coefficient of variation (GCV) estimates for all the characters which indicated the presence of very negligible environmental influence on these characters.

Correlation study revealed that grain yield per plant was positive and significantly correlation of phenotypic level with days to 75% heading, days to maturity, plant height, number of effective tillers per plant, spike length, grain weight per spike, number of grains per spike, biological yield per plant, harvesting index were major yield contributing traits in this investigation.

At the phenotypic level, the path coefficient analysis revealed that the positive direct effect on grain yield per plant was observed for 75% heading, days to maturity, plant height, number of effective tillers per plant, spike length, 100 grain weight, harvest index and number of grains per spike Therefore, direct selection for these characters would be rewarding for improvement of grain yield per plant in barley.

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Allard, R. W. (1956a). The analysis of genetic, environmental interaction by means of diallel crosses. *Genetic* ,**41:** 305-08.

Abdulhamed, Z. A.; Abas, S. A. and Kosaj, K. I. (2022). Genetic and molecular variations using the molecular marker RAPD in barley yield. *International Journal of Agricultural & Statistical Sciences*, **18** (7): 1357-1363.

Abdel-Ghani, A. H. (2013). Selection of high yielding lines from heterogeneous Jordanian barley landraces under well watered and drought stress conditions. *Egyptian Journal of Agricultural Sciences*, **64** (1): 13-29.

Addisu, F. and Shumet, T. (2015). Variability, heritability and genetic advance for some yield and yield related traits in barley (*Hordeum vulgare* L.) landraces in Ethiopia. *International Journal of Plant Breeding and Genetics*, **9** (2): 68-76.

Ahmadi, J.; Vaezi, B. and Pour Aboughadareh, A. (2016). Analysis of variability, heritability, and interrelationships among grain yield and related characters in barley advanced lines. *Genetica*, **48** (1): 73-85.

Aklilu, E.; Dejene, T. and Worede, F. (2020). Genotypic and phenotypic correlation and path coefficient analysis for yield and yield related traits in barley (*Hordeum vulgare* L.) landraces in North Gondar, Ethiopia. *Indian journal of Pure & Applied Biosciences*, **8**: 24-36.

Akgün, N. (2016). Genetic variability and correlation studies in yield and yield related characters of barley (*Hordeum vulgare* L.) genotypes. *Selcuk Journal of Agriculture and Food Sciences*, **30** (2) :88-95.

Akashdeep, K.; Madakemohekar, A.H.; Thakur, G. and Bindal, S. (2021). study of heterosis and combining ability for yield and its component traits in barley (*Hordeum vulgare* L.). *Plant Archives.*, **21** (2): 583-589.

Akanksha; Sirehi, A.; Kumar, S.; kant, S; Pal; Kumar, A. and Singh. M. (2012). Genetic improvement through variability, heritability and genetic advancein barley (*Hordeum vulgare* L.). *environment and ecology*, **30** (4): 1343-1345.

Al-Tabbal, J. A. and Al Fraihat, A. H. (2012). Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Science*, **4**(3): 187-193.

Assefa, A. and Labuschagne, M. T. (2015). Genetic analysis of agronomic traits in barley (*Hordeum vulgare* L.) landrace lines under drained and waterlogged conditions. *Ethiopian journal of crop science*, **4** (1): 15-29.

Al-Jibouri, H. A.; Miller, P. A. and Robinsion, H. F. (1958). Genotypic and environmental variance and covariance in an upland cotton cross of interspecific origin. *Agronomy journal*, **50** (10): 633-636.

Badr, A. and El-Shazly, H. (2012). Molecular approaches to origin, ancestry and domestication history of crop plants: Barley and clover as examples. *Journal of Genetic Engineering and Biotechnology*, **10** (1): 1-12.

Angassa, D. (2021) Genetic Variability of Ethiopian Barley (*Hordeum Vulgare* L.)) Genotypes for Yield and Yield Related Traits. *Plant*, **9**, (4): 101-105.

Baye, A.; Berihun, B.; Bantayehu, M. and Derebe, B. (2020). Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat (*Triticum aestivum* L.) lines. *Cogent Food & Agri*, **6** (1): 175603.

Baik, B. K. and Ullrich, S. E. (2008). Barley for food Characteristics, improvement, and renewed interest. *Journal of cereal science*, **48** (2) :233-242.

Bennett, M. D. and Smith, J. B. (1976). Nuclear DNA amounts in angiosperms. Philosophical Transactions of the Royal Society of London, Series B. Biological Sciences**, 27** (4): 227-274.

Brahim, B. and Mohamed, B. (2014). Analysis of the diallel crosses between six row varieties of durum wheat in semi arid area. *African journal of biotechnology,* **13** (2): 286- 293.

Bocianowski, J.; Warzecha, T.; Nowosad, K. and Bathelt, R. (2019). Genotype by environment interaction using AMMI model and estimation of additive and epistasis gene effects for 1000-kernel weight in spring barley (*Hordeum vulgare* L.). *Journal of applied genetics*, **60**: 127-135.

Bouchetat, F. and Aissat, A. (2019). Evaluation of the genetic determinism of an F_1 generation of barley resulting from a complete diallel cross between autochthones and introduced cultivars. *Heliyon*, **5** (11): 27-44.

Bouchetat, F.; Aissat, A.; Boutellaa, S. and Bellah, S. (2020). Analysis of the main agronomic characters of some barley varieties and the genetic characterization of their descendancy after a full diallel cross. *Acta Scientifica Naturalis***, 7**(1): 98-111.

Calleja, M.; Boutin, C.; Dyrszka, E.; Manès, Y.; Reif, J. C.; Zhao, Y. and Igartua, E. (2023). Identification of adapted breeding lines to improve barley hybrids for Spain. *Crop Science*, **63** (1): 186-203.

Comstock, R. E. and Robinson, H. F. (1952). Genetic parameters, their estimation and significance. Proc. Sixth Intern. *Grassland cong* **1**: 284-291.

Comstock, R. E. and Robinson, H. F. (1948). The components of genetic variance in populations of biparental progenies and their use in estimating the average degree of dominance. Biometrics**, 4** (4): 254-266.

Crumpacker, D. and Allard, R. (1962). A diallel cross analysis of heading date in wheat. Hilgardia, **32**(6): 275-318.

Devi, S.; Kumar, Y.; Bhuker, A. and Niwas, R. (2020). Assessment of genetic variability for metric traits in barley under different sowing conditions. *Forage Res*, **45**: 277-280.

De, L. C. (2020). Edible seeds and nuts in human diet for immunity development. *Int. J. Recent Sci. Res*, **6** (11): 38877-38881.

Dewey, D. R. and Lu, K. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, **51** (9): 515-518.

Dido, Allo A.; M. S. R. Krishna; B. J. K. Singh; Kassahun Tesfaye and Dawit T. Degefu. (2020) "Assessment of variability of yield affecting metric characters in barley (*Hordeum vulgare* L.) landraces. *Research on Crops*, **21** (3): 587-594.

Dido, A. A.; Degefu, D. T.; Assefa, E.; Krishna, M. S. R.; Singh, B. J. K. and Tesfaye, K. (2021). Spatial and temporal genetic variation in

Ethiopian barley (*Hordeum vulgare* L.) landraces as revealed by simple sequence repeat (SSR) markers. *Agriculture & Food Security*, **10:** 1-14.

Dinsa, T.; Mekbib, F. and Letta, T. (2018). Genetic variability, heritability and genetic advance of yield and yield related traits of food barley (*Hordeum vulgare* L.) *Genotypes in Mid Rift Valley of Ethiopia. Adv Crop Sci Tech*, **6** (401): 299-310.

Dyulgerov, N. and Dyulgerova, B. (2020) Variability, heritability, and correlations among grain yield and related traits in hulless barley accessions. *Trakia Journal of Sciences*, **18** (4): 285.

Dyulgerov, N. and Dyulgerova, B. (2021). Variability, correlation, and path coefficient analysis of grain yield and yield-related traits of facultative, barley accessions grown under rainfed conditions. *International Journal of Innovative Approaches in Agricultural Research*, **5** (2): 203-212.

Elakhdar, A.; Kumamaru, T.; Abd El-Aty, M.; Amer, K.; Eldegwy, I.; Elakhdar, I. and Noaman, M. (2017). Inheritance pattern of earliness and yield related-traits in spring barley (*Hordeum vulgare* L.). *Journal of Agricultural Science*, **9** (6): 142- 153.

Fonesca, S. and Patterson, F.L. (1968). Yield component heritabilities and interrelationship in winter wheat (*Triticum aestivum* L.). *Crop Sci*., **8**: 614-617.

Fisher, R. A. and Yates, F. (1938). Statistical tables for biological, agricultural and medical research. Statistical tables for biological, agricultural and medical research, **3**: 1938-2028.

Fotokian, M. H. (2013). Selection of barley advanced lines at rainfed conditions using regression and cluster analysis. *International Journal of Biosciences*, **6 (**4) :80-88.

Farag. H. I. A. (2020). comparative efficiency of breeding methods for selection of improved high yielding genotypes of barley under semiarid regions *egypt. J. Plant Breed***, 24** (1):99– 121.

Feldman, M. and Levy, A. A. (2015). Origin and evolution of wheat and related *Triticeae species*. *Alien introgression in wheat: cytogenetics, molecular biology, and genomics*, **26 :**21-76.

Gilbert, N. E. G. (1958). Diallel cross in plant breeding. *Heredity*, **12** (4): 477-492.

Griffing, J. B. (1956b). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian journal of biological sciences***, 9 (**4): 463-693.

Gocheva, M. and Valcheva, D. (2022). Combining ability of grain weight per spike in spring barley varieties. *Rastenievadni nauki*, **59** (1): 3-6.

Gupta, P. K.; Pandey, A.; Kumar, J. and Bahar, J. (2018). Selection parameters in six rowed exotic barley (*Hordeum vulgare* L.) genotypes. *Society for Advancement of Wheat and Barley Research*, **10** (3): 236-239.

Gupta, P. K.; Malik, P.; Singh, S. K.; Singh, L. and Kumar, S. (2018). Studies on Heritability and Genetic Advance for Seed Yield and Its Component in Barley (*Hordeum vulgare* L.). *Int. J. Pure App. Biosci*, **6** (6): 810-813.

Gupta, C.; Rana, V. and Rana, A. (2022). Selection criteria parameters for improving seed yield in hulled barley (*Hordeum vulgare* L.) under north-western Himalayan conditions: Early selection Indices in barley. *Journal of Cereal Research*, **14** (3): 275-282.

