ESTIMATION OF MORPHOLOGICAL AND GENETIC ASPECTS FOR YIELD AND YIELD CONTRIBUTING TRAITS IN BARLEY (*Hordeum vulgare* L.)

THESIS

By

RAVINDER KUMAR
(A-2015-30-045)

Submitted to

CHAUDHARY SARWAN KUMAR
HIMACHAL PRADESH KRISHI VISHVAVIDYALAYA
PALAMPUR – 176 062 (H.P.) INDIA

in

Partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE IN AGRICULTURE
(DEPARTMENT OF CROP IMPROVEMENT)
(GENETICS AND PLANT BREEDING)

2019

Dr. Naval Kishore,
Scientist (Plant Breeding)

Department of Crop Improvement
CSK HP Krishi Vishvavidyalaya,
Palampur 176 062 (HP) India

CERTIFICATE – I

This is to certify that the thesis entitled **"Estimation of morphological and genetic aspects for yield and yield contributing traits in barley (*Hordeum vulgare* L.)"** submitted in partial fulfilment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the discipline of Genetics and Plant Breeding of Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur is a bonafide research work carried out by **Ravinder Kumar (Admission No. A-2015-30-45)** son of **Shri Rajbir Singh** under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been fully acknowledged.

Place: Palampur
Dated:

(Dr. Naval Kishore)
Major Advisor

CERTIFICATE- II

This is to certify that the thesis entitled **"Estimation of morphological and genetic aspects for yield and yield contributing traits in barley (*Hordeum vulgare* L.)"** submitted by **Ravinder Kumar (A-2015-30-45)** son of **Shri Rajbir Singh** to the Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur in partial fulfilment of the requirements for the degree of **Master of Science (Agriculture)** in the discipline of **Genetics and Plant Breeding** has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

(Dr. Naval Kishore)
Chairperson
Advisory Committee

(   )
External Examiner

(Dr. Rakesh Devlash)
Member

(Dr. H.K. Chaudhary)
Member

(Dr. G.D. Sharma)
Dean's nominee

Head of the Department

Dean, Postgraduate Studies

ACKNOWLEDGEMENTS

First and foremost, I offer my obeisance to THE ALMIGHTY GOD for his boundless blessing, which accompanied me in all the endeavours.

I am pleased to place my profound etiquette to my advisor **Dr. Naval Kishore**, Scientist (Plant Breeding), CSK Himachal Pradesh Krishi Vishvavidyalaya, Hill Agricultural Research and Extension Centre, Bajaura (Kullu) and esteemed Chairman of my Advisory Committee for his learned counsel, unstinted attention, arduous and meticulous guidance on the work in all the stages. His keen interest, patient hearing and constructive criticism have installed in me the spirit of confidence to successfully complete the task.

Cordial thanks are due to the esteemed members of my advisory committee**, Dr. H.K. Chaudhary**, Professor & Head (Department of Crop Improvement), **Dr. Rakesh Devlash,** Sr. Scientist (Plant Pathology) and **Dr. G.D. Sharma** (Principal Scientist) for their valuable suggestions and generous cooperation during the course of investigation and preparation of this manuscript.

My sincere thanks are also due to the faculty members of the department of Crop Improvement, CSKHPKV Palampur, **Dr. Gopal Katna**, **Dr. V.K. Sood**, **Dr. Satish Paul**, **Dr. (Mrs.) Vedna**, **Dr. R.K. Mittal** and also to the entire staff of HAREC, Bajaura. **Dr. S.K. Guleria** needs special mention for providing me with the much needed assistance and help at various occasions during the preparation of this manuscript.

I seize this opportunity with a personal touch of emotions to express my deepest and affectionate gratitude to my adorable and loving parents **Sh. Rajbir Singh** and **Smt. Kamlesh Devi** for their indispensable encouragement, selfless sacrifices, sustained inspiration and invaluable assistance throughout my life. I am also highly grateful for the love and support of my wife Monika and also highly grateful for the support of my brother Ankit Kumar.

I am also indebtly thankful to my seniors Rahul Kamboj, Amaninder and Nimit and my close friends Rahul, Ajay, Naval, Samar, Vashu and Rajan Kamboj for their diligent support during the making of this thesis. I must also thank Sawan for his unforgettable moral and emotional support. I must also thank Shri Bagwan Dev and Walia Ji for their diligent support. I am also highly beholden to the efforts put by the field staff of HAREC, Bajaura without them the completion of my research work would have not been possible.

My heartfelt thanks and appreciation for all those whom I am indebted on various occasions but have not named personally.

Needless to say, all errors and omissions are mine.

Place: Palampur
Dated: July, 2019

(Ravinder Kumar)

TABLE OF CONTENTS

LIST OF ABBREVIATIONS USED

Abbreviation		**Meaning**
a.m.s.l	:	Above mean sea level
°E	:	Degree East
°N	:	Degree North
CD	:	Critical Difference
cm	:	Centimetre
g	:	Gram
mm	:	Millimetre
NS	:	Non-Significant
gca	:	General combining ability
sca	:	Specific combining ability
*	:	Significant
RBD	:	Randomised Block Design
%	:	Per cent
SE	:	Standard error
SC	:	Standard check
BP	:	Better parent
CV	:	Coefficient of variation
h^2(ns)	:	Heritability (narrow-sense)
GA	:	Genetic advance
viz.	:	Vi delicet (namely)

LIST OF TABLES

Department of Crop Improvement, COA
CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur – 176 062 (HP)

Title of thesis : Estimation of morphological and genetic aspects for yield and yield contributing traits in barley (*Hordeum vulgare* L.)
Name of the student : Ravinder Kumar
Admission number : A-2015-30-045
Major discipline : Genetics and Plant Breeding
Minor discipline : Plant Pathology
Date of thesis submission : July, 2019
Total pages of the thesis : 90
Major Advisor : Dr. Naval Kishore

ABSTRACT

Combining ability studies were made by crossing seven lines of barley with four testers in line x tester fashion. The resultant F_1's (28) along with parents were evaluated in randomized block design with three replications at the Experimental Farm of Hill Agricultural Research and Extension Centre, Bajaura, Kullu, HP during *Rabi*, 2016-17. The analysis of variance revealed highly significant differences among the genotypes for all the traits studied. High values of PCV and GCV and high heritability coupled with high genetic advance was observed for number of grain per spike and seed yield/plant. Correlation and path studies showed that traits biological yield/plant, number of effective tillers/plant, harvest index and number of grains/spike may be selected for yield improvement. Line x tester analysis revealed significant differences for lines, testers and lines x testers indicating wide genetic variability among the genotypes and prevalence of additive variance for the significant traits. Predominance of contribution of lines was observed for days to flowering, days to maturity, plant height and harvest index; maximum contribution of testers for number of grains/spike, spike length and peduncle length, whereas contribution of line x tester was more for number of tillers/plant, biological yield/plant, seed yield/plant and 1000 grain weight than lines and testers indicating higher estimates of SCA variances for interaction. Magnitude of dominance variance was higher than additive variance for all the traits studied indicating non-additive gene action. Estimates of GCA showed that line Local Sudhrani for seed yield/plant alongwith HBL 713 and HBL 738 were good general combiners for most number of yield contributing characters. Tester HBL 276 was a good general combiner for seed yield and associated traits. Estimates of SCA effects revealed that cross combinations *viz.*, Local Sudhrani × HBL 276, HBL 722 × DWRUB 64, HBL 748 × DWRUB 64 and HBL 751 x HBL 113 were the best for seed yield and its component traits. Mid parent heterosis indicated that crosses *viz.*, HBL 722 x DWRUB 64, HBL 751 x DWRUB 64, HBL 751 x HBL 113, HBL 738 x HBL 113 and Local Sudhrani x HBL 276 were promising for seed yield and related traits.

Student
(Ravinder Kumar)
Date: July, 2019

Major Advisor
(Dr. Naval Kishore)
Date: July, 2019

Head of the Department

1. INTRODUCTION

Barley (*Hordeum vulgare* L; 2n=14) is the first domesticated crop and ancient among cereals. Barley is currently the fourth most important cereal of India and the World, both in area and tonnage harvested, after rice, wheat and maize. In India, barley is cultivated on about 737 thousand ha area with production of 1986 thousand tonnes and productivity of 26.95 q/ha (Anonymous, 2018). The major barley growing states in India are Rajasthan, Uttar Pradesh, Haryana, Punjab, Madhya Pradesh, Uttrakhand, Himachal Pradesh, Bihar, Jammu and Kashmir, West Bengal, Chhattisgarh and Sikkim. In Himachal Pradesh, next to wheat, barley is the most important winter cereal with respect to area and production, cultivated on about 20.40 thousand ha. area with a production of approximately 35.80 thousand tonnes having productivity of 17.55 q/ha (Anonymous 2018). Since time immemorial, barley is considered as a crop of rainfed situation and problematic soil conditions i.e. saline-alkaline, drought and diara (marginal/coastal area of river). It is the main crop of higher elevation under rainfed conditions and of high hill dry temperature zone, generally grown on marginal land and has several use for the hilly people food, feed, fodder and local beverages (Al-Tabbal and Al Fraihat 2012).

Barley was domesticated about 10,000 years ago in the fertile crescent of the Near-East. It is a staple food in several regions of the world i.e. in some areas of North Africa and the Near East, highlands of Central Asia, Horn of Africa, Andean countries and Baltic States. These regions are characterized by harsh living conditions and home to some of the poorest farmers in the world who depend on the low productive systems. It is considered as the first cereal domesticated for use by man as food and feed (Potla et al., 2013). It is one of the widely grown *Rabi* cereals in the temperate and tropical regions of the world. The major barley producing countries of world are Canada, USA, Germany, France, Spain, Turkey, UK, Denmark, Russia, Central Asian countries and Australia.

Barley belongs to genus *Hordeum* of Poaceae family and tribe Triticeae along with wheat and rye. The genus *Hordeum* comprises of 32 species and 45 taxa.

Hordeum vulgare is the most intensively studied species in barley consisting of both cultivated and wild forms, which are easily crossable and closely related (Fedak 1985). The cultivated form is referred to as subspecies *vulgare*, while the wild form is referred as subspecies *spontaneum* C. Koch. Both subspecies are diploids with 2n = 2x = 14 chromosomes. The subspecies *vulgare* may be two or six-rowed spikes, whereas *spontaneum* is of two-rowed type with brittle rachis.

Barley can grow in a wide range of environments than any other cereal, including extremes of latitude, longitude and high altitude (Kishore et al. 2016). Around 55-60 per cent of barley is used for feed, 30-40 per cent for malt, 2-3 per cent for food and 5 per cent for seed (Ullrich 2010).

From nutritional point of view, barley grain is considered as superior over other cereals due to its higher biological value and rich source of β-glucans, acetylcholine, thiamin, riboflavin, total dietary and water soluble digestible fibre. Recent research regarding dietary composition in food barley has renewed the interest confirming the health benefits of barley in human diets (Brockman et al. 2013; Sullivan et al. 2013). In comparison to other cereal crops, barley has a better fodder value including grain and straw. In most of the developed countries, barley straw is used for animal bedding, whereas it is used as animal feed in the developing countries. Even under variable climate within the growing season, barley gives comparably better yield than wheat and other small grain cereals. Being one of the most widely adapted crops, the barley germplasm pool has the potential to contain enough genetic diversity to breed for adaptation to different environmental conditions. Owing to its vast morphological and environmental adaptability, various types of barley (winter, spring, two rowed, six rowed, awned, awnless, hooded, covered, naked, malting, feed and food types) are grown throughout the world. Moreover, the ample barley germplasm resources available worldwide (Bockelman and Valkoun 2010) likely contain beneficial allelic variation that new genomic and breeding technologies can exploit (Newton et al. 2011).

The production of barley can be increased either by increasing cultivated area or by increasing yield per unit area. Currently, it is nearly impossible to increase area under barley crop due to competition with other crops and restricted supply of irrigation water. Therefore, one of the alternatives is to increase yield per unit area through better crop management techniques and enhancing cultivation of high yielding varieties with adequate resistance against biotic and abiotic stresses. Expansion of the cultivated area of barley in India somehow seems difficult.

The breeding method in any crop depends upon its genetic architecture and the pattern possible only in rainfed areas. A thorough understanding of the genetics and related aspects of a crop is necessary for improvement of yield and quality parameters of inheritance of characters. Therefore, proper understanding of the nature of inheritance of yield and its components by estimation of genetic parameters like heterosis and combining ability is required to put such a breeding programme on sound footing. To evolve an effective breeding programme, combining ability analysis is used to test the performance of parents in different cross combinations and characterize the nature and magnitude of gene effects in the expression of yield and associated traits. The study of heterosis helps the plant breeder in eliminating the less productive crosses in early generations.

Barley crop growth is governed by morphological and genetic factors which directly or indirectly influences the yield of the crop. Identification of genetically superior parents is an important pre-requisite for developing promising strains for effective transfer of targeted genes controlling both quantitative and qualitative traits in the resultant progenies. In order to launch a sound breeding programme, it is essential to have an idea of the nature and magnitude of variability, heritability and expected genetic advance in respect of breeding materials at hand. The choice of such parents would have to be done on some criteria since it become often difficult to predict on the basis of yield *per se* performance and whether any two given cultivars would combine well to produce desirable genotypes. Thus, information concerning the breeding behavior of the parents to be used is of fundamental importance in planning such a programme. Line x tester mating design is one of the powerful tools available to estimate combining ability effect and aids in exploitation of heterosis. The system permits the estimation of the effects of the general combining ability (GCA) of the parents and specific combining ability (SCA) of the hybrids to discriminate for their genetic worth as breeding materials. Thus, there is urgent need of preliminary assessment of barley varieties for breeding work, which would presumably broaden the genetic variability through various breeding tools.

Moderate to high incidence of yellow rust is also responsible for the low production and productivity of the crop. It is a well-known fact that the Central Himalayan region is the foci for infection of yellow rust which causes disease spread in the adjoining North Indian Plains. Therefore, sources of resistance to yellow rust as well as other diseases is required to be introgressed into the barley genetic background to prevent inoculum buildup of the pathogen.

Keeping in consideration the importance of barley as a feed and fodder crop under the rainfed situations of hilly areas, the productivity of barley has to be increased. The barley upgradation programme requires development of high yielding, disease resistant, nutritionally superior varieties to cater the demand of product-specific domestic and international market. Therefore, the present investigation has been proposed to employ line x tester design to screen lines and crosses for their combining abilities and usefulness of heterosis in crop improvement with the following objectives:

To

- assess the general and specific combining ability contributing to yield and related traits in barley, and
- study the genotypic and phenotypic associations among different morphological traits.

2. REVIEW OF LITERATURE

Plant breeder is mainly concerned with quantitative traits showing continuous variation such as yield. Therefore, it is imperative for a breeder to have the information on the complexity of yield and its component traits for an effective genetic improvement programme in various crop species. Among the different biometrical methods available to determine the genetic information from the performance of hybrids and for the identification of appropriate cross-combinations, “Line × Tester” mating design (Kempthorne 1957) gives comparable estimates of the genetic make-up of genotype(s). Further, it is also useful to identify the best general combiners amongst large number of parent lines by attempting relatively less number of crosses as compared to other mating design.

2.1 Variability, heritability and genetic advance

2.2 Correlation coefficient and path analysis

2.3 Combining ability studies

2.4 Heterosis

2.1 Variability, heritability and genetic advance

The observed variability is a combined estimate of genomic content and environmental causes. The magnitude of heritable portion of variability and more particularly its genomic contents is clearly the most important aspect of the breeding material, which have a close bearing on its response to selection. It was necessary to separate the total variation into heritable and non-heritable components with the help of genetic parameters i.e. genotypic and phenotypic coefficients of variation, heritability and genetic advance. Heritability indicates relative degree to which, a character (phenotypic variability) is transmitted from parent to offspring, while the genetic advance provide information on the extent of genetic gain in the population mean. However, the estimates of heritability alone does not provide an idea about the expected gain in the next generation but have to be considered in conjunction with estimates of genetic advance (Shukla et al. 2006; Atta et al. 2008). Therefore, an assessment to the extent of genetic variability, heritability and genetic advance were previously reviewed by following authors:

Singh et al. (2006) observed high heritability coupled with high genetic advance for plant height, ear length, number of grains/spike, 1000-grain weight and grain yield/plant, whereas genetic advance for days to flowering and days to maturity was comparatively low.

Nanak et al. (2008) found higher phenotypic coefficient of variability (PCV) than genotypic coefficient of variability (GCV). Highest estimates of heritability in broad sense were recorded for 1000-grain weight and number of grains/spike followed by biological yield/plant and grain yield/plant. High heritability coupled with higher estimates of genetic advance reflecting additive gene action were registered for grain yield/plant and number of grains/spike followed by biological yield/ plant.

Eshghi et al. (2010) observed highest heritability for number of grain/spike, number of tillers/plant and 1000 grain weight, indicating that these traits are controlled by additive effect, while low heritability and genetic gain were observed for grain yield/plant.

Jalata et al. (2011) studies on variability, heritability and genetic advance for yield and yield related traits in barley revealed that significant ($p<0.01$) variation was observed among materials tested for quantitative traits indicating the presence of variability. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was relatively higher for grain yield/plant, number of kernels/spike and spike weight. High heritability was obtained for spike length and grain yield/plant showing better condition for effective selection in these characters.

Singh (2011) showed significant differences among the genotypes for all the characters. Estimates of heritability ranged from 71.64% for days to maturity to 97.58% for peduncle length, while grain yield/plant showed 84.28% heritability. Heritability coupled with high genetic advance was observed for number of grains/spike, grain yield/plant, peduncle length, flag leaf length, flag leaf width and second leaf width indicating the importance of these traits in selection and crop improvement.

Verma and Verma (2011) revealed high mean, wide range, GCV, PCV, heritability and genetic advance for grain weight, days to heading, biological yield, tillers/metre and harvest index. Correlation coefficients showed significant positive association of grain yield with harvest index, biological yield and days to maturity.

Jalal and Ahmad (2012) revealed significant differences among barley entries for all the characters.

Al-Tabbal and Al-Fraihat (2012) reported that the analysis of variance revealed significant differences among genotypes for all the characters. Estimates of GCV and PCV were high for grain yield/plant, biological yield/plant and number of kernels/main spike. Broad sense heritability estimates for various traits ranged from 68 to 99.7%. Grain yield/plant showed highly significant positive genotypic and phenotypic correlation with only number of kernels/main spike. Multiple correlations of characters *via* tiller number/plant and number of kernels/main spike were significant and positive with grain yield/plant.

Vir and Sultan (2013) studied the genetic variability in thirty-four accessions of barley. Results showed that there were significant genotypic differences for seed yield per plant, 100-seed weight and grains per spike, number of seeds per spike, spike length, plant height and days to 50% flowering. Broad sense heritability estimates were high and ranged from 0.55 (days to 50% flowering) to 0.73 (100-seed weight).

Kumar et al. (2013) observed significant differences among the genotypes for all the characters. The characters *viz.*, number of grains/spike, number of tillers/metre row, ear length and harvest index showed high range of PCV and GCV. Estimates of heritability ranged from 54% (biological yield/plant) to 98% (number of grains/spike), while 57% for grain yield/plant. High heritability coupled with high genetic advance as percent of mean was observed for number of grains/spike, number of tillers/metre row, ear length, harvest index and 1000-grain weight.

Kumar et al. (2013) estimated the variability, heritability and genetic advance for yield and its component traits in barley. Mean squares due to treatments were positive and highly significant for all the characters. High PCV and GCV were recorded for grains/spike and number of grains/ear. High heritability coupled with high genetic advance was noted for biological yield /plant and number of tillers/plant. High heritability along with moderate genetic advance was recorded for plant height, harvest index and 1000 grain weight.

Derbew et al. (2013) found that analysis of variance showed highly significant differences among the tested genotypes for all traits considered in the study, indicating the presence of genetic variability in the traits. Grain yield varied between 436 and 375.5 kg/ha, plant height ranged from 44.95 to 94.1 cm, days to maturity between 92 and 131 days, and days to heading ranged between 57 and 94. Low PCV and GCV were observed for days to maturity. High heritability and high genetic advance was observed for flag leaf width, spikelets/spike and grain yield/plant.

Kumar and Shekhawat (2013a) evaluated twenty two barley genotypes for grain yield/plant and related morphological characters. Genotypes were significantly different for all the characters indicating sufficient variability in the experimental material. The characters *viz.,* plant height, spike length, peduncle length, number of tillers/plant, 1000 grain weight, biological yield/plant and grain yield/plant showed high GCV and PCV. High estimates of heritability along with high genetic advance (% of mean) were observed for plant height, spike length, peduncle length, number of tillers/plant, 1000 grain weight, biological yield/plant and grain yield/plant.

Raikwar et al. (2014) in a study of 10 genetically diverse varieties of barley indicated that heritability percentage ranged from 5.19 $h^{2}n$ (plant height) to 99.75 $h^{2}b$ (number of grains per spike).

Yadav et al. (2014) evaluated 52 genotypes of barley and recorded high estimates broad sense heritability for all traits except days to maturity, number of tillers per plant and grain yield per plant. High heritability estimates coupled with moderate GA were recorded for biological yield per plant, grains per spike, plant height and days to 50 per cent flowering.

Singh et al. (2014) reported high GCV and PCV for number of effective tillers/plant (29.86, 28.97), peduncle length (30.96, 30.67) and grain yield/plant (21.82, 20.72), respectively. High heritability coupled with high genetic advance were also observed for days to heading, grains/spike, biological yield/plant and grain yield/plant.

Addisu and Shumet (2015) evaluated 36 barley landraces in Southern Ethiopia and revealed significant differences among the landraces for the thirteen quantitative characters studied, except spike length. The phenotypic coefficients of variability were higher than genotypic coefficients of variability for all the characters. The greater difference between GCV and PCV was observed for spike and peduncle length, whereas high heritability coupled with high genetic advance was observed for biomass per plant, grain yield and number of tillers per plant indicating that selection for these characters could be more effective due to additive gene action.

Kaur et al. (2016) evaluated 45 genotypes comprising of hulled and hulless type barley from ICARDA along with six check varieties (DWRUB 52, DWRUB 64, DWRB 73, BH 902, RD 2035 and RD 2552) in an augmented design for grain protein content, starch content and agronomic traits. High heritability along with high genetic advance for grain yield, thousand grain weight, ear length and grain filling period showed that these traits were under control of additive genes and hence, can be improved by selection based on phenotypic performance.

Kumar et al. (2018) exhibited high PCV and GCV (>20%) along with high heritability coupled with high genetic advance for number of grains per spike, biological yield per plant and seed yield per plant which indicated the predominance of additive gene action.

2.2 Correlation coefficient and path analysis

Correlation study indicates the degree of interdependence of plant characters, which is an important tool in selection of a pertinent genotype. Therefore, information on association between characters is quite useful to plant breeders to formulate their breeding and selection strategies. The genetic architecture of seed yield can be better resolved through component traits rather than yield *per se*, as yield is the end product of multiplicative interactions between various yield components (Grafius, 1959). The correlations provide information about inter-relationship among yield and its components. The information on character association may be used in the prediction of correlated response to directional selection, construction of selection indices and identification of some characters which may have no value by themselves, but are useful as indicators of the more important ones under consideration (Johnson et al. 1955).

Path coefficient analysis permits partitioning of the correlation coefficients into direct and indirect effects of a set of independence variables on the dependent variable and gives more realistic contribution. This technique was originally developed by Wright (1921) but was first used for plant selection by Dewey and Lu (1959). To use this path coefficient analysis, it required cause and effect situation among the variables in any crop. Grain yield has been associated with a number of yield contributing characters and these characters themselves are inter-related. The available literature on path analysis for seed yield with their component traits in barley is briefly reviewed below.

Sethi and Singh (1971) recorded significant positive correlation among grain yield and number of spikes/plant. Positive correlation of grain yield with number of tillers/plant, nodes/tiller, plant height and days to 70% heading and maturity was observed.

Sethi et al. (1972) working in hulled barley reported that yield/plant, plant height, number of tillers/plant, grains/plant, days to flowering and test weight showed high heritability, GCV, PCV and GA. The regression analysis indicated that tillers/plant contributed about 75% of total variability for yield.

Naik et al. (1988) studied twenty genotypes of six-rowed barley and found that yield was positively correlated with productive tillers per plant. Path coefficient analysis indicated that direct selection for productive tillers/m and grains/spike against plant height could improve yield

Irfan-ul-Haq et al. (1997) carried out correlation analysis of grain yield and its components in twelve husked barley lines and observed positive association of grain yield with 1000-grain weight and number of spikelets per spike. However, grain yield was negatively associated with days to heading.