Hailu, A.; Alamerew, S.; Nigussie, M. and Assefa, E. (2016). Phenotypic diversity for qualitative characters of some barley (*Hordeum vulgare* L.) germplasm. *Elixir Agriculture International Journal***, 91**: 38495-38500.

Hashash, E. F. and Agwa, A. M. (2018). Genetic parameters and stress tolerance index for quantitative traits in barley under different drought stress severities. *Asian Journal of Research in Crop Science*, **1**(1): 1-16.

Habouh, M. A. F. (2019) Inheritance of plant height, grain yield and its components in three barley crosses. *Plant Production*, *Mansoura Univ*, **10** (3): 293- 297.

Hayman, B. I. (1954). The theory and analysis of diallel crosses. *Genetics*, **39**: 789-809.

Hayman, B. I. (1954). Interaction, heterosis and diallel crosses. *Genetics*, **42**: 336-355.

Hitaishi, S. K.; Kumar, S.; Choudhary, A. M. and Yadav, C. B. (2019). Worth of genetic parameters to sort out new elite barley lines over heterogeneous environments. *Journal of Pharmacognosy and Phytochemistry*, **8** (3): 332-334.

Hudzenko, V. M.; Polishchuk, T. P.; Lysenko, A. A.; Fedorenko, I. V.; Fedorenko, M. V.; Khudolii, L. V.; Ishchenko, V. A.; Kozelets, H. M.; Babenko, A. I.; Tanchyk, S. P. and Mandrovska, S. M. (2022). Elucidation of gene action and combining ability for productive tillering in spring barley. *Regulatory Mechanisms in Biosystems*, **13** (2): 197-206.

Iannucci, A.; Suriano, S. and Codianni, P. (2021). Genetic diversity for agronomic traits and phytochemical compounds in coloured naked barley lines. *Plants*, **10** (8): 1575.

Jain, S. K. and Sastry, E. V. D. (2012). Heterosis and combining ability for grain yiled and its contributing traits in bread wheat (*Triticum aestivum* L.). *Journal of Agriculture and Allied Science* **1** (1): 17-22.

Jalata, z.; Ayana, A. and Zeleke, H. (2011). Variability, heritability and genetic advance for some yield and yield related traits in Ethiopian barley (*Hordeum vulgare* L.) landraces and crosses. *International Journal of Plant Breeding and Genetics* **5** (1): 44 -52.

Jalata, Z. (2011). GGE-biplot analysis of multi-environment yield trials of barley (*Hordeium vulgare* L.) genotypes in Southeastern Ethiopia highlands. *International journal of plant breeding and genetics*, **5** (1), 59-75.

Jalata, Z.; Mekbib, F. and Lakew, B. (2019). Generation mean analysis of net blotch and scald diseases on barley. *World J. Agric. Res***, 4:** 142-149.

Johnson, H. W.; Robinson, H. F. and Comstock, R. E. (1995). Estimates of genetic and environmental variability in soyabean, *Agron, J.*, **47 (7)**: 314-318.

Johnson, H. W.; Robinson, H. F. and Comstock, R. E. (1955). Genotypic and phenotypic correlations in soybean and their implications in selection. *Agron. J*, **47** (1): 477- 483.

Katiyar, A.; Sharma, A.; Srivastava, A.; Singh, S. and Vishwakarma, S. R. (2020). Heterosis for Yield and Yield Attributing Traits in Barley (Hordeum vulgare L.). *Int. J. Curr. Microbiol. App. Sci*, **9** (10), 248-254.

Katiyar, A.; Sharma, A.; Singh, S.; Srivastava, A. and Vishwakarma, S. R. (2021). Combining ability analysis for yield traits in barley (*Hordeum vulgare* L.). *Electronic Journal of Plant Breeding*, **12** (2): 583-588.

Khatab, I. A.; El-Mouhamady, A. A.; Mariey, S. A. and Elewa, T. A. (2019). Assessment of water deficiency tolerance indices and their relation with ISSR markers in barley (*Hordeum vulgare* L.). *Cur Sci Int*, **8** (1): 83-100.

Kempthorne, O. and Curnow. (1961). The partial diallel cross biometrics, 17(2): 229-250.

Kozachenko, M. and Zimogliad, O. (2022). Definition of performance determinants in spring barley by path analysis. 25 (3): 26 -35.

Kumar, Y.; Sehrawat, K. D.; Singh, J. and Shehrawat, S. (2021). Identification of promising barley genotypes based on morphological genetic diversity. *Journal of Cereal Research* **13** (1): 79-88.

Kumar, M., and Shekhawat, S. S. (2013). Genetic variability in barley (*Hordeum vulgare* L.) *Electronic journal of plant breeding*, **4** (4): 1309-1312.

Kumar, Y.; Kumar, N.; Bishnoi, O. P. and Devi, N. (2018). Estimation of genetic parameters and character association in barley (*Hordeum vulgare* L.) under irrigated condition. *Forage Res***, 44** (1): 56-59.

Kumar, A.; Kishore, N.; Devlash, R. and Singh, G. (2018). Genetic variability and association study in some hulled and hullness genotypes of barley (*Hordeum vulgare* L.) in north western Himalayan region. *Wheat and Barley Research*, **10** (3): 185-189.

Kumari, A.; Vishwakarma, S. R.; Verma, O. P. and Yadav, H. (2019). Assessment of nature and magnitude of genetic variability, heritability and genetic advance for yield component traits of barley. *International Journal of Genetics*, **11** (9): 646 - 649.

Kumari, A.; Vishwakarma, S. R. and Singh, Y. (2020). Evaluation of combining ability and gene action in barley (*Hordeum vulgare* L.) using Line x Tester analysis. *Electronic Journal of Plant Breeding*, **11** (1): 97-102.

Kumari, A.; Vishwakarma, S. R. and Singh, Y. (2020). Evaluation of combining ability and gene action in barley (*Hordeum vulgare* L.) using Line x Tester analysis. *Electronic Journal of Plant Breeding*, **11** (1): 97-102.

Kumari, A. and Vishwakarma, S. R. (2022) Evaluation of correlation and path analysis for yield contributing traits in Barley (*Hordeum vulgare* L.). *Journal of Agricultural Research Advances*, **4** (1): 8-11.

Lal, C.; Shekhawat, A. S.; Singh, J. and Kumar, V. (2018). Study of heterosis in six-rowed barley (*Hordeum vulgare* L.). *Journal of Pharmacognosy and Phytochemistry*, **7** (5): 2287-2292.

Lal, C. (2018). Heterosis and inbreeding depression studies for grain yield and related traits in barley (*Hordeum vulgare* L.) under early and timely sown conditions. *International Journal of Agriculture Sciences*, **10**: 0975-3710.

Lodhi, R.; Prasad, L. C.; Madakemohekar, A. H.; Bornare, S. and Prasad, R. (2015). Study of Genetic parameters for yield and yield contributing trait of elite genotypes of barley (*Hordeum vulgare* L.). *Indian Research Journal of Genetics and Biotechnology*, **7** (1): 17-21.

Madakemohekar, A. H.; Prasad, L. C.; Lal, J. P.; Bornare, S. S. and Prasad, R. (2015). Study of Heterosis and combining ability in exotic and indigenous crosses of barley (*Hordeum vulgare* L.) under rainfed environment. *The Bioscan*, **10** (2): 751-756.

Madakemogekar, A. H.; Talekar, N. S.; Kamboj, A. D. and Thakur, G. (2018). Scope of hulless barley (*Hordeum vulgare* L.) as a nutritious and medicinal food: A review. *Acta Scientific Agriculture*, **2** (12): 11-13.

Madhukar, K.; Prasad, L. C.; Lal, J. P.; Prasad, R. and Chandra, K. (2018). Generation mean analysis for yield and drought related traits in barley (*Hordeum vulgare* L.). *International Journal of Pure and Applied Biological Science*, **6** (1): 1399 -1408.

Madic, M.; Djurovic, D. S.; Knezevic, D. S.; Paunovic, A. S. and Tanaskovic, S. T. (2014). Combining ability for spike traits in a diallel cross of barley (*Hordeum vulgare* L.). *Journal of Central European Agriculture*, **15** (1): 2882-2888.

Malik, P.; Singh, S. K.; Singh, L.; Gupta P. K.; Kumar, S.; Yadav, R. K. and Kumar, A. (2018). Studies on genetic heritability and genetic advance for seed yield and its component in barley (*Hordeum vulgare* L.). *International Journal of Pure and Applied Bioscience* **6 (**6): 810-813.

Matin, M. Q. I.; Amiruzzaman, M.; Billah, M. M.; Banu, M. B.; Nazmun Naher, N. and Choudhury, D. A. (2019) Genetic variability and path analysis studies in barley (*Hordeum vulgare* L.), *Int. J. Appl. Sci. Biotech*, **7** (2): 243-247.

Mareiy, S. A.; Farid, M. A. and Karima, A. R. (2018). Morphological and molecular characterization of some Egyptian barley cultivars under calcareous soil conditions. *Middle East J. Agric. Res*, **7**: 408-420.

Maurer, A.; Draba, V.; Jiang, Y.; Schnaithmann, F.; Sharma, R.; Schumann, E. and Pillen, K. (2015). Modelling the genetic architecture of flowering time control in barley through nested association mapping. BMC genomics, **16** (1): 1-12.

Mansour E. and Moustafa E. S. (2016). Estimation of combining ability and gene action for yield contributing traits in spring barley under normal and salinity conditions. *Egyptian Journal of Agronomy*, **31** (3): 431-83.

Mansour, M. (2017). Genetic analysis of earliness and yield component traits in five barley crosses. *Journal of Sustainable Agricultural Sciences*, **43** (3): 165-173.

Mansour, M.; Elshawy, E. E.: Abdel-Azim, A. M.; Mohdly, B. R. and Hamden, S. (2023). Estimation of Inheritance Leaf Rust, Powdery Mildew, Yield and Yield Components in Barley through Generation Means Analysis. *Asian Journal of Research in Crop Science*, **8** (3): 124-137.

Marzougui, S. and Chargui, A. (2018). Estimation of correlation, regression and heritability among barley (*Hordeum vulgare* L.) accessions. *J. New Sci. Agr. Biotec*, **60**: 3838-3843.

Medimagh, S. and Mansouri, S. (2020) Genetic Analysis for Seed Quality Traits in a Diallel Cross of Spring Barley. *Crop Sci*, **53**: 819-824.

Meena, B. S.; Dashora, A.; Dodiya, N. S.; Kumar, D. and Verma, R. P. S. (2022) Study of Heterosis for Yield and Grain Quality Traits in Barley (*Hordeum vulgare* L.). -Indian Institute of Wheat and Barley Research, **1**: 360-S366.