Hennawy (1997) in an interrelationship study found positive and significant phenotypic and genotypic correlations between grain yield per plant, grains/spike, 100-grain weight and harvest index.

Kishore et al. (2000) showed that grain yield/plant exhibited significant and positive association with plant height, number of tillers/plant, number of grains/ear and 1000-grain weight. The 1000-grain weight was also positively and significantly associated with plant height and number of tillers/plant.

Kumar and Prasad (2002) revealed that grain yield per plant showed significant positive genotypic correlation with grain number per ear, number of tillers, biological yield, harvest index and chlorophyll content. On the other hand, grain number per ear showed significant positive correlation with number of tillers per plant and biological yield per plant.

Yadav et al. (2002) observed that grain yield was significantly and positively correlated with number of grains/spike, biological yield, harvest index, grain weight and husk content, while 1000 grain weight, protein content and whole nitrogen content were significantly and negatively correlated with grain yield in the parents, F_1 and F_2 generations.

Najeeb and Wani (2004) studied the relationships of important characters of 10 barley cultivars. The magnitude of genotypic correlation was significant and positive for spike length, grains per spike, 1000-grain weight and biological yield per plant with grain yield per plant. Similarly, significant and positive correlation was observed for biological yield per plant with 1000 grain weight. Test weight also displayed significant, positive correlations with spike length, number of tillers per plant and grains per spike. Grains per spike showed positive correlations with spike length and number of tillers per plant. Spike length exhibited significant positive correlations with days to flowering, days to maturity and plant height. Significant and positive correlation was also exhibited by plant height with days to flowering and days to maturity. Days to maturity showed significant positive correlation with days to flowering. Path analysis indicated high and positive direct effects of number of tillers per plant, plant height, grains per spike, days to flowering and 1000 grain weight on grain yield per plant. Spike length and days to maturity had high direct negative influence on grain yield per plant.

Shahinnia et al. (2005) found highly significant positive phenotypic and genotypic correlations between grain yield per plant and harvest index, biological yield per plant, test weight, kernel weight per spike and kernel number per spike. Path analysis showed highest direct effect of kernel number/spike and indirect effect of kernel weight/spike via kernel number/spike on grain yield.

Bhatta et al. (2005) observed higher genotypic correlation coefficients than their respective phenotypic ones. Data revealed significant positive correlations of grain yield with 1000-grain weight and number of grains per spike. Grain yield was negatively correlated with days to heading.

Ataei (2006) studied correlations among some yield related charaters for 20 advanced lines. Result showed positive significant correlation coefficient of grain number per spike and 1000-grain weight with grain yield per plant. The direct effects of 1000-kernel weight and number of grain yield per plant were positive.

Singh et al. (2006) observed that the grain yield per plant had positive and significant correlation with the number of tillers per plant, number of grains per spike, grain weight per spike and 1000-grain weight at both genotypic and phenotypic levels. Path analysis showed that grain weight per plant and number of tillers per plant had the highest direct effects on the grain yield per plant. 1000-grain weight showed negative direct effect on yield. The positive indirect effect of grain weight per spike on grain yield through the number of grains per spike, 1000-grain weight, ear length and plant height was also considerable.

Singh et al. (2008) found that grain yield per plant exhibited positive association with spikes per plant followed by 100-grain weight and tillers per plant. Path analysis exhibited high positive and direct influence of 100-grain weight towards grains yield per plant followed by spikes per plant and tillers per plant. Spikes per plant also contributed to grain yield mainly through indirect effect via tillers per plant. The results indicated that selection for spikes per plant, 1000 seed weight and tillers per plant would lead to higher yield.

Yang et al. (2008) studied the partial correlation and showed that the coefficient of 1000 grain weight to yield was highest and most correlations were found negative among the yield components. He also noted positive direct effect of three yield components to yield per plant. Among them, the contribution of the 1000 grain weight was the largest indicating that increase of 1000 grain was the efficient way to increase grain yield during the late growing stage of barley. The indirect path coefficients were positive only between grains per spike and 1000 grain weight, the others were negative.

Dadashi (2010) observed that number of grains per spike, 1000 grain weight and number of fertile tillers per plant had significant positive correlation with grain yield per plant. The results derived from path analysis indicated that almost 70% of the yield increase was due to the direct effect of 1000 kernel weight. Number of kernels per spike was positively significant and tillers per plant were also found to have positive and significant direct effect on yield, but number of fertile tillers was indirectly affected by higher 1000 kernel weight.

Pal et al. (2010) revealed that grain yield per plant was correlated positively with tillers/plant, flag leaf area, spike length, spikelets/spike, fertile spikelets/spike and biological yield per plant. Path coefficient analysis indicated that grains/spike and fertile spikelets/spike had positive direct effect on grain yield per plant.

Drikvand (2011) showed that grain yield had positive significant correlation with number of spikes per square meter, harvest index, biological yield and straw yield per square meter, and negatively correlated with spike length and awn length. Using stepwise regression, 1000 grain weight, number of spikes per square meter, grains per spike and harvest index were the most important yield components. Path analysis showed that the number of spike per square metre and harvest index had positive direct effect on grain yield per plant.

Zaefizadeh et al. (2011) studied 22 hulless barley genotypes in a randomized complete block design with 3 replications. Correlation analysis showed that the trait number of seeds per spike was most effective which meant that to achieve high performance this attribute could be used. The maximum direct effect was related to harvest index. The maximum direct negative effect on yield performance was related to the days to heading.

Carpc and Celk (2012) indicated that grain yield was positively and significantly associated with all the yield components except 1000-kernel weight. The highest correlation coefficients were found between grain yield and kernel number per spike, and between grain yield and harvest index. Path analysis indicated that harvest index had the highest direct effect on grain yield followed by spike number and kernel number per spike. Percentages of their direct effect were 71.97, 48.47 and 28.22, respectively. On the other hand, most of the indirect effects of yield components on grain yield were found to be significant and positive.

Singh et al. (2014) revealed significant positive association of grain yield/plant with 1000 grain weight, peduncle length, number of effective tillers/plant and plant height. Path coefficient analysis exhibited high positive direct effect of 1000 grain weight followed by number of effective tillers/plant, number of grains/ear and plant height.

Kumar et al. (2018) showed significant and positive correlation of biological yield per plant, number of grains per spike and number of tiller per plant with seed yield per plant. Path coefficient analysis also exhibited high positive direct and indirect contribution of these traits towards seed yield per plant indicating further selection based on these traits for effective improvement in barley.

2.3 Combining ability studies

Combining ability can be defined as the ability of a genotype to transmit superior attributes to its crosses. General combining ability (GCA) indicates the average performance of a line in a series of cross combination, whereas specific combining ability (SCA) shows those effects in some definite combinations which significantly departed from what would be expected on the basis of the average performance of the lines involved (Sprague and Tatum, 1942). The significance of combining ability was first revealed by Davis (1927). Combining ability studies are useful in assessing the nicking ability of parents and thus, help in selecting parents that would give rise to more desirable segregants during hybridization programme. It also helps to characterize the nature and magnitude of a pragmatic breeding approach.

Spargue and Tatum (1942) initially defined combining ability as the relative ability of a biotype to transmit desirable performance to the crosses. According to them general combining ability (GCA) is the performance of a variety when crossed to many other lines or varieties. Specific combining ability (SCA) was similarly defined as the performance of a variety or line when crossed to another specific variety or line, do relatively better or worse than would be expected on the basis of average performance of parental lines involved. The general combining ability is primarily due to additive as well as additive × additive effects of genes and specific combining ability is due to non-additive (i.e. Intra-allelic and/or inter-allelic interaction) effects of genes.

Griffing (1956), Carnahm et al. (1960) and others suggested that GCA include both additive as well as additive × additive interaction. It has also been realized that high yielding lines may not necessarily be able to transmit their superiority to their hybrids (Allard, 1960). Hence, an estimate of GCA and SCA effects may be more reliable test rather than their *per se* performance.

Hayman (1957) explained general combining ability and reported that general combining ability was composed of additive and dominance portion, while specific combining ability involved dominance alone. However, when epistasis was present, both general and specific combining ability contained epistasis portion.

Riggs and Hayter (1972) reported that the large effects of general and specific combining ability both for early and late heading were detected. They further reported small effects for general and specific combining ability both for high and low grain number per ear, but significant positive correlations were found between the general combining ability effects and the corresponding parental expression of the characters. Significant interactions were detected between additive and non-additive effects at the F_1 and F_2 years in analysis conducted over both seasons.

Choudhary et al. (1974) reported that high SCA effects for plant height, ear length, grain yield, 100 grain weight and number of grains per ear were the results of crosses between high and low GCA parents line, indicating additive x dominant type of interaction for number of effective tillers. High SCA was produced by low x low general combiners, indicating dominant x dominant gene interaction.

Sharma (1978) studies on the parents, F_1's and F_2's at two plant desired densities revealed significant effects of years on yield, ears per plant, 1000 grain weight, height and of plant density on yield and ears per plant in F_1 and F_2 and 1000 grain weight in F_1. GCA effects were found to be no less affected by environmental interaction than SCA effects. A general decrease in the relative magnitude of SCA variance was observed in F_2.

Abdulamonov (1984) reported significant differences in GCA between varieties for all the characters except 1000-grain weight. Significant differences in SCA, indicative of the involvement of non-additive gene effect were found for plant height, grain weight, number (from the main ear) and 1000-grain weight.

Chauhan (1985) observed that significant genotype differences were found among the parental lines and F_1 population in all these characters except 250 grain weight. The variances of GCA were greater than those of SCA in all characters except number of spikelet per ear and of grains per ear, the highest SCA for grain yield and a high positive SCA value for 250 grain weight also. In a few cases in which both lines had high GCA but SCA was low, it was found that there was only silent genetic diversity between the lines. The highest heterosis was obtained for yield (60.84% above the better parent), though the parental lines had low and negative GCA.

Singh and Singh (1990) reported that the GCA and SCA effects were highly significant, indicating that both additive and non-additive effects were controlling days to heading and days to maturity. Significant GCA and SCA for 1000-grain weight were also reported.

Arabi et al. (1992) observed high genetic variability for the traits studied. Significant GCA and SCA were observed for all traits and the values were, in some cases, significantly modified by net blotch of barley.

Phogat et al. (1995) reported additive gene action for grain yield and some important associated traits.

Singh et al. (1996) reported that GCA effects were significant for most of the characters. Variance of GCA was significant for all the examined traits, whereas variance of SCA was important only for spikes per plant and lodging grade.

Madic (1996) reported that highest GCA value was observed for spike length. High heritability values were obtained for spike length (63.3%) and grain weight per plant (70%).

El-Seidy (1997a&b) reported additive gene action for grain yield and some important associated traits.

Bhatnagar and Sharma (1997) reported that the GCA and SCA components of variance were highly significant for all the characters evaluated in both F_1 and F_2 generations except variances due to SCA for grain yield. The GCA component of variance was higher than SCA in both F_1 and F_2 generations, indicating the predominance of additive gene effects. However, both GCA and SCA effects were highly influenced by the environment.

Bouzerzour and Djakoune (1998) reported additive gene action for grain yield and some important associated traits.

Bhatnagar and Sharma (1998) studied 45 crosses of barley grown under three environments (early, normal and late) and indicated that both GCA and SCA variances were important in controlling the inheritance grain yield and harvest index. However, GCA variances were predominant.

Martinez and Foster (1998a) reported additive gene action for grain yield and some important associated traits.

Manmohan et al. (2003) reported that the GCA and SCA variances were significant for spike per plant, grains per spike, spikelets per spike, grain yield and 1000 grain weight in both the environments (normal and heat stress). Only SCA for grains per spike was found non-significant under heat stress environment.

Ajmal et al. (2004) depicted greater proportion of variance components due to specific combining ability than that of general combining ability for days to maturity, spike length, spikelet per spike, 100-grain weight and grain yield which denoted the preponderance of non-additive type of gene-action for these characters. However the inheritance of plant height was shown to be conditioned by genes acting additively.

Singh et al. (2005) observed highly significant GCA and SCA for days to maturity, days to reproductive phase, peduncle length, number of grains/spike, biological yield/plant, harvest index, 1000 grain weight and protein content.

Dhadhal and Dobariya (2006) analyzed combining ability of 14 parents and their 33 F_1s under timely and late sowing conditions. Estimates of general combining ability effects revealed that none of the parents was a good general combiner simultaneously for days to heading, days to maturity, number of tillers per plant, length of main spike, number of spikelets per spike, number of grains per spike, grain yield per plant, harvest index, 1000-grain weight and protein content.

Singh et al. (2007) reported that the variance due to parents was significant for days to 50% flowering, plant height, spike length, grain per spike, 1000 grain weight and grain yield per plant indicating that parents possess good amount of variability. Variation due to hybrids was also highly significant for the all traits, suggesting that good amount of variability was generated among the hybrids. The relative estimates of variance due to SCA were higher than variance due to GCA for the all traits studied except for days to the flowering indicating the predominance of non-additive gene action.

Kakani et al. (2007) studies on diverse parents in barley and their F_1 and F_2 progenies indicated significant difference among the parents for GCA and among crosses for SCA for all characters studied. The GCA and SCA components for variance were significant for all the traits. The GCA/SCA ratio showed preponderance of non-additive gene action for characters, namely days to maturity, plant height, effective tillers per plant, biological age per plant, grain yield per plant, and harvest index. However, the additive gene action was predominant for days to heading and test weight.

Amiruzzaman et al. (2008) observed that variance due to GCA and SCA showed additive gene action for all the characters except spikes per plant. Significant mean sum of squares due to lines and testers for all the characters indicated enough variability among the lines and testers. Most of the crosses involving low x low or low x high general combiners produced high GCA effects for yield. Cross combinations between general combiners of high x low and high x high for spikes per plant, low x low and low x average for spike length, low x low and high x high for grain weight and low x low and low x average for grain number also revealed high SCA. The mode of genetic interaction varied from character to character ranging from epistatic to dominant type of gene action.

Singh et al. (2012) conducted an experiment to find out combining ability for high temperature tolerance. The observations were recorded in parents, F_1s and F_2s for 14 morphological parameters. The experimental results manifested significant differences among the parents for GCA and crosses for SCA for all the characters studied. The GCA and SCA components of variance were significant for all the traits. The GCA/SCA variance ratio below unity in both the generations showed the preponderance of non-additive gene effects for all the characters.

Potla et al. (2013) reported significant differences among the parents for GCA, among crosses for SCA for all the quantitative traits. It is therefore, the selective parents and crosses could be utilized for developing desirable genotypes/hybrids/ varieties with better yielding towards exploiting the hybrid vigour or other associated traits under crop improvement.

Bornare et al. (2013) revealed that the variance due to GCA and SCA were highly significant for most of the traits studied. The relative magnitude of these two variances indicated the predominance of additive gene action for plant height and thousand seed weight, while rest of the traits showed preponderance of non-additive gene action.

Zhang et al. (2015) showed that GCA and SCA was significantly different among parents and crosses.The performance of hybrid was significantly correlated with the sum of female and male GCA (TGCA), SCA and heterosis.

Shendy (2015a) reported that variances due to both general and specific combining ability were highly significant for all studied traits in both F_1 and F_2 generations. High ratios of GCA/SCA mean squares were detected for all traits studied in both F_1 and F_2 generations except for number of spike per plant in the F_1, spike length in F_2, number of grain per spike in F_2, plant height and 100-grain weight in the F_1 and F_2 generations, indicating the predominant role of additive gene action in the inheritance of these characters.

Patial et al. (2016) reported significant differences among parents, crosses and parent vs. crossed for all the traits studied indicating the presence of sufficient variability. 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 (dominance, over-dominance and epistasis) type of gene action in the inheritance of the traits. Hence, selection of superior plants should be deferred to later generation. Two crosses were found to be good specific cross combinations for grain yield and its related traits having high significant SCA.

Pesaraklu et al. (2016a) estimated the combining ability and heterosis in barley for a number of qualitative traits. Results of variance analysis showed that there were significant differences between genotypes for all the measured traits. General combining ability effect was significant for all traits, whereas specific combining ability effect was also significant for all traits except for plant height, days to physiologic maturity and spikelet density. Moreover, dominance variance was the most effective factor in genetic control of traits.

Rathore and Chauhan (2017) studied the GCA and SCA effects of ten parents and 45 F_1 hybrids of six-rowed barley and revealed that Ritambhara, Gitanjali, Jagrati and Lakhan were good general combiners for grain yield per plant and 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 expressed positive and highly significant desirable SCA effect for seed yield per plant.

Abdel-Moneam and Leilah (2018) observed that specific combining abilities (GCA and SCA) mean squares were highly significant for all studied traits.

2.4 Heterosis

The phenomenon of hybrid vigour in artificial plant hybrid was first studied by Koelreuter in 1776. Bruce (1910) explained heterosis on the combined action of favourable dominant or partial dominant factors. Shull (1914) first coined the term heterosis while defining it as the superiority of heterozygous genotypes with respect to one or more characters. Hull (1945) explained this phenomenon based upon over dominance. Hayes (1964) from his studies concluded that heterosis is normal expression of complex character when the genes are in highly heterozygous condition with dominance or partial dominance. Heterosis represents percentage increase or decrease in the mean value of F_1 hybrid over its mid parental value. Barley being a highly self-pollinated crop has been largely neglected in hybrid breeding research of autogamous cereals. Thus, scope for exploitation of hybrid vigour depends on the direction and magnitude of heterosis, biological feasibility of crop and nature of gene action. The phenomenon of heterosis has been observed to manifest for yield and its component traits by several workers.

Nasar and Khayrallah (1976) studied the F_1 hybrids of barley involving 5 parents. Significant heterosis was detected for grain yield in two of the ten crosses for number of tillers per plant in one cross, for number of grains per plant in two crosses, for plant height in three crosses and for grain weight in none of the crosses.

Garkavyi et al. (1980) reported that all the F_1 showed heterosis for number of productive tillers, but heritability for this trait was not high. Heritability for ear length was 10.51 to 58.5%. Over dominance was generally found for number of grains per plant, yield per plant, heritability being about 50% or higher.

Zhao et al. (1983) observed heterosis for height, grain weight per plant and grain weight per spike. Transgressive heterosis for all characters was less than 10%. Heading date and height were positively correlated with those of the male parents and spike numbers per plant and grain weight per plant were also positively correlated with those of the male parent, but less closely.

Huang (1984) observed the highest heterosis exceeding the mid parental values by 25-30%. Additive effects were important, so general combing ability values were high for most characters (76-96 %). Heritability eastimates were also high (61-89 %).

Burgazova and Burgasova (1985) observed heterosis in relation to the better barley parent for grain weight per plant and 1000 grain weight and plant height.

Sethi et al. (1987) reported that heterosis over the better parent was 26.54% for harvest index and 159.38% for grain yield per plant. Parents and crosses with good combining ability for both traits were identified and recommended for use in breeding programme.

Ulker and Ozgen (1993) studies on eight barley genotypes and their F_1 hybrids observed favorable heterosis for tiller number per plant and grain yield per spike and same for plant height, spike length and 1000-grain weight. Traits 1000-grain weight and grains per spike also contributed to yield heterosis (Guo and Xu 1994).

El-Seidy (1997a) observed significant heterotic effects over the mid parents detected for all traits except for 1000 kernel weight. Significant heterosis over better parents was noted for all the traits studied except for heading date in the second cross, while heterotic effect for 1000 kernel weight were absent.

Martinez and Foster (1998a) observed heterosis over the mid parent which was quite similar among crosses for heading date, but there was no heterosis over the high parent.

Singh et al. (1999) observed significant and positive heterosis for days to heading and plant height. It was noteworthy that significant and positive inbreeding depression was observed for days to heading indicating a possibility for selection of early maturing genotypes in advanced generation.

Subhani et al. (2000) reported significant average heterosis and heterobeltiosis values in barley for flag leaf area, tillers per plant, plant height, grains per spike, 1000-grain weight, biomass per plant and grain yield per plant under irrigated and drought stress conditions. The maximum heterosis was reported for grain yield per plant (36.39%), tillers per plant (15.71%) and spike length (12.54%) in cross LU 265 x Roh 90 under irrigated conditions, whereas cross combination Inq. 91 x 4072 exhibited maximum heterosis and heterobeltiosis for 1000-grain weight under irrigated and drought stress conditions.

Singh et al. (2002) noted the positive heterosis for plant height, number of spikes/plant and grain yield/plant except 1000 grain weight.

Daya et al. (2009) estimated highest economic heterosis for grain yield (48.82%) followed by number of productive tillers per plant (38.09%), 1000-grain weight (21.43%), length of spike (19.05%), number of grains per spike (11.63%) and plant height (11.72) indicating estimates of inbreeding depression due to additive x additive and additive x dominance types of epistatic gene action. Non-additive gene action was predominantly responsible for the expression of grain yield.

Abd El-Aty et al. (2011) reported that positive heterotic effects relative to the mid-parent were found for most of the traits in the five crosses, except for heading and maturity dates that showed negative heterotic effects. Also positive heterotic effects relative to the better parent were found for the most of crosses.

Vishwakarma et al. (2011) reported that considerable amount of heterosis over better parent was observed for almost all the characters. Highest heterobeltiosis (better parent heterosis) were observed for days to heading as well as days to maturity.

Amer et al. (2012) observed that variance due to lines, testers and line x testers were highly significant for most of the traits studied. Positive and negative heterosis over better parent and mid parent were detected for most traits.

Muhleisen et al. (2013) reported that mid-parent heterosis averaged 11.3% and ranged from 0.7 to 19.9%. Better-parent heterosis was slightly lower with an average of 9.2%. Maximum commercial heterosis (i.e., the difference between the hybrid performance and the performance of the best line variety) was 7.6%, which clearly underlines the significance of hybrid barley breeding. Accuracy to predict hybrid performance was only moderate based on mid-parent values ($r=0.46$; $P<0.001$) and GCA effects ($r=0.38$; $P<0.001$).

Shendy (2015b) studied heterosis and combining ability for grain yield and its contributing characters. Percentages of heterotic effects of the F_1 hybrids over their respective mid and better parents for grain yield ranged from 13.77 to 41.28 per cent and from 9.91 to 38.69 per cent, respectively.

Mansour (2016) reported positive heterotic effects relative to the mid parent and better parent for most of the studied traits. Generally, the most promising crosses were 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 the most studied traits in barley under saline conditions.

Pesaraklu et al. (2016) observed highest values of heterosis for grain number per spike, grain weight per spike and 1000-grain weight.

Ram and Shekhawat (2017c) observed sufficient degree of heterosis and heterobeltiosis for all the studied characters. Among top three crosses for grain yield per plant in all the environments, two crosses showed desirable heterosis and heterobeltiosis for one or more characters in all the environments. Significant inbreeding depression was reported for different traits in all the three environments. However, few crosses for grain yield per plant in E2 and E3 exhibited significant negative inbreeding depression.

Bernhard et al. (2017) studied that heterosis for biomass and grain yield facilitated breeding of productive dual-purpose winter barley hybrids and revealed that the average best-parent heterosis of grain yield was 7.7%, whereas average best-parent heterosis of dry matter yield was 9.1%. The higher grain yield of hybrids was mainly caused by the higher kernel number per ear.

Madhukar et al. (2018) carried out an experiment to study the heterosis in barley and found that the expression of heterosis varied with the crosses as well yield attributing traits. For grain yield, the maximum per cent 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.

3. MATERIALS AND METHODS

The present investigation entitled "Estimation of morphological and genetic aspects for yield and yield contributing traits in barley (*Hordeum vulgare* L.)" was carried out at Experimental Farm of Hill Agricultural Research and Extension Centre, Bajaura, Kullu-175125, HP. The details of the materials used and methods employed in the present investigation are described in this chapter under the following headings:

3.1 Experimental site

3.2 Experimental material

3.3 Layout of the experiment

3.4 Observations recorded

3.5 Biometrical analysis

  3.5.1 Analysis of variance

  3.5.2 Genetic parameters of variation

  3.5.3 Estimation of correlation coefficients

  3.5.4 Path analysis

  3.5.5 Line x tester analysis

  3.5.6 Estimation of heterosis

3.1 Experimental site

The Experimental Farm is situated at an elevation of 1090 m above mean sea level with $31^0$48' N latitude and $77^0$9' E longitude. Agro-climatically, the location represents the mid-hill zone of Himachal Pradesh (zone-II) and is characterized by humid sub-temperate climate with high rainfall (944 mm). The soil is neutral in nature with pH ranging from 6.5 to 7.0 and soil texture is silty clay loam.