Moti R. and Shekhawat, A. S. (2015). Genotypic variances and interactions with environments in barley genotypes using half diallele analysis for grain yield and its associate characters. *Forage Research*, **43** (1): 22-25.

Mustafa, K. M.; Ewadh, M. J.; Al-Shuhaib, M. B. S. and Hasan, H. G. (2018). The in-silico prediction of the chloroplast maturase k gene polymorphism in several barley varieties. *Agriculture (Pol'nohospodárstvo)*, **64** (1): 3-16.

Mustafa, K. M. (2018). Estimation Heterosis and Combining Ability for Yield and Yield Contributing Traits in Two-Rowed Barley Using Line X Tester. *Journal of Zankoi Sulaimani*, **2**: 707-716.

Naresh, K. S. and Kumar, Y. (2023). assessment of genetic variability for agronomic and biochemical characters in barley (*Hordeum vulgare* L.). Forage Res., **48** (4): 445-452.

Negash, G.; Lule, D. and Jalata, Z. (2019). Correlations and path Analysis of some quantitative characters in barley (*Hordeum vulgare* L.) landraces in western Oromia, Ethiopia. *African Journal of Plant Science*, **13** (2): 34-46.

Neykov, N.; Doneva, M.; Chavdarov, P. and Alexiev, I. (2022). Correlation, path-coefficient and principal component analysis of yield and some traits related to the productivity of winter barley accessions with Bulgarian origin. *Bulgarian Journal of Agricultural Science*, **28** (4): 658-661.

Panse, V. G. and Sukhatme, P. V. (1967). Statistical method for agriculture work. **2:** 152- 157.

Panwar, D. (2022). Analysis of heterosis in barley (*Hordeum vulgare* L.) for yield, its attributing and quality traits. *the Pharma Innovation Journal*, **11** (4): 1469-1475.

Panwar, D. and Sharma, H. (2019). Study of combining ability analysis in barley (*Hordeum vulgare* L.). *International Journal of Current Microbiology and Applied Sciences*, **8** (12): 3004-3011.

Patial, M.; Pal, D. and Kumar, J. (2016). Combining ability and gene action studies for grain yield and its component traits in barley (*Hordeum vulgare* L.). *SABRAO Journal of Breeding and Genetics*, **48** (1): 90-96.

Patial, M.; Pal, D.; Kapoor, R. and Pramanick, K. K. (2018). Inheritance and combining ability of grain yield. in half diallel barley population. *Wheat and Barley Research*, **10** (3): 173-178.

Pawar, K. K. and Singh, A. K. (2013). Combining ability analysis for grain yield and its attributing traits in barley. *Int. J. Agric. Sc. Vet. Med*, **1** (2): 83-87.

Pesaraklu, S.; Soltanloo, H.; Ramezanpour, S. and Kalateh Arabi, M. (2016). Study of the Inheritability of Morphological Traits in some Barley Genotypes (*Hordeum vulgar* L.) by Analysis Diallel Crosses. *Journal of Crop Breeding*, **9** (22): 41-52.

Preiti, G.; Calvi, A.; Romeo, M.; Badagliacca, G. and Bacchi, M. (2021). Seeding density and nitrogen fertilization effects on agronomic responses of some hybrid barley lines in a Mediterranean environment. Agronomy, **11** (10): 19- 42.

Potla, K. R.; Bornare, S. S.; Prasad, L. C.; Prasad, R. and Madakemohekar, A. H. (2013). Study of heterosis and combining ability for yield and yield contributing traits in barley (*Hordeum vulgar* L.). *The Bioscan*, **8** (4): 1231-1235.

Porumb, J.; Rusu, F. and Tritean, N. (2016). The variability and heritability of some morpho-productive traits of spring barley. *Res. J. Agricult. Sci*, **48** (4): 132-138.

Rathore, R. K. S., & Chauhan, Y. (2017). GCA and SCA effects analysis for grain yield and its quantitative traits in six-rowed barley (Hordeum vulgare L.) in Agra region. *Indian Journal of Scientific Research*, (1): 56-64.

Ram, M. O. T. I. and Shekhawat, A. S. (2017). Genotypic variances and interactions with environments in barley genotypes using half diallel analysis for grain yield and its associate characters. *Forage Res*, **43** (1): 22-25.

Ram, M. (2017). The genetic analysis of combining ability and gene action for yield and its associated traits in Barley (*Hordeum vulgare* L.) *Journal of Progressive Agriculture*, **8** (2): 29-35.

Rahimi Darabad, J.; Rashidi, V.; Shahbazi, H.; Moghaddam Vahed, M. and Khalilvand, E. (2021). Genetic analysis of agronomic traits of barley (*Hordeum vulgare* L.) cultivars under salinity stress using diallel cross. *Plant Genetic Researches*, **7** (2): 83-96.

Raikwar, R. S.; Upadhyay, A. K. and Tyagi P. K. (2014). Heritability and genetic variability for yield components under two regimes of soil in barley (*Hordeum vulgare* L.). *The Bioscan*, **9** (4): 1613-1617.

Raikwar, R. S. and Mishra, A. (2018). Study of Simple Scaling Tests and Gene Effects in Barley (*Hordeum vulgare* L.). *A Journal of Multidisciplinary Advance Research*, **7** (2): 76 – 83.

Raikwar, R. S. (2020). Heterosis and inbreeding depression for yield and its components traits in barley (*Hordeum vulgare* L.). *Indian Journal of Agricultutal Sciences* **90** (2): 307-311.

Robinson, H. F.; Comstock, R. E. and Harvey, P. H. (1949). Estimates of heritability and the degree of dominance in corn. *Res. J. Agricult. Sci*, **4** (1): 353-539.

Saroei, E.; Cheghamirza, K. and Leila Zarei L. (2017) Genetic diversity of characteristics in barley cultivars. *Genetica*, **49**, (2): 495-510.

Sankar, T. V.; Zynudheen, A. A.; Anandan, R. and Nair, P. V. (2006). Distribution of organochlorine pesticides and heavy metal residues in fish and shellfish from Calicut region, Kerala, India. *Chemosphere*, **65** (4), 583-590.

Sharief, A. E.; Attia, A. N.; Saied, M.; El-Sayed, A. A. and Ei-Hag, A. (2011). Agronomic studies on barley yield analysis. *Crop and Enviroment*, **2** (1): 11-18.

Shiferaw, T.; Abate, B. and Lakew, B. (2020). Genetic variability and association of traits in Ethiopian barley (*Hordeum vulgare* L.) genotypes at Holetta, Central Ethiopia. *Journal of Agricultural and Crop Research*, **8** (1): 11-19.

Shen, Y.; Lansky, E.P. and Nevo, E. (2010). Wild barley Harbinger of biodiversity. *Biodiversity*, **11 (**3): 19-25.

Sharma, S. K.; Sharma, A. K.; Sharma, L. D.; Singh, S.; Rajput, A. P. and Yadav, M. (2022). Heterosis investigation in six rowed barley (*Hordeum vulgare* L.). *The Pharma Innovation Journal*, **11** (2): 1842-1846

Sharma, S. K.; Sharma, A. K.; Shekhawat, A. S. and Rajput, S. S. (2023). Nature of gene action for grain yield and its contributing character in Barley (*Hordeum vulgare* L.) under different environmental conditions, *The Pharma Innovation Journal*; **12** (2): 3304-3312.

Shekhawat, A. S.; Singh, J.; Kumar, P. and Kumar, V. (2018). GCA and SCA effects analysis for grain yield and related traits in barley (*Hordeum vulgare* L.) in early and normal sowing conditions. *IJCS*, **6** (5): 1215-1221.

Shiferaw, T.; Abate, B. and Lakew B. (2020) Genetic variability and association of traits in Ethiopian barley (*Hordeum vulgare* L.) genotypes at Holetta. *Cent. Ethio. Jour. Agricl. And Crop Res*, **8** (1): 11-19.

Shoaib, M.; Ayub, M.; Shehzad, M.; Akhtar, N.; Tahir, M. and Arif, M. (2014). Dry matter yield and forage quality of oat, barley and canola mixture. *Pakistan Journal of Agricultural Sciences*, **51** (2): 236-241.

Shrimali, J.; Shekhawat A. S. and Kumari, S. (2017) Correlation and path analysis studies in barley (*Hordeum vulgare* L.) genotypes under normal and limited moisture conditions. *Int. J. Curr. Microbiol .App. Sci*, **6** (8): 1850-1856**.**

Shrimali, J.; Shekhawat, A. S. and Kumari, S. (2017). Genetic variation and heritability studies for yield and yield components in barley genotypes under normal and limited moisture conditions. *Journal of Pharmacognosy and Phytochemistry*, **6** (4): 233-235.

Srivastava, S.; Sirohi, A.; Kumar, S. and Kumar, A. (2012). Correlation and path coefficient studies for yield and yield contributing traits in malt barley (*hordeum vulgare* L). *Internation conference on Agriculture science, science and engineering*, **3** (2): 1-7.

Singh, M. and Singh, R. K. (1973). correlation and path-coefficient analysis in barley (*Hordeum vulgare* L). *Indian Journal of Agricultural Sciences*, **43**(5): 455-458.

Singh, H. C. and Singh, S.K. (2011). Combining ability and heterosis in six rowed barley. *Indian journal of plant genetic resources*, **16** (2): 90-98.

Singh, S. K.; Gupta, P. K.; Singh, L.; Nigam, P.N.; Kumar, j. and Singh, R. (2014). Variability and correlation studies for some quantitative traits in barley (*Hordeum vulgare* L.). *Society for Sci. Dev. in Agric. and Tech*, **9** (1): 219-221.

Singh, S.; Madakemohekar, A. H.; Prasad, L. C. and Prasad, R. (2015). Genetic variability and correlation analysis of yield and its contributing traits in barley (*Hordeum vulgare* L.) for drought tolerance. *Indian Research Journal of Genetics and Biotechnology*, **7** (1): 103-108.

Singh, S.; Prasad, L. C.; Madhukar, K.; Chandra, K. and Prasad, R. (2017). Heterosis and combining ability of indigenous and exotic crosses of barley. *Plant Archives*, **17** (2): 813-820.

Sootrakar, K.; Joshi, R. P.; Payasi, S. K. and Shukla, D. (2020). Genetic Variability and Heritability Studies in Two-Rowed Barley (*Hordeum Vulgare* L.). *International Journal for Research in Applied Science & Engineering Technology*, **45** (98): 2321-9653.