3.2 Experimental material

The experimental material used for the present investigation consisted of F_1 population of 28 crosses developed (Table 3.1) by crossing 7 lines/genotypes *viz.*,

HBL 713, HBL 722, HBL 723, HBL 738, HBL 748, HBL 751 and Local Sudhrani with four testers *viz*., HBL 113, HBL 276, DWRUB 64 and Atahualpa. All the lines used as female parents were crossed to each of the testers by hand pollination using the standard procedure as per line x tester model and thus true to type seeds were produced during *Rabi*, 2015-16.

Table 3.1 List of barley genotypes used in making crosses in line x tester mating design

S. No.	Lines	Pedigree	Type	Source
1	HBL 713	HBL 276 × HBL 364	6R, Hulled	CSKHPKV, Palampur
2	HBL 722	IBYT-LRAC-17(2010-2011)	2R, Hulled	CSKHPKV, Palampur
3	HBL 723	IBYT-LRAC-18(2010-2011)	6R, Hulled	CSKHPKV, Palampur
4	HBL 738	IBOHI-65 (EIBGN 2012-2013)	2R, Hulled	CSKHPKV, Palampur
5	HBL 748	P.STO/3/LBIRAN/UNA80/LIGNEE640/4/BLLU15/PETUNIA1/6/LEGAGU/PENCO/CHEVRON-BAR	6R, Hulless	CSKHPKV, Palampur
6	HBL 751	ZIGZIG/4/TOCTE//HIOG/LINO/3/ PETUN18 A 1	6R, Hulless	CSKHPKV, Palampur
7	Local Sudhrani	Local collection	6R, Hulled	Local collection, vill. Sudhrani, Kullu
	Testers			
8	Atahualpa	Selection from Ecuador	2R, Hulless	Ecuador
9	DWRUB 64	DL472/PL705	6R, Hulled	IIWBR,Karnal
10	HBL 113	Selection from Zephyre	2R, Hulled	CSKHPKV, Palampur
11	HBL 276	HBL 233 × HBL 238	6R, Hulless	CSKHPKV, Palampur

3.3 Layout of the experiment

The experimental material comprising of parents (seven lines and four testers) and the resultant 28 F_1s were evaluated in Randomized Block Design with three replications at the Experimental Farm, Hill Agricultural Research and Extension Centre, Bajaura, Kullu-175125, HP during *Rabi* 2016-17. Parents and F_1s were grown in single row of 1 m length. The row to row distance was 30 cm apart. Recommended package of practices were followed for raising the crop.

3.4 Observations recorded

The data were recorded on five random competitive plants for parents (lines and testers) and individual plants were sampled for F_1s in each replication for all the traits, whereas days to 50% flowering and days to maturity were recorded on plot basis.

1. Days to 50 per cent flowering

The number of days taken from the date of sowing to 50 per cent blooming of the plants was recorded on plot basis.

2. Number of effective tillers/plant

The number of effective tillers per plant were counted at the time of harvest.

3. Peduncle length (cm)

Length from the base of the spike to the first node was measured in centimetre.

4. Spike length (cm)

It was recorded from the base of spike to tip of the spike (excluding awns) in centimetre.

5. Number of grains/spike

Total number of seeds in each spike per plant in each plot were counted and then averaged.

6. Plant height (cm)

The height of plant from the base to the tip of the spike on the main stem was recorded in centimetres and mean value was obtained.

7. Days to maturity

The number of days taken from the date of sowing to maturity of the plants was recorded on plot basis.

8. Biological yield/plant (g)

Five randomly taken sun dried plants were weighed (g) and average weight per plant was calculated.

9. 1000-grain weight (g)

A random sample of 1000 dry seeds of each genotype was taken and weight was recorded in grams.

10. Seed yield/plant (g)

Total seed weight of five randomly selected plants in each plot were recorded and averaged.

11. Harvest index (%)

Harvest index was estimated as per cent of seed yield per plant and biological yield per plant.

$$\text{HI (\%)} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

3.5 Biometrical analysis

The data recorded on 28 crosses along with seven lines and four testers for different characters were analyzed as per the design i.e. line x tester for working out the following values.

3.5.1 Analysis of variance

For working out the analysis of variance the data was analyzed by using the following model as suggested by Panse and Sukhatme (1984).

$Y_{ij} = \mu + g_i + r_j + e_{ij}$

Where,

Y_{ij} = phenotypic observation of i^{th} entry in j^{th} replication,

μ = general mean,

g_i = effect of i^{th} entry,

r_j = effect of j^{th} replication, and

e_{ij} = error component

Analysis of variance

Sources of variation	df	Mean sum of squares	Expected mean sum of squares
Replications	(r-1)	Mr	$\sigma^2 e + g\sigma^2 r$
Genotypes	(g-1)	Mg	$\sigma^2 e + r\sigma^2 g$
Error	(r-1)(g-1)	Me	$\sigma^2 e$

Where,

r = number of replications,

g= number of genotypes,

$\sigma^2 g$ = variance due to entries,

$\sigma^2 r$ = variance due to replications, and

$\sigma^2 e$ = error variance.

The replications and entries mean squares for entries were tested against error mean squares by ‘F’ test for (r-1), (g-1) and (r-1)(g-1) degrees of freedom at P=0.05. From this analysis the following standard errors were calculated where the ‘F’ test was significant.

Standard error for the entry mean

$$SE(m) = \pm \sqrt{Me/r}$$

Standard error for the difference of entry mean

$$SE(d) = \pm \sqrt{2Me/r}$$

The critical difference (CD) at 5% level of probability was obtained by multiplying SE(d) ± by the table value of ‘t’ for error degree of freedom at P = 0.05.

CD = SE(d) ± x ‘t’ value for error degree of freedom at P = 0.05.

3.5.2 Genetic parameters of variation

3.5.2.1 Phenotypic and Genotypic coefficient of variance

The genotypic, phenotypic and environmental coefficients of variation were estimated following Burton and De Vane (1953):

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV \%)} = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

where,

$\sqrt{\sigma^2_g}$ = Genotypic standard deviation

$\sqrt{\sigma^2_p}$ = Phenotypic standard deviation

$\bar{x}$ = Grand mean

For categorizing the magnitude of PCV and GCV, the following limits were used:

PCV and GCV	> 25%	-	High
	20% - 25%	-	Moderate
	< 20%	-	Low

3.5.2.2 Estimation of heritability (%)

Heritability in broad sense (h^2_{ns}) was calculated as per the following formula

$$\text{Heritability } (h^2_{bs}) = \frac{\sigma^2 g}{\sigma^2 p}$$

Where,

h^2_{bs} = estimated heritability

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

For categorizing the magnitude of heritability, the following limits were used:

Heritability (h^2_{bs}) =	> 60%	High
	30% - 60%	Moderate
	<30%	Low

3.5.2.3 Genetic advance (%)

The expected genetic advance (GA) resulting from the selection of 5 per cent superior individuals was calculated as per Burton and De Vane (1953) and Johnson et al. (1955).

$$GA = K \times \sigma_p \times h^2_{(bs)}$$

where,

K = 2.06 (selection differential at 5 per cent selection intensity)

$h^2_{(bs)}$ = heritability (broad sense)

σ_p = phenotypic standard deviation

$$\text{Genetic advance as percentage of mean (GA \%)} = \frac{\text{Expected GA}}{\bar{X}} \times 100$$

3.5.3 Estimation of correlation coefficients

Phenotypic and genotypic coefficients of correlation were worked out following the procedure of Al-Jibouri et al. (1958) and Dewey and Lu (1959).

Analysis of covariance

Source	Degree of freedom	Mean sum of product	Expected mean sum of product
Replication	(r–1)	$Mr_{\times y}$	$\sigma e_{\times y} + g.\ \sigma r_{\times y}$
Genotypes	(g–1)	$Mg_{\times y}$	$\sigma e_{\times y} + r.\ \sigma g_{\times y}$
Error	(r-1)(g-1)	$Me_{\times y}$	$\sigma e_{\times y}$

where,

r = number of replications

g = number of genotypes

$\sigma g_{\times y}$ = genotypic covariance between traits × and y = $(Mg_{\times y} – Me_{\times y})/r$

$\sigma e_{\times y}$ = environmental covariance between traits × and y = $Me_{\times y}$

$\sigma p_{\times y}$ = phenotypic covariance between traits × and y = $\sigma g_{\times y} + \sigma e_{\times y}$

$Mg_{\times y}$ = mean sum of squares due to genotypes from the analysis of covariance between traits × and y

$Me_{\times y}$ = mean sum of squares due to error from the analysis of covariance between traits × and y

Phenotypic coefficient of correlation ($rp_{\times y}$)

$$rp_{\times y} = \frac{\sigma p_{\times y}}{(\sigma^2 p_{\times} \times \sigma^2 p_y)^{½}}$$

where,

$\sigma p_{\times y}$ = phenotypic covariance between two traits ‘×’ and ‘y’

$\sigma^2 p_{\times}$ = phenotypic variance of trait ‘×’

$\sigma^2 p_y$ = phenotypic variance of trait ‘y’

Genotypic coefficient of correlation ($rg_{\times y}$)

$$rg_{\times y} = \frac{\sigma g_{\times y}}{(\sigma^2 g_{\times} \times \sigma^2 g_y)^{1/2}}$$

where,

$\sigma g_{\times y}$ = genotypic covariance between two traits ‘×’ and ‘y’

$\sigma^2 g_{\times}$ = genotypic variance of trait ‘×’

$\sigma^2 g_y$ = genotypic variance of trait ‘y’

Test of significance

The significance of phenotypic coefficient of correlation at (g–2) degrees of freedom, where g stand for number of genotypes, was tested at 5 per cent level of significance against the table values of correlation coefficient (Fisher and Yates 1963).

To test the significance of genotypic coefficient of correlation, the F value was calculated using:

$F = [(g-2)\ r^2]/\ (1-r^2)$

It was compared with the F-distribution at 1 and (g–2) degrees of freedom, where g and r stand for number of genotypes and genotypic coefficient of correlation, respectively (Mead and Curnow 1983).

3.5.4 Path analysis

Path coefficient is a standardized partial regression coefficient, which permits the partitioning of the correlation coefficients into direct and indirect effects. The path analysis of important component traits and quality traits with green forage yield was done following Dewey and Lu (1959) as under:

$Py_1 + Py_2.r_{12} + Py_3.r_{13} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + Py_n.r_{1n} = ry_1$

$Py_1.r_{12} + Py_2 + Py_3.r_{23} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + Py_n.r_{2n} = ry_2$

$Py_1.r_{13} + Py_2.r_{23} + Py_3 + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + Py_n.r_{3n} = ry_3$

:

:

$Py_1.r_{1n} + Py_2.r_{2n} + Py_3.r_{3n} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + Py_n = ry_n$

where,

Py_1, Py_2, Py_3 ………….. Py_n are the direct path effects of 1, 2, 3, ………….., n variables on the dependent variable ‘y’.

r_{12}, r_{13}, ………….. r (n-1) n are the coefficients of correlation between various independent variables and ry_1, ry_2, ry_3, …………… ry_n are the correlation coefficients of independent variables with dependent variable ‘y’.

The variation in the dependent variable which remained undetermined by included variables was assumed to be due to variables (s) not included in the present investigation. The degree of determination of such variables was calculated as follows:

$$\text{Residual effect} = 1 - R^2$$

where,

$$R^2 = \sum_{i=1}^{n} p_{iy}\, r_{iy}$$

where,

R^2 is the squared multiple correlation coefficient and is the amount of variation in the yield that can be accounted for any yield component characters included in the present investigation. For performing path analysis, adjusted treatment means have been used.