Sravani, M.; Madakemohekar, A. H.; Rajaneesh, K.; Swetha, M.; Kamboj, A. D.; Thakur, G.; Kumar, B. and Nilesh, T. (2018). Evaluation of barley (*Hordeum vulgare* L.) genotypes for yield and yield contributing traits in normal sown condition. *Plant Archives*, **18** (2): 1638-1642.

Sunil, K. D.; Sehrawat and Khan, M. (2017) Investigation of genetic variability for yield and yield related traits in barley (*Hordeum vulgare* L.) genotypes, *Indian Journal of Ecology*, **44** (4): 869-872.

Swati, K.C.; Tiwari, J. P.; Jaiswal, A; Kumar and P Goel. (2018). Genetic architeture of barley (*Hordeum vulgare* L.) genotypes for grain yield and yield attributing traits. *Wheat and Barley Research*, **10** (3): 179-184.

Tehulie, N. S. (2022) Genetic variability and agronomic association on some genotypes of barley (*Hordeum vulgare* L). *AGBIR*, **38**.361-365.

Tripathi, R. K.; Aguirre, J. A. and Singh, J. (2021). Genome-wide analysis of wall associated kinase (WAK) gene family in barley. Genomics, **113** (1): 523-530.

Tokhetova, L.; Makhmadjanov, S.; Savin, T. and Baimbetova, G. (2022). combining ability analysis in spring barley *(Hordeum vulgare* L.) for yield traits. *Sabrao Journal of Breeding and Genetics***,** **54** (4): 710-721.

Thakur, V. S.; Mishra, V.; Tamrakar, A.; Kumar, K. and Kumar, C. M., 2022. Assessment of genetic diversity and yield performance in barley (*Hordeum vulgare* L.) under rainfed condition. *The Pharma Innovation Journal*, **11** (2): 1888-1891.

Verma P. K.; Vijay Rana V. and Rupali Choudhary R. (2022) Genetic variability for yield and yield related traits in barley (*Hordeum vulgare* L.) *Himachal Journal of Agricultural Research* **48** (2): 272-275.

Varzaru, S. and Ciulca, S. (2012). Assessment of heterosis for grain yield per spike in winter barley. *Analele universitati din Craiova – biologie, Horticulture, Tehnology Prelucrarii Produselor Agricol, Ingieria Mediului*, **17**: 859-862.

Vaschenko, V.; Shevchenko, O.; Vinyukov, A. and Bondareva, O., (2021). correlation of effects of the general combination ability and the sign of the duration of the spring-hilling period in spring barley varieties. *agrolife scientific journal*, **10** (2): 2372- 289.

Vishwakarma, S. R.; Shukla, A.; Bahadur, R. and Singh, N. (2011). Expression of heterosis for yield and chlorophyll content in barley. *Plant Archives*, **11** (2): 891-894.

Vinesh, B.; Prasad, L.C.; Prasad, R. and Madhukar, K. (2018). Association studies of yield and it's attributing traits in indigenous and exotic Barley (*Hordeum vulgare* L.) germplasm. Journal of Pharmacognosy and Phytochemistry, **7** (5): 1500-1502.

Wright, S. (1921). Systems of mating. The biometric relations between parent and offspring. Genetics, **6** (2): 111-123.

Yadav, D. N.; Balasubramanian, S.; Kaur, J.; Anand, T. and Singh, A. K. (2014). Non-wheat pasta based on pearl millet flour containing barley and whey protein concentrate. *Journal of Food Science and Technology*, **51**: 2592-2599.

Yadav, K.; Maurya, K. N.; Shrivastava, S. P.; Lal, V. S. K.; Maurya, S. K. and Yadav, H. (2019). Assessment of genetic variability, correlation and path coefficient for yield and its contributing traits in exotic and indigenous barley (Hordeum vulgare L.). *International J Chemical Studies*, **7** (2): 1584-158.

Yadav, A. S. and Singh, G. (2021). Estimation of genetic variability, expected genetic advance, correlation and path analysis in barley (*Hordeum vulgare* L.) *the Pharma Innovation Journal* ,**10** (10): 561-563.

Zohary, D., and Hopf, M. (1993). Domestication of plants in the old World - The origin and spread of cultivated plants in West Asia, Europe, and the Nile Valley. Clarendon Press, Oxford.

Zohary, D.; Hopf, M. and Weiss, E. (2012). Domestication of Plants in the Old World: The origin and spread of domesticated plants in Southwest Asia, Europe, and the Mediterranean Basin. *Oxford University Press*.

Yates, F. (1947). Analysis of data from all possible reciprocal crosses between a set of parental lines. *Heredity*, **1 (**3): 287-301.

Yang, T.; Zeng, Y.; Yang, S. and Pu, X. (2019). Genetic analysis of four main flavonoids in barley grain. *Bangladesh Journal of Botany*, **48** (2): 231-237.

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Table 1: Analysis of variance of parents and F_1s for eleven characters in a set of 8 parents diallel cross of barley

S. N.	Sourced of variation	d.f.	Days to 75% heading	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Spike length (cm)	Number of grains per spike	Grain weight per spike (g)	100 grain weight (g)	Biologic al yield per plant	Harvest index (%)	Grain yield per plan (g)
1.	Replication	2	4.75 *	8.62**	3.86	0.70	0.59	15.25	0.03	0.010	14.96	9.52	6.73
2.	Treatment	35	14.56 **	3.99**	84.12**	3.17*	3.41**	145.28**	0.26**	0.11**	81.88**	24.03**	17.47**
3.	Parents	7	12.42 **	4.48**	32.67**	6.93**	3.48**	173.23**	0.47**	0.20**	45.82	20.80*	15.79**
4.	F_1	27	12.84 **	3.36**	80.70**	1.69	1.66**	54.52**	0.05**	0.09**	48.87**	22.89**	6.530
5.	P vs F_1	1	76.00 **	17.79**	536.90**	16.93	50.38**	2400.19**	4.42**	0.03	1225.57**	77.63**	324.70**
6.	Error	70	1.09	1.23	10.62	1.93	0.31	6.73	0.01	0.018	22.50	7.46	4.60

***Significant at 5% level; **Significant at 1% level**

Table 2: Mean and range of parents and F_1s for eleven characters in a set of 8 parents diallel cross of barley

S. N.	Characters	General mean		Range			
		Parents	F_1s	Parents		F_1s	
				Minimum	Maximum	Minimum	Maximum
1.	**Days to 75% heading**	73.70	75.73	71.33	77.00	69.67	79.00
2.	**Days to maturity**	118.33	119.31	116.00	120.00	117.00	122.00
3.	**Plant height (cm)**	77.87	83.24	73.83	84.43	74.60	94.00
4.	**Number of effective tillers per plant**	8.08	9.04	6.33	11.00	7.66	11.00
5.	**Spike length (cm)**	8.06	9.70	5.93	9.13	5.93	11.80
6.	**Number of grains per spike**	42.21	53.55	30.33	53.00	45.00	59.67
7.	**Grain weight per spike(g)**	2.03	2.52	1.45	2.50	2.30	2.73
8.	**100 grain weight (g)**	4.89	4.93	4.54	5.37	4.52	5.17
9.	**Biological yield per plant (g)**	51.37	59.48	45.49	56.12	47.33	69.75
10.	**Harvest index (%)**	36.45	38.49	32.12	39.57	32.79	44.28
11.	**Grain yield per plant (g)**	18.54	22.71	15.32	21.10	20.22	25.95

Table 3: Estimate values of regression (b), SEb, (b-0)/SEb, (1-b) / SEb and t^2 for eleven characters in a set 8 of diallel cross of barley.

S. N.	Characters	b	SEb	T test		
				(b-0)/ SEb	**(1-b)/SEb**	**t^2**
1.	**Days to 75% heading**	0.23	0 .13	5.95*	2.50	10.93**
2.	**Days to maturity**	0.44	0.30	1.47	1.87	0.17
3.	**Plant height (cm)**	0.16	0.16	1	5.25**	6.0**
4.	**Number of effective tillers per plant**	0.47	0.35	1.34	1.51	0.00
5.	**Spike length (cm)**	0.58	0.25	2.32	1.69	0.27
6.	**Number of grains per spike**	0.77	0.17	4.54*	1.36	0.41
7.	**Grains weight per spike (g)**	0.64	0.12	5.33*	2.90	3.99*
8.	**100-grains weight (g)**	0.56	0.47	1.19	0.96	0.64
9.	**Biological yield per plant (g)**	0.62	0.26	3.38	1.77	0.142
10.	**Harvest index (%)**	0.56	0.31	1.81	1.48	0.03
11.	**Grain yield per plant**	0.77	0 .16	4.81*	1.44	0.39

***Significant at 5% level; **Significant at 1% level**

Table 4: Estimates of genetic components and related parameters for eleven characters in a set of 8 parents diallel cross of barley

S. N.	Characters	Genetic component						Related parameter (genetic ratio)			
		$\hat{D}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{F}$	h^2	$\hat{E}$	$(\hat{H}_1/\hat{D})^{0.5}$	$\hat{H}_2/4\hat{H}_1$	$\frac{(4DH_1)^{0.5}+F}{(4DH_1)^{0.5}-F}$	$h^2/\hat{H}_2$
1.	Days to 75% heading	3.74*	20.15*	17.02*	5.58	12.2*	0.40	2.32	0.21	1.95	0.72
	SE±	1.49	3.42	2.98	3.52	1.99	0.50	-	-	-	-
2.	Days to maturity	1.01*	4.13*	3.73*	1.11	2.71*	0.48*	2.02	0.20	1.74	0.72
	SE±	0.45	1.04	0.90	1.07	0.60	0.15	-	-	-	-
3.	Plant height (cm)	7.41	105.31*	86.37*	12.09	86.56*	3.48	3.77	0.21	1.55	1.00
	SE±	7.18	16.50	14.36	16.96	9.63	2.39	-	-	-	-
4.	Number of effective tillers per plant	1.68*	2.88*	1.77*	2.57*	2.50*	0.63*	1.30	0.15	3.56	1.41
	SE±	0.33	0.76	0.66	0.78	0.44	0.11	-	-	-	-
5.	Spike length(cm)	1.05*	4.18*	3.37*	1.65	8.21*	0.10	1.99	0.20	2.31	2.43
	SE±	0.45	1.03	0.90	1.06	0.60	0.15	-	-	-	-
6.	Number of grains per spike	55.41*	188.55*	148.84*	90.82*	392.75*	2.32	1.84	0.20	2.60	2.64
	SE±	8.37	19.25	16.75	19.79	11.23	2.79	-	-	-	-
7.	Grain weight per spike (g)	0.15*	0.34*	0.24*	0.25*	0.72*	0.004	1.53	0.18	3.5	2.98
	SE±	0.02	0.04	0.03	0.04	0.025	0.006	-	-	-	-
8.	100-grain weight (g)	0.06*	0.15*	0.10*	0.09*	0.026	0.005	1.58	0.17	3.03	0.26
	SE±	0.01	0.03	0.02	0.03	0.02	0.004	-	-	-	-
9.	Biological yield per plant	7.84	93.47*	77.73*	20.08	197.81*	7.43*	3.45	0.21	2.17	2.54
	SE±	6.43	14.80	12.87	15.21	8.63	2.15	-	-	-	-
10.	Harvest index	4.42*	26.37*	18.72*	7.09	11.63*	2.51*	2.44	0.18	1.97	0.62
	SE±	2.23	5.13	4.46	5.27	2.99	0.74	-	-	-	-
11.	Grain yield per plant (g)	3.71*	17.09*	13.09*	6.34*	52.09*	1.55*	2.15	0.19	2.3	3.94
	SE±	0.88	2.03	1.76	2.09	1.18	0.29	-	-	-	-