3.5.5 Line x tester analysis

In this case the replication wise mean values of F_1 generation of 28 crosses for each trait were subjected to statistical analysis using following model given by Kempthorne (1957).

$$Yijk = \mu + gi + gj + sij + eijk$$

Where,

Yijk = value of the ijkth observation of the cross involving ith line and jth tester in kth replication,

μ = general mean (an effect common to all hybrids in all replications),

gi = general combining ability (gca) effect of ith line,

gj = general combining ability (gca) effect of jth tester,

sij = specific combining ability (sca) effect of the cross involving ith line and jth tester,

eijk = error associated with ijkth observation ,

i = ith line (1, 2, 3........10)

j = jth tester (1, 2, 3), and

k = kth replication (1, 2, 3)

Analysis of variance for combining ability

Source of variation	df	Mean square	Expected mean square
Replication	(r-1)	-	-
Crosses	(fm-1)	-	-
Lines	(f-1)	M(f)	$\sigma^2e + r\ \sigma^2fm + rm\,\sigma^2f$
Testers	(m-1)	M(m)	$\sigma^2e + r\ \sigma^2fm + rf\,\sigma^2m$
Line x Tester	(f-1)(m-1)	M(f x m)	$\sigma^2e + r\ \sigma^2fm$
Error	(fm-1)(r-1)	Me	σ^2e
Total	(fmr-1)		-

Where,

f = number of lines,

m = number of testers,

M(f) = mean squares due to lines,

M(m) = mean squares due to testers,

M(fm) = mean squares due to line x tester interactions,

Me = error mean squares,

σ^2f = variance due to lines/progeny variance arising from differences among female parents/lines,

σ^2m = variance due to testers/progeny variance arising from differences among male parents/testers,

σ^2f x m = variance due to lines x testers/progeny variance arising from interaction of the contribution of female and male parents, and

σ^2e = environmental variance per error variance among individuals from same mating.

3.5.5.1 Estimation of general and specific combining ability effects

GCA and SCA effects were obtained from the two way table of female parents vs. male parents in which each figures was total over replications. The individual effects were estimated as follows:

i) gca effects of ith line

$$gi = \frac{Xi..}{mr} - \frac{X...}{fmr}$$

where,

X... = sum total of all crosses,

Xi.. = total of ith female parent over all males and replications,

r = number of replications,

f = number of lines/female parents, and

m = number of testers/male parents.

Check, $\sum gi = 0$

gca effects of j^th tester

$$gj = \frac{Xj..}{fr} - \frac{X...}{fmr}$$

where,

Xj.. = total of j^{th} male parent overall females and replications.

Check, $\sum gi = 0$

ii) sca effects of ij^{th} cross

$$sij = \frac{xi\,j.}{r} - \frac{xi..}{mr} - \frac{xj..}{fr} + \frac{x...}{fmr}$$

where,

xij. = ij^{th} combination total over all replications.

Check, $\sum_{i} Sij = \sum_{j} Sij = \sum_{i}\sum_{j} Sij = 0$

Standard errors for different combining ability effects

SE (gi) lines = $(Me / mr)^{½}$

SE (gj) testers = $(Me / fr)^{½}$

SE (si j) crosses = $(Me / r)^{½}$

SE (gi - gj) lines = $(2Me / mr)^{½}$

SE (gj - gj) testers = $(2Me / fr)^{½}$

SE (si j - skl) crosses = $(2Me / r)^{½}$

Where,

Me = mean sum of squares due to error.

Critical difference (CD) = SE (difference) x ‘t’ table value for error degree of freedom at P = 0.05

Test of significance for gca and sca effects

$$\text{For gca of lines (females)} = t_i = \frac{g_i - 0}{SE\ (g_i)}$$

$$\text{For gca of testers (males)} = t_j = \frac{g_j - 0}{SE\ (g_j)}$$

$$\text{For sca of crosses} = t_{ij} = \frac{s_{ij} - 0}{SE\ (s_{ij})}$$

Where,

ti, tj and tij are the calculated ‘t’ values,

gi = gca effect of ith line,

gj = gca effect of jth tester, and

sij = sca effect of i jth cross.

Calculated ‘t’ values were compared with the tabulated ‘t’ values for error degree of freedom at P= 0.05.

3.5.5.2 Estimation of variance components

The co variances were calculated as suggested by Singh and Chaudhary (1977).

$$\text{Cov (HS)} = \sigma^2 f \text{ (females)} = \frac{M_f - M_{fm}}{mr}$$

$$\text{Cov (HS)} = \sigma^2 m \text{ (males)} = \frac{M_m - M_{fm}}{fr}$$

$$\sigma^2 fm \text{ (females x males)} = \frac{M_{fm} - M_e}{r} = \sigma^2 sca$$

Estimation of Cov HS (Average) and Cov (FS)

These were calculated as:

$$\text{Cov HS (average)} = \frac{(m\, \sigma^2 f + f\, \sigma^2 m)}{(f + m)}$$

$$\text{Cov (FS)} = \sigma^2 fm + 2 \text{ Cov (HS)}$$

This can also be calculated from the expection of mean squares as:

$$\text{Cov HS (average)} = \frac{M_f + M_m - 2M_{fm}}{2\,(f + m)}$$

$$\text{Cov (FS)} = \frac{M_f + M_m + M_{fm} - 3M_e}{3r} + \frac{6r \text{ Cov (HS)} - r\,(f + m) \text{ Cov (HS)}}{3r}$$

Estimation of gca and sca variances

From the estimates of Cov (HS) and Cov (FS), variances due to general combining ability and specific combining ability were calculated as:

$$\sigma^2 gca = \text{Cov (HS)} = \frac{M_f + M_m - 2\, M_{fm}}{r\,(f + m)}$$

$$\sigma^2 sca = Cov\,(FS) - 2Cov\,(HS) = \frac{M_{fm} - M_e}{r}$$

Estimation of additive (σ^2A) and dominance (σ^2D) components of variances

For computing the additive and dominance components of variances following formulae have been used (Singh and Chaudhary, 1977).

$$\sigma^2 gca = [\,1 + F / 4]\ \sigma^2 a = \tfrac{1}{2}\,\sigma^2 A$$

$$\sigma^2 sca = [\,1 + F / 2]^2\ \sigma^2 D = \sigma^2 D$$

where,

F = inbreeding coefficient,

σ^2A = additive variance, and

σ^2D = dominance variance.

3.5.5.3 Percent contribution of lines, testers and their interactions

There were computed as per the formulae suggested by Singh and Chaudhary (1977).

$$\text{Percent contribution of lines} = \frac{\text{SS (lines)}}{\text{SS (crosses)}} \text{ X } 100$$

$$\text{Percent contribution of testers} = \frac{\text{SS (testers)}}{\text{SS (crosses)}} \text{ X } 100$$

$$\text{Percent contribution of lines x testers} = \frac{\text{SS (lines x testers)}}{\text{SS (crosses)}} \text{ X } 100$$

3.5.6 Estimation of heterosis

The estimates of heterosis were calculated as the deviation of F_1 mean from the mid parent (MP).

$$\text{Heterosis over mid parent (\%)} = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

(i) Calculations of standard errors

$$\text{SE for testing heterosis over MP} = \pm\sqrt{2Me/r} = SE\,(H_1)$$

(ii) Test of significance for heterosis

$$\text{Heterosis over MP} = \frac{\overline{F_1} - \overline{MP}}{SE\,(H_1)} = \text{‘}t_1\text{’ Calculated value}$$

The ‘t’ calculated values (t_1) for heterosis over mid parent (MP) were compared with ‘t’ tabulated values for error degree of freedom at $P = 0.05$.

4. RESULTS AND DISCUSSION

The results obtained from the present investigation are presented under following heads.

4.1 Analysis of variance

4.2 Mean performance

4.3 Genetic parameter of variation

4.4 Correlation coefficient analysis

4.5 Path coefficient analysis

4.6 Line x tester analysis

4.7 Heterosis

4.1 Analysis of variance

The results of analysis of variance for 11 traits were carried out to partition the total variation into the variation due to genotypes and other sources. The analysis of variance revealed highly significant differences amongst the genotypes for all the traits studied. The analysis of variance for seed yield and its component traits are presented in Table 4.1.

4.2 Mean performance of barley genotypes

The variation in different traits under study revealed the measure of free variability in the population of different genotypes which would reflect the unforeseen impact of potential variability on yield. The mean performance for grain yield and its contributing characters are presented in Table 4.2.

4.2.1 Days to 50% flowering

Days to 50% flowering ranged from 117 days for the cross HBL 738 × Atahualpa to 139 days for the parent Local Sudhrani. Two crosses, namely HBL 738 × Atahualpa (117 days) and HBL 738 × DWRUB 64 (118 days) followed by parent HBL 738 (118 days) were significantly early in flowering than the best check, Atahualpa (121 days).

Table 4.1 Analysis of variance for seed yield and its component traits in barley

S.No.	Characters	Source	Replication	Genotypes	Error
			Mean Squares		
		df	**2**	**38**	**76**
1.	Days to 50% flowering		27.27	90.70**	5.78
2.	Days to maturity		79.09	101.72**	4.92
3.	Plant height (cm)		316.48	340.99**	52.93
4.	No. of tillers/plant		8.24	20.69**	3.76
5.	No. of grains/spike		29.60	738.47**	10.64
6.	Spike length (cm)		11.89	4.67**	1.07
7.	Peduncle length (cm)		7.54	65.79**	17.38
8.	1000 grain weight (g)		2.65	349.20**	5.42
9.	Biological yield/plant (g)		76.21	1021.28**	104.00
10.	Seed yield/plant (g)		6.57	155.25**	11.50
11.	Harvest index (%)		3.06	47.19**	7.06

* Significant at 5 per cent level; **Significant at 1 per cent level

Table 4.2 Genetic parameters of variability for seed yield and related traits in barley

S. No.	Character	Mean ± SE(m)	Range	PCV (%)	GCV (%)	h^2bs (%)	Genetic advance (% of Mean)
1.	Days to 50% flowering	5.78±1.39	117- 139	4.51	4.11	83.04	7.72
2.	Days to maturity	4.92±1.28	154-175	3.72	3.47	86.77	6.66
3.	Plant height (cm)	52.93±4.20	84-124	11.45	9.19	64.46	15.20
4.	No of tillers/plant	3.76±1.12	4-14	31.75	24.60	60.04	39.27
5.	No. of grains/spike	10.64±1.88	22-67	37.81	37.00	95.80	74.61
6.	Spike length (cm)	1.07±0.60	6.65-11.55	16.92	12.31	52.95	18.46
7.	Peduncle length (cm)	17.38±2.41	18.13-42.40	18.29	12.69	48.15	18.14
8.	1000 grain weight (g)	5.42±1.34	32-68	20.63	20.16	95.48	40.58
9.	Biological yield/plant (g)	104.00±5.89	31.28-115.64	33.26	28.73	74.62	51.13
10.	Seed yield/plant (g)	11.50±1.96	8.85-38.36	36.51	32.79	80.65	60.65
11.	Harvest index (%)	7.06±1.53	27.65-42	13.10	10.60	65.44	17.66

PCV: Phenotypic Coefficient of Variation; GCV: Genotypic Coefficient of Variation; h^2bs (%): heritability in broad sense

4.2.2 Days to maturity

Days to maturity ranged from 154 days for the parent Local Sudhrani to 175 days for the cross HBL 723 × HBL 113. None of the parents/crosses were significantly early in maturity than the best check, Atahualpa (155 days). However, parent Local Sudhrani (154 days) was at par with the best check.

4.2.3 Plant height (cm)

Plant height ranged from 84 cm for parent HBL 723 to 124 cm for the cross HBL 748 × Atahualpa. None of the parents/crosses were significantly lower in plant height than the best check, DWRUB 64 (94cm). Less plant height is desirable in barley to prevent losses due to lodging.

4.2.4 Number of tillers per plant

Numbers of tillers per plant ranged from 4 to 14 for the parents DWRUB 64 and HBL 113, respectively. None of the parents/crosses were significant for number of tillers per plant than the best check, HBL 113 (14). However, cross HBL 738 × HBL 113 (14) was at par with the best check.

4.2.6 Number of grains per spike

Number of grains per spike ranged from 22 to 67 for the crosses HBL 723 × Atahualpa and HBL 713 × HBL 276, respectively. However, none of the parents/crosses were significant for number of grains per spike than the best check, HBL 276 (66). However, crosses HBL 713 × HBL 276 and HBL 751 × HBL 276 were at par with the best check.

4.2.5 Spike length (cm)

Spike length ranged from 6.65 cm to 11.65 cm for the crosses HBL 748 × DWRUB 64 and Local Sudhrani × HBL 113, respectively. None of the parents/crosses showed significant values for spike length than the best check, HBL 113 (11.07cm). However, cross Local Sudhrani × HBL 113 (11.55cm) was found at par with the best check.

4.2.7 Peduncle length (cm)

Peduncle length ranged from 18.13 cm to 42.40 cm for the parent HBL 113 and cross HBL 738 × HBL 276, respectively. None of the parents/crosses were significant for peduncle length than the best check, HBL 276 (35.73). However, seven crosses *viz*., HBL 738 × HBL 276 (42.40cm), HBL 713 × Atahualpa (40.13cm), Local Sudhrani × Atahualpa (38.93cm), HBL 748 × Atahualpa (38.45cm), HBL 738 × Atahualpa (37cm), HBL 748 × HBL 276 (36.27cm) and HBL 751 × Atahualpa (36.27cm) were at par with the best check.