***Significant at 5% level; **Significant at 1% level**

Table 5: Analysis of variance (ANOVA) for combining ability for eleven characters in a set of 8 parents diallel cross in barley

S. N.	Source of Variation	d. f.	Days to 75% heading	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Spike length (cm)	Number of grains per spike	Grain weight per spike (g)	100 grain weight (g)	Biological yield per plant	Harvest index (%)	Grain yield per plan (g)
1.	**GCA**	7	3.50**	1.29**	27.08**	1.26	0.70**	22.06**	0.05**	0.05**	9.81	10.89**	4.09*
2.	**SCA**	28	5.19**	1.34**	28.28**	1.005	1.24**	55.01**	0.09**	0.03**	31.67**	7.30**	6.25**
3.	**Error**	70	0.36	0.40	3.54	0.64	0.10	2.25	0.004	0.006	7.50	2.49	1.53
4.	**$\delta^2 g$**	-	0.31	0.09	2.35	0.06	0.06	1.98	0.005	0.004	0.23	0.84	0.25
5.	**$\delta^2 s$**	-	4.83	0.93	24.74	0.36	1.14	52.77	0.09	0.028	24.16	4.80	4.72
6.	**$\delta^2 g / \delta^2 s$**	-	0.06	0.095	0.095	0.172	0.053	0.038	0.051	0.16	0.01	0.17	0.14
7.	**$(\delta^2 s / \delta^2 g)^{0.5}$**	-	3.95	3.21	3.24	2.45	4.35	5.16	4.24	2.65	10.24	2.39	4.34

***Significant at 5% level; **Significant at 1% level**

GCA= General combining ability **SCA = Specific combining ability;**

$(\delta^2 s / \delta^2 g)^{0.5}$ =Average degree of dominance **$\delta^2 g / \delta^2 s$ = Ratio of GCA variance to SCA variance**

Table 6: Estimates of GCA effects of parents for eleven characters in a set of 8 parents diallel cross in barley

S.N.	Parents	Days to 75% heading	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Spike length (cm)	Number of grains per spike	Grain weight per spike(g)	100 grain weight (g)	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
1.	RD 2907	0.21	0.18	-1.9**	-0.17	-0.04	-0.79	0.02	0.10**	-1.69 *	-0.77	-1.07 **
2.	KB 1425	-0.75**	0.28	1.13 *	0.02	-0.07	-1.82**	-0.09**	0.01	0.38	-0.04	0.24
3.	KB 1506	-0.18	-0.31	2.57 **	0.79**	0.18	-1.19**	-0.03	0.011	0.05	0.17	0.25
4.	KB 1762	-0.48 **	-0.71 **	0.012	-0.44	-0.48**	-1.23**	-0.07**	-0.07**	0.90	-1.69**	-0.75*
5.	KB 1634	0.08	-0.08	1.27*	-0.18	0.12	2.44**	0.12**	0.06 *	0.38	1.07*	0.78*
6.	HUB 113	-0.32	0.25	-1.47**	-0.04	-0.03	0.74	0.06**	-0.003	-1.16	1.70 **	0.53
7.	K 603	0.25	0.31	0.278	-0.01	-0.13	0.51	-0.05*	-0.14**	1.24	-0.28	0.29
8.	DWRB 137	1.18 **	0.08	-1.89**	0.03	0.44**	1.34**	0.05*	0.03	-0.11	-0.17	-0.26
	SE (gi) ±	0.18	0.19	0.56	0.24	0.09	0.44	0.02	0.02	0.81	0.47	0.37
	SE (gi-gj) ±	0.27	0.29	0.84	0.36	0.14	0.67	0.03	0.03	1.22	0.71	0.55

***Significant at 5% level; **Significant at 1% level**

Table 7: Estimates of SCA effects and *per se* performance of 28 F_1s for eleven characters in a set of 8 parents diallel cross in barley

S. N.	Cross combination	Days to 75% heading		Days to maturity		Plant height (cm)		Number of effective tillers per plant		Spike length (cm)		Number of grains per spike	
		SCA	*Per se*	SCA	*Per se*	SCA	*Per se*	SCA	*Per se*	SCA	*Per se*	SCA	*Per se*
1.	**RD 2907 X KB 1425**	2.59 **	77.33	-0.56	119.00	-4.88**	76.40	0.66	9.33	-0.66 *	8.57	1.26	49.67
2.	**RD 2907 X KB 1506**	1.36*	76.67	1.04	120.00	4.52 *	87.23	-0.44	9.00	0.96**	10.43	5.62**	54.67
3.	**RD 2907 X KB 1762**	0.99	76.00	1.11	119.67	6.21 **	86.37	-0.54	7.67	-0.19	8.63	-2.68	46.33
4.	**RD 2907 X KB 1634**	1.42 *	77.00	-0.86	118.33	5.88 **	87.30	0.19	8.67	1.15**	10.57	-7.68**	45.00
5.	**RD 2907 X HUB 113**	1.82 **	77.00	0.47	120.00	0.49	79.17	1.06	9.67	0.01	9.37	0.69	51.67
6.	**RD 2907 X K 603**	-2.74 **	73.00	-0.59	119.00	-5.83**	74.60	0.03	8.67	0.16	9.33	7.92**	58.67
7.	**RD 2907 X DWRB 137**	0.66	77.33	0.97	120.33	-1.42	76.83	0.66	9.33	0.09	9.83	7.76**	59.33
8.	**KB 1425 X KB 1506**	-0.34	74.00	-0.73	118.33	2.45	88.20	0.69	10.33	0.19	9.63	7.32**	55.33
9.	**KB 1425 X KB 1762**	1.96**	76.00	2.01 **	120.67	10.81 **	94.00	0.59	9.00	1.08**	9.87	2.02	50.00
10.	**KB 1425 X KB 1634**	-0.94	73.67	0.04	119.33	1.21	85.67	1.66 *	10.33	-0.09	9.30	5.69**	57.33
11.	**KB 1425 X HUB 113**	-0.21	74.00	0.37	120.00	2.79	84.50	-0.47	8.33	0.60 *	9.83	4.39**	54.33
12.	**KB 1425 X K 603**	-3.78 **	71.00	0.64	120.33	2.71	86.17	0.49	9.33	0.63 *	9.77	9.62**	59.33
13.	**KB 1425 X DWRB 137**	0.29	76.00	-0.46	119.00	-3.92*	77.37	0.126	9.00	0.12	9.83	3.79**	54.33
14.	**KB 1506 X KB 1762**	2.39 **	77.00	0.94	119.00	-5.56 **	79.07	-0.17	9.00	-0.07	8.97	-0.61	48.00
15.	**KB 1506 X KB 1634**	1.49 *	76.67	1.31 *	120.00	2.64	88.53	-0.44	9.00	1.07**	10.70	2.06	54.33

Table 7: Continued

S. N.	Cross combination	Days to 75% heading		Days to maturity		Plant height (cm)		Number of effective tillers per plant		Spike length (cm)		Number of grains per spike	
		SCA	***Per se***	**SCA**	***Per se***	**SCA**	***Per se***	**SCA**	***Per se***	**SCA**	***Per se***	**SCA**	***Per se***
1.	**KB 1506 X HUB 113**	1.89 **	76.67	-1.03	118.00	3.33	86.47	-1.24	8.33	0.25	9.73	3.76**	54.33
2.	**KB 1506 X K 603**	1.66 **	77.00	0.91	120.00	5.91 **	90.80	1.39	11.00	1.08**	10.47	4.32**	54.67
3.	**KB 1506 X DWRB 137**	-1.28 *	75.00	-0.19	118.67	5.35 **	88.07	-0.97	8.67	0.58	10.53	1.49	52.67
4.	**KB 1762 X KB 1634**	-5.21 **	69.67	0.71	119.00	2.00	85.33	1.46	9.67	0.99**	9.97	7.42**	59.67
5.	**KB 1762 X HUB 113**	0.52	75.00	-0.29	118.33	-5.22 **	75.37	-0.01	8.33	-0.19	8.63	-1.21	49.33
6.	**KB 1762 X K 603**	0.96	76.00	-1.36 *	117.33	2.03	84.37	-0.04	8.33	0.80**	9.53	6.36**	56.67
7.	**KB 1762 X DWRB 137**	3.02**	79.00	0.21	118.67	6.20 **	86.37	0.59	9.00	2.49**	11.80	8.52**	59.67
8.	**KB 1634 X HUB 113**	0.62	75.67	1.07	120.33	3.12	84.97	1.39	10.00	-0.02	9.40	-0.88	53.33
9.	**KB 1634 X K 603**	3.06 **	78.67	-0.33	119.00	-2.37	81.23	0.36	9.00	-0.29	9.03	0.02	54.00
10.	**KB 1634 X DWRB 137**	0.46	77.00	-2.09 **	117.00	-1.96	79.47	-0.34	8.33	-0.83**	9.07	-0.81	54.00
11.	**HUB 113 X K 603**	1.79 **	77.00	0.01	119.67	-5.78 **	75.07	0.23	9.00	0.53	9.70	5.06**	57.33
12.	**HUB 113 X DWRB 137**	-1.14 *	75.00	2.57**	122.00	2.99	81.67	-0.81	8.00	-0.98**	8.77	-4.78**	48.33
13.	**K 603 X DWRB 137**	-0.71	76.00	0.17	119.67	-0.33	80.10	-0.17	8.67	0.72*	10.37	-5.88**	47.00
	SE (Sij)±	1.123		1.123		1.123		1.123		1.123		2.79	
	SE (Sij-Sik) ±	1.66		1.76		5.18		2.21		0.88		4.125	

***Significant at 5% level; **Significant at 1% level**

Table 7: Continued

S. N.	Cross combination	Grain weight per spike(g)		100-gain weight (g)		Biological yield per plant		Harvest index (%)		Grain yield per plant (g)	
		SCA	*Per se*	SCA	*Per se*	SCA	*Per se*	SCA	*Per se*	SCA	*Per se*
1.	RD 2907 X KB 1425	0.08	2.42	0.05	5.07	1.03	56.40	0.03	39.30	2.07	21.99
2.	RD 2907 X KB 1506	0.22**	2.62	-0.15*	4.87	1.34	57.57	1.53	37.74	0.30	22.31
3.	RD 2907 X KB 1762	-0.01	2.34	0.21**	5.16	1.12	63.27	6.38*	32.79	-2.78	21.09
4.	RD 2907 X KB 1634	-0.20**	2.34	-0.04	5.03	-1.34	58.16	1.79	34.75	-3.59*	20.15
5.	RD 2907 X HUB 113	-0.14*	2.34	-0.15*	4.86	0.50	54.42	-0.41	39.77	0.81	21.75
6.	RD 2907 X K 603	0.07	2.45	-0.07	4.81	0.91	61.66	4.43	37.79	0.80	21.92
7.	RD 2907 X DWRB 137	0.23**	2.70	-0.36**	4.68	2.26	59.72	3.841	38.73	1.63	22.71
8.	KB 1425 X KB 1506	0.29**	2.59	-0.13	4.81	1.93	60.61	2.50	40.09	1.93	24.21
9.	KB 1425 X KB 1762	0.16*	2.41	0.11	4.98	2.17	67.49	8.52**	34.66	-1.64	23.45
10.	KB 1425 X KB 1634	0.29**	2.73	0.15*	5.14	2.85*	61.06	2.62	42.17	3.10*	25.66
11.	KB 1425 X HUB 113	0.23**	2.61	-0.01	4.92	1.60	58.33	1.43	41.79	2.10	24.16
12.	KB 1425 X K 603	0.39**	2.67	0.003	4.80	1.28	56.97	-2.33	41.90	4.19**	23.59
13.	KB 1425 X DWRB 137	0.11	2.47	0.17*	5.12	0.63	59.32	1.37	37.72	-0.11	22.40
14.	KB 1506 X KB 1762	0.14*	2.45	0.16*	5.03	1.09	56.89	-1.74	39.31	2.79	22.37
15.	KB 1506 X KB 1634	0.04	2.54	-0.03	4.95	0.73	56.65	-1.45	41.69	2.41	23.54

Table 7: Continued

S. N.	Cross combination	Grain weight per spike(g)		100-gain weight (g)		Biological yield per plant		Harvest index (%)		Grain yield per plant (g)	
		SCA	*Per se*	SCA	*Per se*	SCA	*Per se*	SCA	*Per se*	SCA	*Per se*
16.	KB 1506 X HUB 113	0.16*	2.60	-0.09	4.83	1.10	62.40	5.83*	37.96	-1.94	23.67
17.	KB 1506 X K 603	0.32**	2.65	0.34**	5.14	3.62**	69.75	10.78**	36.73	1.20	25.95
18.	KB 1506 X DWRB 137	0.06	2.49	0.08	5.04	-0.73	61.06	3.44	34.39	-3.65*	21.04
19.	KB 1762 X KB 1634	0.22**	2.67	-0.06	4.85	2.41*	64.92	5.96*	37.36	-0.06	24.23
20.	KB 1762 X HUB 113	-0.14*	2.26	-0.15 *	4.69	0.37	54.70	-2.72	40.48	2.44	21.94
21.	KB 1762 X K 603	0.33**	2.62	-0.07	4.65	0.75	60.35	0.53	36.32	0.26	22.08
22.	KB 1762 X DWRB 137	0.17**	2.56	-0.14	4.74	2.04	63.89	5.42*	35.90	-0.28	22.82
23.	KB 1634 X HUB 113	-0.05	2.53	0.19**	5.17	1.15	60.40	3.51	40.33	-0.48	24.25
24.	KB 1634 X K 603	0.11	2.59	0.20**	5.04	0.29	59.26	-0.04	38.93	0.10	23.14
25.	KB 1634 X DWRB 137	0.045	2.62	0.17*	5.17	-1.14	53.87	-4.08	41.29	2.349	21.17
26.	HUB 113 X K 603	0.12	2.54	-0.26**	4.52	0.69	52.60	-5.16*	44.28	4.83**	23.30
27.	HUB 113 X DWRB 137	0.11	2.41	0.05	5.00	-1.83	54.95	-1.45	38.00	-1.56	20.22
28.	K 603 X DWRB 137	0.11	2.30	0.07	4.88	-0.88	58.68	-0.13	35.45	-2.13	20.93
	SE (Sij)±	0.127		0.143		2.30		5.09		2.935	
	SE(Sij-Sik)±	0.19		0.21		3.41		7.54		4.34	

***Significant at 5% level; **Significant at 1% level**

Table 8: Per cent heterosis over economic parent (KB 1425) for eleven characters in barley

S.No.	Cross combination	Days to75% heading	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Spike length (cm)	Number of grains per spike	Grain weight per spike(g)	100-gain weight (g)	Biological yield per plant	Harvest index (%)	Grain yield per plant (g)
1	RD 2907 X KB 1425	0.43	-0.83	-9.51 **	-15.15	-6.2	-6.29	-3.07	-5.65 **	0.5	-0.71	4.32
2	RD 2907 X KB 1506	-0.43	0	3.32	-18.18	14.23 **	3.14	4.93	-9.31 **	2.58	-4.63	5.82
3	RD 2907 X KB 1762	-1.3	-0.28	2.29	-30.30 **	-5.47	-12.58 **	-6.4	-4.03	12.74	-17.14 **	0.03
4	RD 2907 X KB 1634	0	-1.39	3.4	-21.21 *	15.69 **	-15.09 **	-6.27	-6.33 **	3.62	-12.19 *	-4.4
5	RD 2907 X HUB 113	0	0	-6.24	-12.12	2.55	-2.52	-6.27	-9.55 **	-3.04	0.5	3.16
6	RD 2907 X K 603	-5.19 **	-0.83	-11.65 **	-21.21 *	2.19	10.69 **	-2	-10.55 **	9.87	-4.52	3.97
7	RD 2907 X DWRB 137	0.43	0.28	**	-15.15	7.66	11.95 **	8.13 *	-12.90 **	6.4	-2.15	7.73
8	KB 1425 X KB 1506	-3.90 **	-1.39	4.46	-6.06	5.47	4.4	3.47	-10.42 **	8	1.31	14.83
9	KB 1425 X KB 1762	-1.3	0.56	11.33 **	-18.18	8.03	-5.66	-3.6	-7.38 **	20.25 **	-12.42 *	11.24
10	KB 1425 X KB 1634	-4.33 **	-0.56	1.46	-6.06	1.82	8.18	9.07 *	-4.34 *	8.79	6.55	21.71 *
11	KB 1425 X HUB 113	-3.90 **	0	0.08	-24.24 *	7.66	2.52	4.4	-8.44 **	3.93	5.59	14.63
12	KB 1425 X K 603	-7.79 **	0.28	2.05	-15.15	6.93	11.95 **	6.67	-10.73 **	1.51	5.86	11.92
13	KB 1425 X DWRB 137	-1.3	-0.83	-8.37 **	-18.18	7.66	2.52	-1.07	-4.65 *	5.69	-4.7	6.25
14	KB 1506 X KB 1762	0	-0.83	-6.36	-18.18	-1.82	-9.43 *	-2.13	-6.45 **	1.37	-0.67	6.14
15	KB 1506 X KB 1634	-0.43	0	4.86	-18.18	17.15 **	2.52	1.6	-7.82 **	0.94	5.35	11.67

Table 8: Continued.

S.N.	Cross combination	Days to75% heading	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Spike length (cm)	Number of grains per spike	Grain weight per spike(g)	100-gain weight (g)	Biological yield per plant	Harvest index (%)	Grain yield per plant (g)
16	KB 1506 X HUB 113	-0.43	-1.67 *	2.41	-24.24 *	6.57	2.52	3.87	-10.05 **	11.18	-4.08	12.27
17	KB 1506 X K 603	0	0	7.54 *	0	14.60 **	3.14	6	-4.40 *	24.27 **	-7.2	23.09 **
18	KB 1506 X DWRB 137	-2.60 *	-1.11	4.3	-21.21 *	15.33 **	-0.63	-0.53	-6.27 **	8.8	-13.11 *	-0.17
19	KB 1762 X KB 1634	-9.52 **	-0.83	1.07	-12.12	9.12	12.58 **	6.8	-9.68 **	15.67 *	-5.6	14.93
20	KB 1762 X HUB 113	-2.60 *	-1.39	-10.74 **	-24.24 *	-5.47	-6.92	-9.73 *	-12.66 **	-2.54	2.28	4.08
21	KB 1762 X K 603	-1.3	-2.22 **	-0.08	-24.24 *	4.38	6.92	4.67	-13.52 **	7.54	-8.23	4.74
22	KB 1762 X DWRB 137	2.60 *	-1.11	2.29	-18.18	29.20 **	12.58 **	2.27	-11.72 **	13.84	-9.3	8.24
23	KB 1634 X HUB 113	-1.73	0.28	0.63	-9.09	2.92	0.63	1.33	-3.85	7.62	1.9	15.02
24	KB 1634 X K 603	2.16	-0.83	-3.79	-18.18	-1.09	1.89	3.47	-6.20 **	5.59	-1.64	9.77
25	KB 1634 X DWRB 137	0	-2.50 **	-5.88	-24.24 *	-0.73	1.89	4.67	-3.66	-4.02	4.33	0.41
26	HUB 113 X K 603	0	-0.28	-11.09 **	-18.18	6.2	8.18	1.6	-15.94 **	-6.28	11.89 *	10.53
27	HUB 113 X DWRB 137	-2.60 *	1.67 *	-3.28	-27.27 *	-4.01	-8.81 *	-3.6	-7.01 **	-2.08	-3.98	-4.06
28	K 603 X DWRB 137	-1.3	-0.28	-5.13	-21.21 *	13.50 **	-11.32 **	-7.87	-9.18 **	4.56	-10.42	-0.71
	SE±	0.60	0.64	1.88	0.80	0.32	1.50	0.07	0.08	2.74	1.58	1.24
	CD at 5%	1.70	1.81	5.31	2.26	0.90	4.22	0.19	0.22	7.72	4.44	3.49

***Significant at 5% level; **Significant at 1% level**

Table 9: Grand mean, GCV, PCV, heritability (narrow sense) and genetic advance % over mean in eleven characters of barley.