4.2.8 1000 grain weight (g)

The range of 1000 grain weight was observed from 32g for the parent HBL 276 to 68g the parent HBL 748 and crosses HBL 722 × DWRUB 64 and HBL 738 × HBL 276. Sixteen crosses, namely HBL 722 × DWRUB 64 (68g), HBL 738 × HBL 276 (68g), HBL 723 × HBL 113 (67g), HBL 722 × HBL 276 (66g), HBL 723 × Atahualpa (66g), HBL 723 × Atahualpa (66g), HBL 738 × DWRUB 64 (65g), Local Sudhrani × Atahualpa (65g), HBL 748 × Atahualpa (64g), HBL 748 × HBL 113 (62g), HBL 722 × HBL 113 (60g), HBL 738 × Atahualpa (59g), HBL 751 × HBL 113 (59g), Local Sudhrani × HBL 113 (59g), HBL 723 × DWRUB 64 (58g), HBL 751 × Atahualpa (56g) and one parent HBL 748 (68g) were significant than the best check, Atahualpa (51g).

4.2.9 Biological yield per plant (g)

Biological yield per plant ranged from 31.28 g for the cross HBL 751 × Atahualpa to 64g for parent HBL 723 (115.64g). None of the crosses were significant for biological yield per plant. However, crosses Local Sudhrani × HBL 276 (95.92g) and HBL 722 × DWRUB 64 (88.34g) were at par with the best check HBL 276 (84.05g).

4.2.10 Seed yield per plant (g)

Seed yield per plant ranged from 8.85 to 38.36g for the crosses HBL 751 × Atahualpa and Local Sudhrani × HBL 276. Only one cross Local Sudhrani × HBL 276 (38.36g) significantly outyielded the best check, HBL 276 (32.34). However, parents HBL 723 (36.83g) and HBL 713 (34.75g) were found at par with the best check.

4.2.11 Harvest index (%)

Harvest index ranged from 27.67% for the cross HBL 722 × HBL to 42% for parent Atahualpa. None of the parents/crosses were significant and at par for harvest index than the best check, Atahualpa (42%).

4.3 Genetic parameters of variation

The extent of phenotypic and genotypic coefficient of variability, heritability in broad sense and genetic advance as percent of mean recorded for various seed yield and component traits per plant in the present study are presented in Table 4.2.

4.3.1 Phenotypic and Genotypic coefficient of variance

It was observed that phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) for most of the traits were either high or moderate.

High values of PCV and GCV were observed for number of grains per spike (37.81, 37.0) and seed yield per plant (36.51, 32.79), respectively. Moderate estimates of PCV and GCV were observed for 1000 grain weight (20.63, 20.16), respectively. High PCV with moderate GCV were recorded for biological yield (33.26, 28.73) and number of tillers per plant (31.75, 24.60), respectively. Moderate PCV with low GCV was exhibited for peduncle length (18.29, 12.64) and spike length (16.92, 12.31), respectively. Low PCV and GCV were observed for days to 50% flowering (4.51, 4.11), days to maturity (3.72, 3.47), plant height (11.4, 9.19) and harvest index (13.10, 10.60), respectively.

4.3.2 Heritability

Heritability is a measure of the extent of phenotypic variation caused by the additive gene action. A perusal of the data presented in Table 4.2 revealed that the estimates of heritability in broad sense for all the 11 characters under study ranged from 48 to 95 per cent. High heritability estimates (above 80%) were observed for number of grains per spike (95.80%) followed by 1000 grain weight (95.48%), days to maturity (86.77%), days to 50% flowering (83.04%) and seed yield per plant (80.65%). Moderate estimates (30% to 80%) were obtained for biological yield per plant (74.62%) followed by harvest index (65.44%), plant height (64.46%), number of tillers per plant (60.04%), spike length (52.95%) and peduncle length (48.15%).

4.3.3 Genetic advance

Genetic advance as percent of mean varied from 6.66 to 74.61 per cent. Highest genetic advance as percentage of mean (above 50%) was observed for number of grains per spike (74.61%) followed by seed yield (60.65%) and biological yield per plant (51.13%), whereas moderate estimates (30% to 50%) of genetic advance were obtained for 1000 grain weight (40.58%) and number of tillers per plant (39.27%). Similarly, lower values of genetic advance were observed for spike length (18.46%), followed by peduncle length (18.14%), harvest index (17.66%), plant height (15.20%), days to 50% flowering (7.72%) and days to maturity (6.66%). High heritability coupled with high genetic advance was observed for number of grains per spike and seed yield per plant. 1000 grain weight recorded high heritability coupled with moderate genetic advance, whereas moderate heritability coupled with high genetic advance was observed for biological yield per plant. Therefore, the traits having high values for heritability and genetic advance are under the influence of additive gene action and selection would be more operational for their improvement.

The above studies for all the parameters of variability are in conformity with the findings of the earlier workers *viz*. Eshghi et al. (2010), Jalata et al. (2011), Singh et al. (2014) and Kumar et al. (2018).

4.4 Correlation coefficient analysis

The grain yield or economic yield, in almost all the crops, is referred to as super character which results from the multiplicative interactions of several component characters that are termed as yield components. Thus, genetic architecture of grain yield in barley as well as in other crops is based on the balance or overall net effect produced by various yield components directly or indirectly by interacting with one another. Therefore, identification of important yield components and information about their association with yield and also with each other is very useful for developing efficient selection criteria for evolving high yielding varieties. In this respect, the correlation coefficient which provides symmetrical measurement of degree of association between two variables or characters, help us in understanding the nature and magnitude of association among yield and yield components.

The phenotypic and genotypic correlation coefficients between studied characters are presented in Table 4.3. The genotypic correlation coefficients between different characters were generally similar in sign or nature to the corresponding phenotypic correlation coefficients in the experiment. However, genotypic correlations were higher in magnitude than the corresponding phenotypic correlations.

In the present study, high significant positive correlation of days to 50% flowering was observed with days to maturity, spike length, number of grains/spike and biological yield/plant, whereas it showed significant and negative correlation with peduncle length. Days to maturity showed significant and positive association with spike length, whereas significantly negative correlation was observed with peduncle length and harvest index.

Plant height was significantly and positively correlated with number of tillers/plant, spike length, peduncle length and harvest index, whereas significant negative association was observed with biological yield/plant. Number of tillers per plant was observed to be significantly and positively correlated with spike length, biological yield per plant, harvest index and seed yield per plant, whereas it was negatively correlated with number of grains per spike i.e. with increase in tiller number, there was reduction in grain number.

Number of grains per spike also showed significant positive association with biological yield per plant and seed yield per plant besides being negatively correlated with spike length and 1000 grain weight.

Biological yield per plant also showed negative correlation with peduncle length but it was positively correlated with harvest index. Harvest index was also positively correlated with spike and peduncle length. Therefore, harvest index could be increased with longer spikes and peduncle resulting in higher biomass of the plant.

Similarly, seed yield per plant showed significant and positive association with biological yield and harvest index. It was also observed that none of the traits exhibited significant negative association with seed yield. Therefore, the traits *viz.* number of tillers/plant, number of grains/spike, biological yield/plant and harvest index with significant positive associations with seed yield/plant emerged as yield contributing traits to be further selected for future breeding programme for higher grain yield in barley.

Similar correlations between yield and yield components in barley has also been reported by Yadav et al. (2002), Najeeb and Wani (2004), Singh et al. (2014), Kumar et al. (2018).

4.5 Path coefficient analysis

Path-coefficient analysis is a tool to partition the observed correlation coefficient into direct and indirect effects of yield components on seed yield to provide clear cut picture of character associations for formulating efficient selection criteria. Path analysis differs from simple correlations because it point out the causes and their relative importance, whereas correlation measures simply the mutual association ignoring the causation. The results of path analysis were given in the Table 4.4.

4.5.1 Direct effects of various characters on seed yield per plant

Four characters *viz*., biological yield per plant followed by harvest index, number of tillers per plant and number of grains per spike exerted positive direct effects on seed yield per plant at both genotypic and phenotypic levels, whereas the direct effects of other traits on seed yield/plant were negligible. The results from the present study indicated that the biological yield per plant and harvest index alongwith number of tillers/plant and grains/spike could be considered as the best selection indices for improvement of seed yield in barley.

4.5.2 Indirect effects of various characters on seed yield per plant

(i) Days to 50% flowering

Days to 50% flowering showed positive indirect effects on seed yield/plant through biological yield/plant followed by number of grains per spike and days to maturity, whereas negative indirect effects were exerted via harvest index.

(ii) Days to maturity

Days to maturity reported positive indirect effects on seed yield per plant through biological yield/plant, whereas negative indirect effects were observed via harvest index.

(iii) Plant height

Plant height exerted positive indirect effects on seed yield/plant through harvest index. The negative indirect effects via other traits were negligible.

(iv) Number of tillers per plant

Positive indirect effects of number of tillers per plant was observed on seed yield per plant via biological yield/plant and harvest index, whereas negative indirect effects were observed through number of grains per spike.

Table 4.3 Estimates of correlation coefficients at phenotypic (P) and genotypic (G) levels among different traits in barley

Traits		Days to maturity	Plant height (cm)	No. of tillers/ plant	No. of grains/ spike	Spike length (cm)	Peduncle length (cm)	1000 grain weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield/ plant (g)
Days to 50% flowering	P	0.4499**	0.0206	-0.0012	0.2774**	0.2578**	-0.3013**	-0.1526	0.1761	-0.1285	0.1278
	G	0.5089**	0.0331	0.0027	0.3233**	0.3371**	-0.4625**	-0.1679	0.2103*	-0.1589	0.1500
Days to maturity	P		-0.0568	0.0066	-0.0102	0.1885*	-0.1540	0.0343	0.0120	-0.2934**	-0.0660
	G		-0.0403	0.0173	-0.0228	0.2490**	-0.2224*	0.0322	-0.0230	-0.3648**	-0.1046
Plant height (cm)	P			0.1936*	-0.0515	0.4636**	0.5599**	-0.1015	-0.0047	0.4533**	0.1540
	G			0.1121	-0.0896	0.5924**	0.6934**	-0.1185	-0.1986*	0.6935**	0.0529
No of tillers/plant	P				-0.2468**	0.2499**	0.0135	0.0763	0.4725**	0.4205**	0.5805**
	G				-0.3149**	0.2418**	-0.0122	0.0828	0.4557**	0.6254**	0.5838**
No. of grains/spike	P					-0.1901*	-0.1086	-0.6466**	0.3961**	0.0205	0.3642**
	G					-0.3564**	-0.1682	-0.6785**	0.4399**	0.0260	0.3918**
Spike length (cm)	P						0.0877	0.0893	0.0323	0.1690	0.0933
	G						0.1734	0.1215	-0.0946	0.2383**	-0.0130
Peduncle length (cm)	P							-0.0070	-0.1389	0.3278**	-0.0085
	G							0.0103	-0.3171**	0.4718**	-0.1141
1000-grain weight (g)	P								0.0334	-0.1234	-0.0194
	G								0.0373	-0.1764	-0.0280
Biological yield/plant (g)	P									0.1283	0.9329**
	G									0.3315**	0.9529**
Harvest index (%)	P										0.4610**
	G										0.5928**

* Significant at 5 per cent level; **Significant at 1 per cent level

Table 4.4 Estimates of direct and indirect effects of different traits on seed yield/plant at phenotypic (P) and genotypic (G) level in barley