S. N.	Characters	Grand mean	GCV	PCV	Narrow sense heritability [(h^2) %]	Genetic Advance	Genetic advance % over mean
1.	Days to 75% heading	75.28	2.81	3.14	12.2	7.35	5.2
2.	Days to maturity	119.09	0.81	1.23	9.8	12.23	1.07
3.	Plant height (cm)	82.05	6.03	7.22	22.1	11.40	10.38
4.	Number of effective tillers per plant	8.82	7.283	17.35	9.1	6.03	6.29
5.	Spike length (cm)	9.33	10.90	12.41	10.2	0.64	19.73
6.	Number of grains per spike	51.02	13.32	14.26	5.2	2.18	25.63
7.	Grain weight per spike (g)	2.41	11.85	12.82	6.2	8.29	22.55
8.	100 grain weight (g)	4.92	3.62	4.52	22.7	5.30	5.98
9.	Biological yield per plant (g)	57.67	7.71	11.27	6.1	5.00	10.87
10.	Harvest index (%)	38.03	6.18	9.47	25.8	3.02	8.3
11.	Grain yield per plant (g)	21.79	9.51	13.69	12.5	5.46	13.60

***Significant at 5% level, ** Significant at 1% level**

Table 10: Phenotypic (upper) and genotypic (lower) correlation for eleven characters in a set of 8 parents diallel cross of barley.

S. N.	Character \ Character	Days to 75% heading	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Spike length (cm)	Grain weight /spike (g)	100 grain weight (g)	Harvest index (%)	Biological yield per plant (g)	Number of grains umber per spike	Grain yield per plant (g)
1.	**Days of 75 % heading**	$r^P{}_g$	0.216*	0.135	0.003	0.413**	0.251**	0.009	0.056	0.300**	0.194*	0.306**
2.	**Days to maturity**	0.180	$r^P{}_g$	0.458**	0.181	0.466**	0.323**	0.015	0.128	0.464**	0.296**	0.497**
3.	**Plant height (cm)**	0.109	0.209*	$r^P{}_g$	0.515**	0.607**	0.385**	0.174	-0.172	0.827**	0.308**	0.644**
4.	**Number of effective tillers per plant**	0.039	0.135	0.126	$r^P{}_g$	0.552**	0.639**	0.321**	0.653**	0.054	0.605**	0.460**
5.	**Spike length (cm)**	0.324**	0.200*	0.435**	0.314**	$r^P{}_g$	0.715**	0.132	0.225*	0.705**	0.699**	0.770**
6.	**Grain weight /spike (g)**	0.183	0.149	0.270**	0.223*	0.612**	$r^P{}_g$	0.262**	0.657**	0.673**	0.938**	0.987**
7.	**100 grain weight (g)**	0.011	0.071	0.088	0.111	0.048	0.241*	$r^P{}_g$	-0.067	0.137	-0.038	0.087
8.	**harvest index (%)**	-0.009	0.144	-0.186	0.291**	0.112	0.401**	0.056	$r^P{}_g$	-0.102	0.677**	0.554**
9.	**Biological yield per plant (g)**	0.233*	0.225*	0.562**	0.545**	0.533**	0.422**	0.005	-0.165	$r^P{}_g$	0.695**	0.777**
10.	**Number of grains per spike**	0.173	0.156	0.204*	0.256**	0.616**	0.896**	-0.031	0.415**	0.446**	$r^P{}_g$	0.985**
11.	**Grain yield per plant (g)**	0.214*	0.317**	0.358**	0.686**	0.543**	0.613**	0.054	0.520**	0.723**	0.642**	$r^P{}_g$

***Significant at 5% level, ** Significant at 1% level**

Table 11 (a): Direct and indirect effects of eleven characters on grain yield of barley as independent variable at genotype level.

S. N.	Characters	Days to75 % flowering	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Spike length (cm)	Grain weight per spike (g)	100-grains weight (g)	Harvest index (%)	Biological yield per plant (g)	Number of grains per spike	Grain yield per plants (g)
1.	Days to75 % flowering	**0.085**	0.089	-0.064	0.003	-0.309	0.886	-0.009	-0.097	-0.092	-0.186	0.306**
2.	Days to maturity	0.018	**0.414**	-0.216	0.156	-0.349	1.138	-0.016	-0.222	-0.142	-0.284	0.497**
3.	Plant height (cm)	0.011	0.190	**-0.472**	0.444	-0.454	1.356	-0.182	0.299	-0.253	-0.296	0.644**
4.	Number of effective tillers per plant	0.000	0.075	-0.243	**0.863**	-0.413	2.250	-0.337	-1.139	-0.016	-0.580	0.460**
5.	Spike length (cm)	0.035	0.193	-0.287	0.477	**-0.748**	2.518	-0.139	-0.393	-0.215	-0.671	0.770**
6.	Grain weight per spike (g)	0.021	0.134	-0.182	0.551	-0.535	**3.523**	-0.275	-1.145	-0.206	-0.900	0.987**
7.	100-grains weight (g)	0.001	0.006	-0.082	0.277	-0.099	0.922	**-1.049**	0.117	-0.042	0.037	0.087
8.	Harvest index (%)	0.005	0.053	0.081	0.564	-0.169	2.313	0.070	**-1.744**	0.031	-0.650	0.554**
9.	Biological yield per plant (g)	0.026	0.192	-0.391	0.046	-0.527	2.370	-0.144	0.177	**-0.306**	-0.667	0.777**
10.	Number of grains per spike	0.017	0.123	-0.146	0.522	-0.523	3.306	0.040	-1.182	-0.212	**-0.959**	0.985**

***Significant at 5% level, ** Significant at 1% level;**

Direct effects in bold letters and indirect effects in normal letters.

Residual effect = 0.1154

Table 11(b): Direct and indirect effects of eleven characters on grain yield of barley as independent variable at phenotype level.

S. N.	Characters	Days to 75 % flowering	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Spike length (cm)	Grain weight per spike (g)	100 grains weight (g)	Harvest index (%)	Biological yield per plant (g)	number of grains per spike	Grain yield per plants (g)
1.	**Days to75 % flowering**	**0.0293**	0.0065	0.0034	0.0038	0.0070	-0.0012	0.0000	-0.0057	0.1672	0.0039	0.214*
2.	**Days to maturity**	0.0053	**0.0363**	0.0065	0.0132	0.0043	-0.0010	0.0001	0.0870	0.1613	0.0035	0.317**
3.	**Plant height (cm)**	0.0032	0.0076	**0.0312**	0.0123	0.0093	-0.0018	0.0001	-0.1120	0.4033	0.0046	0.358**
4.	**Number of effective tillers per plant**	0.0012	0.0049	0.0039	**0.0979**	0.0067	-0.0015	0.0002	0.1752	0.3913	0.0058	0.686**
5.	**Spike length (cm)**	0.0095	0.0073	0.0136	0.0307	**0.0214**	-0.0040	0.0001	0.0677	0.3830	0.0140	0.543**
6.	**Grain weight per spike (g)**	0.0054	0.0054	0.0084	0.0219	0.0131	**-0.0065**	0.0004	0.2417	0.3028	0.0203	0.613**
7.	**100-grains weight (g)**	0.0003	0.0026	0.0027	0.0109	0.0010	-0.0016	**0.0016**	0.0338	0.0034	-0.0007	0.054
8.	**Harvest index (%)**	-0.0003	0.0052	-0.0058	0.0285	0.0024	-0.0026	0.0001	**0.6021**	-0.1187	0.0094	0.520**
9.	**Biological yield per plant (g)**	0.0068	0.0082	0.0175	0.0533	0.0114	-0.0027	0.0000	-0.0996	**0.7179**	0.0101	0.723**
10.	**Number of grains per spike**	0.0051	0.0057	0.0064	0.0250	0.0132	-0.0058	0.0000	0.2497	0.3202	**0.0227**	0.642**

***Significant at 5% level, ** Significant at 1% level;**

Direct effects in bold letters and indirect effects in normal letters.

Residual effect = 0.2219

Table 12: Ranking top three desirable parents based on GCA effect and *per se* performance for eleven characters in barley.

Characters	Good General Combiner based on GCA effects	Good parents based on *per se* mean performance	Best common parents *per se* performance and GCA effects
Days to 75% heading	KB 1425	KB 1506	
	KB 1762	RD 2907	KB 1762
	HUB 113	KB 1762	
Days to maturity	KB 1762	KB 1762	KB 1762
	KB 1506	KB 1506	KB 1506
	KB1634	HUB 113	
Plant height (cm)	RD 2907	KB 1762	RD 2907
	DWRB 137	DWRB 137	DWRB 137
	HUB 113	RD 2907	
Number of effective tillers per plant	KB 1506	KB 1506	KB 1506
	DWRB 137	HUB 113	DWRB 137
	KB 1425	DWRB 137	
Spike length (cm)	DWRB 137	DWRB 137	DWRB 137
	KB 1506	HUB 113	
	KB1634	KB1634	KB1634
Number of grains per spike	KB1634	KB1634	KB1634
	DWRB 137	HUB 113	DWRB 137
	HUB 113	DWRB 137	HUB 113

Grain weight per spike(g)	KB1634	HUB 113	KB1634
	HUB 113	KB1634	HUB 113
	DWRB 137	RD 2907	
100 grain weight (g)	RD 2907	RD 2907	RD 2907
	KB1634	DWRB 137	
	DWRB 137	KB 1506	DWRB 137
Biological yield per plant (g)	K 603	K 603	K 603
	KB 1762	HUB 113	
	KB 1425	KB1634	
Harvest index (%)	HUB 113	K 603	HUB 113
	KB1634	HUB 113	KB1634
	KB 1506	KB1634	
Grain yield per plant (g)	KB1634	DWRB 137	KB1634
	HUB 113	HUB 113	HUB 113
	K 603	KB1634	

Table 13: Ranking top three desirable combinations based on SCA effect and *per se* performance for eleven characters in barley.

Characters	Superior Combiners based on SCA effects	Good Specific Combiners based on *per se* performance	Common Specific Combiners based on *per se* performance and SCA effects
Days to 75% heading	KB 1762 X KB 1634	KB 1762 X KB 1634	KB 1762 X KB 1634
	KB 1425 X K 603	KB 1425 X K 603	KB 1425 X K 603
	RD 2907 X K 603	RD 2907 X K 603	RD 2907 X K 603
Days to maturity	KB 1634 X DWRB 137	KB 1634 X DWRB 137	KB 1634 X DWRB 137
	KB 1762 X K 603	KB 1762 X K 603	KB 1762 X K 603
	KB 1506 X HUB 113	KB 1506 X HUB 113	KB 1506 X HUB 113
Plant height (cm)	RD 2907 X K 603	RD 2907 X KB 1425	
	HUB113 X K 603	HUB113 X K 603	HUB113 X K 603
	KB 1506 X KB 1762	KB 1506 X KB 1762	KB 1506 X KB 1762
Number of effective tillers per plant	KB 1425 X KB 1634	KB 1506 X K 603	
	KB 1762 X KB 1634	KB 1425 X KB 1634	KB 1425 X KB 1634
	KB1634 X HUB113	KB1634 X HUB113	KB1634 X HUB113
Spike length (cm)	KB 1762 X DWRB 137	KB 1762 X DWRB 137	KB 1762 X DWRB 137
	RD 2907 X KB1634	KB 1506 X KB 1634	RD 2907 X KB1634
	KB 1425 X KB 1762	RD 2907 X KB1634	
Number of grains per spike	KB 1425 X K 603	KB 1762 X KB 1634	
	KB 1762 X DWRB 137	KB 1762 X DWRB 137	KB 1762 X DWRB 137

	RD 2907 X K 603	RD 2907 X K 603	RD 2907 X K 603
Grain weight per spike(g)	KB 1425 X K 603	KB 1425 X KB 1634	
	KB 1762 X K 603	KB 1762 X KB 1634	
	KB 1506 X K 603	KB 1506 X K 603	KB 1506 X K 603
100 grain weight (g)	KB 1506 X K 603	KB 1634 X DWRB 137	KB 1506 X K 603
	RD 2907 X KB 1762	KB 1506 X K 603	
	KB1634 X K 603	KB 1425 X DWRB 13	
Biological yield per plant (g)	KB 1425 X K 603	KB 1506 X K 603	KB 1425 X K 603
	KB 1425 X KB 1762	KB 1425 X K 603	
	KB 1762 X DWRB 137	KB 1425 X DWRB 137	
Harvest index (%)	HUB 113 X K 603	HUB 113 X K 603	HUB 113 X K 603
	KB 1425 X K 603	KB 1425 X K 603	KB 1425 X K 603
	KB 1425 X KB1634	KB 1425 X KB1634	KB 1425 X KB1634
Grain yield per plant (g)	KB 1506 X K 603	KB 1506 X K 603	KB 1506 X K 603
	KB 1425 X KB1634	KB 1425 X KB1634	KB 1425 X KB1634
	KB 1762 X KB1634	KB 1762 X KB1634	KB 1762 X KB1634

Table 14: Ranking of desirable specific cross combination for grain yield per plant and their performance in other traits in 8 parent- diallel cross in F_1 generation of barley.

Desirable cross	*Per se* performance	SCA effects	GCA		Traits for which cross also exhibited desirable SCA effects
			P_1	P_2	
KB 1506 X KB 603	25.95	1.20	0.25	0.29	Spike length, number of grains of per spike, Harvest index, biological yield per plant, 100 grain weight and grain weight per spike
KB 1425 X KB 1634	25.66	3.10	0.24	0.78	Number of effective tillers per plant, number of grains per spike, grain weight per spike and harvest index

Table 15: Significant economic crosses for grain yield per plant in order to merit and their performance in related parameters in barley.

Genetic parameter	**Cross combination**	
	KB 1506 X K 603	KB 1425 X KB 1634
Mean performances:		
$\bar{x}_{E_P}$	17.74	16.52
$\bar{x}_{F_1}$	25.95	25.66
Heterosis (%) over economic	23.09	21.71
Traits for which cross exhibited desirable heterosis response over economic parent	III*, V**, IX**	I**, VII*,
GCA effect: P_1 P_2	 0.25 0.29	 0.24 0.78
SCA effects:	4.32	5.69
Character for which cross showed desirable SCA effects:	I*, III**, V**, VI**, VII**, VIII**, IX**, X**	IV*, VI**, VII**, VIII*,

Appendix: *Per se* performance of parents and F_1s for eleven characters in barley

S.N.	Parent/Cross combination	Days to 75% heading	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Spike length (cm)	Number of grains per spike	Grain weight /spike (g)	100 grain weight (g)	Harvest index (%)	Biological yield per plant (g)	Grain yield per plant (g)
	Parents											
1	RD 2907	72.67	118.67	75.77	7.67	8.47	43.00	2.32	5.37	36.89	45.49	16.74
2	KB 1425	74.00	119.00	78.73	7.00	8.27	30.33	1.45	4.76	32.13	51.37	16.52
3	KB 1506	71.33	117.33	77.87	11.00	7.67	36.67	1.73	4.85	38.06	47.33	17.74
4	KB 1762	72.00	116.00	73.83	7.00	5.93	38.67	1.83	4.75	34.29	48.31	15.32
5	KB 1634	75.00	119.00	79.33	6.33	8.60	53.00	2.41	4.74	38.27	54.28	20.87
6	HUB 113	72.00	118.00	78.23	8.67	9.13	49.00	2.50	5.12	38.32	54.84	21.07
7	K 603	75.67	120.00	84.43	7.67	7.27	38.33	1.71	4.55	34.05	56.12	19.03
8	DWRB 137	77.00	118.67	74.80	9.33	9.13	48.67	2.30	4.95	39.57	53.25	21.08
	F_1's											
9	RD 2907 X KB 1425	77.33	119.00	76.40	9.33	8.57	49.67	2.42	5.07	39.30	56.40	21.99
10	RD 2907 X KB 1506	76.67	120.00	87.23	9.00	10.43	54.67	2.62	4.87	37.74	57.57	22.31
11	RD 2907 X KB 1762	76.00	119.67	86.37	7.67	8.63	46.33	2.34	5.16	32.79	63.27	21.09
12	RD 2907 X KB 1634	77.00	118.33	87.30	8.67	10.57	45.00	2.34	5.03	34.75	58.16	20.15
13	RD 2907 X HUB 113	77.00	120.00	79.17	9.67	9.37	51.67	2.34	4.86	39.77	54.42	21.75
14	RD 2907 X K 603	73.00	119.00	74.60	8.67	9.33	58.67	2.45	4.81	37.79	61.66	21.92
15	RD 2907 X DWRB 137	77.33	120.33	76.83	9.33	9.83	59.33	2.70	4.68	38.73	59.72	22.71
16	KB 1425 X KB 1506	74.00	118.33	88.20	10.33	9.63	55.33	2.59	4.81	40.09	60.61	24.21
17	KB 1425 X KB 1762	76.00	120.67	94.00	9.00	9.87	50.00	2.41	4.98	34.66	67.49	23.45
18	KB 1425 X KB 1634	73.67	119.33	85.67	10.33	9.30	57.33	2.73	5.14	42.17	61.06	25.66
19	KB 1425 X HUB 113	74.00	120.00	84.50	8.33	9.83	54.33	2.61	4.92	41.79	58.33	24.16
20	KB 1425 X K 603	71.00	120.33	86.17	9.33	9.77	59.33	2.67	4.80	41.90	56.97	23.59
21	KB 1425 X DWRB 137	76.00	119.00	77.37	9.00	9.83	54.33	2.47	5.12	37.72	59.32	22.40
22	KB 1506 X KB 1762	77.00	119.00	79.07	9.00	8.97	48.00	2.45	5.03	39.31	56.89	22.37

23	KB 1506 X KB 1634	76.67	120.00	88.53	9.00	10.70	54.33	2.54	4.95	41.69	56.65	23.54
24	KB 1506 X HUB 113	76.67	118.00	86.47	8.33	9.73	54.33	2.60	4.83	37.96	62.40	23.67
25	KB 1506 X K 603	77.00	120.00	90.80	11.00	10.47	54.67	2.65	5.14	36.73	69.75	25.95
26	KB 1506 X DWRB 137	75.00	118.67	88.07	8.67	10.53	52.67	2.49	5.04	34.39	61.06	21.04
27	KB 1762 X KB 1634	69.67	119.00	85.33	9.67	9.97	59.67	2.67	4.85	37.36	64.92	24.23
28	KB 1762 X HUB 113	75.00	118.33	75.37	8.33	8.63	49.33	2.26	4.69	40.48	54.70	21.94
29	KB 1762 X K 603	76.00	117.33	84.37	8.33	9.53	56.67	2.62	4.65	36.32	60.35	22.08
30	KB 1762 X DWRB 137	79.00	118.67	86.37	9.00	11.80	59.67	2.56	4.74	35.90	63.89	22.82
31	KB 1634 X HUB 113	75.67	120.33	84.97	10.00	9.40	53.33	2.53	5.17	40.33	60.40	24.25
32	KB 1634 X K 603	78.67	119.00	81.23	9.00	9.03	54.00	2.59	5.04	38.93	59.26	23.14
33	KB 1634 XDWRB 137	77.00	117.00	79.47	8.33	9.07	54.00	2.62	5.17	41.29	53.87	21.17
34	HUB 113 X K 603	77.00	119.67	75.07	9.00	9.70	57.33	2.54	4.52	44.28	52.60	23.30
35	HUB 113 XDWRB 137	75.00	122.00	81.67	8.00	8.77	48.33	2.41	5.00	38.00	54.95	20.22
36	K 603 X DWRB 137	76.00	119.67	80.10	8.67	10.37	47.00	2.30	4.88	35.45	58.68	20.93
	Parent mean & range											
	Mean	**73.70**	**118.33**	**77.87**	**8.08**	**8.06**	**42.21**	**2.03**	**4.89**	**36.45**	**51.37**	**18.54**
	Min	71.33	116.00	73.83	6.33	5.93	30.33	1.45	4.54	32.12	45.49	15.317
	Max	77.00	120.00	84.43	11.00	9.13	53.00	2.50	5.37	39.57	56.12	21.10
	F_1s mean & range											
	Mean	**75.73**	**119.31**	**83.24**	**9.04**	**9.70**	**53.55**	**2.52**	**4.93**	**38.47**	**59.48**	**22.71**
	Min	69.67	117.00	74.60	7.66	5.93	45	2.30	4.52	32.79	47.33	20.22
	Max	79.00	122.00	94.00	11.00	11.80	59.67	2.73	5.17	44.28	69.75	25.95
	SE(d)	0.85	0.91	2.66	1.13	0.45	2.12	0.09	0.10	2.23	3.87	2.11
	C.D. at 5%	1.70	1.81	5.31	2.26	0.90	4.23	0.19	0.22	4.45	7.72	3.49
	C.V. (%)	1.39	0.93	3.97	15.75	5.93	5.09	4.90	2.70	7.18	8.22	9.85