Characters		Days to flowering	Days to maturity	Plant height (cm)	No. of tillers/ plant	No. of grains/ spike	Spike length (cm)	Peduncle length (cm)	1000 grain weight (g)	Biological yield/plant (g)	Harvest Index (%)	Correlation with seed yield/plant (g)
Days to 50% flowering	P	**0.0066**	0.0098	-0.0001	-0.0001	0.0119	-0.0002	-0.0032	-0.0028	0.1497	-0.0438	0.1278
	G	**0.0019**	0.0056	0.0017	0.0003	0.0429	-0.0081	-0.0033	-0.0129	0.1613	-0.0395	0.1500
Days to maturity	P	0.0030	**0.0217**	0.0003	0.0003	-0.0004	-0.0001	-0.0016	0.0006	0.0102	-0.0999	-0.0660
	G	0.0010	**0.0110**	-0.0020	0.0020	-0.0030	-0.0060	-0.0016	0.0025	-0.0176	-0.0907	-0.1046
Plant height (cm)	P	0.0001	-0.0012	**-0.0056**	0.0089	-0.0022	-0.0004	0.0060	-0.0019	-0.0040	0.1543	0.1540
	G	0.0001	-0.0004	**0.0506**	0.0128	-0.0119	-0.0142	0.0050	-0.0091	-0.1524	0.1725	0.0529
No of tillers/plant	P	0.0000	0.0001	-0.0011	**0.0460**	-0.0106	-0.0002	0.0001	0.0014	0.4016	0.1431	0.5805^{**}
	G	0.0000	0.0002	0.0057	**0.1141**	-0.0418	-0.0058	-0.0001	0.0063	0.3496	0.1555	0.5838^{**}
No. of grains/spike	P	0.0018	-0.0002	0.0003	-0.0113	**0.0428**	0.0001	-0.0012	-0.0118	0.3367	0.0070	0.3642^{**}
	G	0.0006	-0.0003	-0.0045	-0.0359	**0.1327**	0.0085	-0.0012	-0.0520	0.3374	0.0065	0.3918^{**}
Spike length (cm)	P	0.0017	0.0041	-0.0026	0.0115	-0.0081	**-0.0008**	0.0009	0.0016	0.0275	0.0575	0.0933
	G	0.0007	0.0027	0.0300	0.0276	-0.0473	**-0.0239**	0.0012	0.0093	-0.0726	0.0593	-0.0130
Peduncle length (cm)	P	-0.0020	-0.0033	-0.0032	0.0006	-0.0047	-0.0001	**0.0106**	-0.0001	-0.1180	0.1116	-0.0085
	G	-0.0009	-0.0024	0.0351	-0.0014	-0.0223	-0.0041	**0.0071**	0.0008	-0.2432	0.1174	-0.1141
1000 grain weight (g)	P	-0.0010	0.0007	0.0006	0.0035	-0.0277	-0.0001	-0.0001	**0.0182**	0.0284	-0.0420	-0.0194
	G	-0.0003	0.0004	-0.0060	0.0095	-0.0900	-0.0029	0.0001	**0.0767**	0.0286	-0.0439	-0.0280
Biological yield/plant (g)	P	0.0012	0.0003	0.0000	0.0217	0.0170	0.0000	-0.0015	0.0006	**0.8499**	0.0437	0.9329^{**}
	G	0.0004	-0.0003	-0.0100	0.0520	0.0584	0.0023	-0.0023	0.0029	**0.7671**	0.0825	0.9529^{**}
Harvest index (%)	P	-0.0009	-0.0064	-0.0026	0.0193	0.0009	-0.0001	0.0035	-0.0023	0.1090	**0.3404**	0.4610^{**}
	G	-0.0003	-0.0040	0.0351	0.0714	0.0035	-0.0057	0.0034	-0.0135	0.2543	**0.2487**	0.5928^{**}

Note: Values in bold depict the direct effects

(v) Number of grains per spike

Number of grains per spike exhibited positive indirect effects on seed yield per plant through biological yield per plant and harvest index, whereas negative indirect effects were exhibited via 1000 grain weight and number of tillers per plant.

(vi) Spike length

Spike length revealed positive indirect effects on seed yield per plant through harvest index (0.0575) followed by biological yield per plant and number of tillers per plant. The negative indirect effects via other traits were negligible.

(vii) Peduncle length

Peduncle length exerted positive indirect effects on seed yield per plant through harvest index, whereas negative indirect effects were reported via biological yield/plant.

(viii) 1000 grain weight

The indirect effects of 1000 grain weight on seed yield per plant were positive through biological yield per plant, whereas negative indirect effects were exhibited via harvest index and number of grains per spike.

(ix) Biological yield per plant

Biological yield per plant exhibited positive indirect effects on seed yield per plant through harvest index followed by number of tillers per plant and number of grains per spike, whereas the indirect effects via other traits were negligible.

(x) Harvest index

Positive indirect effects of harvest index on seed yield/plant were exerted via biological yield per plant and number of tillers per plant. The negative indirect effects via other traits were negligible.

The traits biological yield/plant and harvest index proved to be of high significance through which all the characters exerted positive indirect effects on seed yield/plant. Besides, the traits plant height, spike length and harvest index also exhibited positive indirect effects on seed yield/plant via number of tillers/plant, whereas biological yield/plant showed positive indirect effects both via number of tillers/plant and number of grains/spike. However, negative indirect effects on seed yield/plant were also exerted by days to 50% flowering, days to maturity and 1000 grain weight via harvest index. 1000 grain weight and tillers/plant also exerted negative effects via grains/spike. To sum up, it was evident from the study that the traits number of tillers/plant, number of grains/spike, biological yield/plant and harvest index directly or indirectly influenced seed yield/plant and these may be selected for further improvement in seed yield of barley.

4.6 Line x tester analysis

4.6.1 Analysis of variance for parents and crosses

Analysis of variance for combining ability for yield and yield contributing traits are presented in Table 4.5. Significant differences among the parents and crosses were observed for all the traits studied. The mean squares due to testers (males) were recorded to be significant for all characters except for days to maturity and number of tillers per plant, which were found to be non-significant. The mean squares due to lines (females) were highly significant for all the traits except spike length. The mean squares due to line vs. tester were highly significant for all the characters except peduncle length. The mean squares for parents vs. crosses were found to be significant for all characters except days to 50% flowering and number of tillers/plant and revealed good scope for manifestation of heterosis in the significant traits. The genotypes were also found to be significant for all the traits studied.

Larger mean square values for four characters *viz.*, days to 50% flowering, 1000 grain weight, biological yield/plant and seed yield/plant in lines and high mean square values for the remaining seven traits in testers indicated enough diversity for combining ability in lines and testers for the respective traits. Therefore, both lines and testers were more or less equally responsible for combining ability of the crosses and indicated prevalence of additive variances for the traits studied. The mean squares due to line × tester interactions were found to be significant for seed yield and related traits except peduncle length suggesting that lines may have different combining ability patterns and performed differently in crosses depending on type of testers used.

Table 4.5 Analysis of variance for yield and yield attributing traits for lines, testers and crosses in barley

Source of variation / Traits	df	Days to flowering	Days to maturity	Plant height (cm)	No. of tillers/ plant	No. of grains /spike	Spike length (cm)	Peduncle length (cm)	1000 grain weight (g)	Biological yield/plant (g)	Seed yield/ plant (g)	Harvest index (%)
Replications	2	27.29*	79.09**	316.47**	8.24	29.60	11.89**	7.54	2.64	76.02	6.56	3.04
Treatments	38	90.70**	101.72**	340.99**	20.69**	738.47**	4.67**	65.79**	349.20**	1021.27**	155.25**	47.18**
Parents	10	138.19**	149.02**	190.65**	34.63**	848.45**	4.19**	74.31**	311.03**	2014.74**	255.21**	42.14**
Crosses	27	76.42**	83.56**	299.85**	16.13**	625.90**	4.47**	47.35**	332.47**	604.42**	115.97**	50.60**
Parents vs crosses	1	1.47	119.02**	2954.87**	4.46	2678.18**	15.09**	478.52**	1182.56**	2341.51**	216.25**	5.26**
Lines	6	151.16**	155.16**	161.86**	21.60**	824.22**	2.29	42.16**	325.19**	2844.85**	328.93**	15.75**
Testers	3	104.00**	172.00	171.33*	65.56	1162.75**	5.47**	162.96**	242.75**	793.27**	189.41**	90.13**
Line × tester	18	18.58**	42.34**	149.47**	16.75**	269.04**	2.59**	20.71	242.77**	605.61**	107.19**	25.03**
Error	76	5.78	4.92	52.94	3.76	10.64	1.07	17.38	5.42	104.01	11.50	7.06
Contribution of lines (%)	-	66.40	65.35	49.77	26.01	34.93	7.98	26.24	30.58	20.00	32.21	56.52
Contribution of testers (%)	-	17.39	0.87	17.00	4.75	36.41	53.36	44.60	20.74	13.20	6.17	10.50
Contribution of crosses (%)	-	16.21	33.78	33.23	69.23	28.66	38.66	29.16	48.68	66.80	61.62	32.98

* Significant at 5 per cent level; **Significant at 1 per cent level

It also indicated that specific combining ability (SCA) attributed heavily in expression of these traits and suggest importance of dominance or non-additive variances. Therefore, significant differences for lines, testers and lines x testers indicated wide genetic variability among the genotypes and prevalence of additive variance for the significant traits.

4.6.2 Contribution of lines, testers and crosses

The proportional contribution of lines, testers and crosses for different characters are shown in Table 4.5. Highest percent contribution due to lines was observed in days to 50% flowering (66.4%) followed by days to maturity (65.35%), harvest index (56.52%), plant height (49.77%), number of grains per spike (34.93%), seed yield per plant (32.21%), 1000 grain weight (30.58%), peduncle length (26.24%), number of tillers per plant (26.01%), biological yield/plant (20%) and spike length (7.98%). Maximum percent contribution due to testers was observed for the trait spike length (53.36 %) followed by peduncle length (44.6%), number of grains per spike (36.41%), 1000 grain weight (20.74%), days to 50 % flowering (17.39%), plant height (17.0%), biological yield per plant (13.2%), harvest index (10.5%), seed yield per plant (6.17%), number of tillers per plant (4.75%) and days to maturity (0.87%). Similarly, percent contribution due to crosses was observed in number of tillers per plant (69.23%) followed by biological yield per plant (66.8%), seed yield per plant (61.62%), 1000 grain weight (48.68%), spike length (38.66%), days to maturity (33.78%), harvest index (32.98%), peduncle length (29.16%), number of grains per spike (28.66%) and days to 50% flowering (16. 21%). Though there was predominance of lines contribution for days to flowering, days to maturity, plant height and harvest index; testers also showed maximum influence for number of grains/spike, spike length and peduncle length. Similarly, line x tester interaction was observed more for number of tillers/plant, biological yield/plant, seed yield/plant and 1000 grain weight than lines and testers indicating higher estimates of SCA variances for interaction.

4.6.3 Estimation of genetic variances

The estimates of genetic variances, namely additive and dominance were computed for the various traits studied (Table 4.6). The dominance variance recorded larger values than additive variance for all characters indicating that the gene effect was predominantly of non-additive type which showed that most of the characters were controlled by non-additive type of gene action. Higher values of variance due to SCA than the GCA variance suggested the major role of non-additive effects in the manifestation of all the traits. The ratio of GCA and SCA was also less than one for all the traits studied indicating predominance of non-additive gene effects. Narrow sense heritability was observed to be very low (0.02% to 20.68%) for all the traits studied also indicating that non-additive effects play an important role in controlling the traits. Therefore, it suggests greater importance of non-additive gene action and hence, hybridization may be choice for utilizing the putative heterosis in specific crosses to exploit the non-additive genetic variation.

4.6.4 Combining ability studies

The success of any breeding program largely depends on the choice of parents and breeding procedure adopted. Combining ability is a powerful tool to discriminate good as well as poor combiners and for crossing suitable parents in the hybridization program. It also provides information of promising specific combiners to exploit heterosis. Knowledge of relative importance of additive and non-additive gene action is essential to plant breeder for the development of an efficient hybridization program. General combining ability (GCA) is primarily additive genetic variance. On the other side, specific combining ability (SCA) is mainly a function of dominance variance. The detection of suitable parents with desirable characters having good general combining ability effects for yield and its component characters and superior cross combinations having high estimates of specific combining ability effects are essential for commercial exploitation of heterosis.

Results presented earlier by Singh and Singh (1990), Ajmal et al. (2004), Singh et al. (2007), Potla et al. (2013), Zhang et al. (2015) and Rathore and Chauhan (2017) also indicated preponderance of non-additive gene effects in the expression of various quantitative traits.

Table 4.6: Estimates of genetic components of variance, degree of dominance and heritability for various agro-morphological traits in barley

Components of variance	Days to flowering	Days to maturity	Plant height (cm)	No. of tillers/plant	No. of grains/spike	Spike length (cm)	Peduncle length (cm)	1000 grain weight (g)	Biological yield/plant (g)	Seed yield/ plant (g)	Harvest index (%)
σ^2lines	17.48**	16.95**	43.50**	0.18**	59.57**	-0.08**	2.93**	17.90**	-5.13**	5.08**	8.64**
σ^2testers	4.81**	-1.70**	14.73**	-0.47**	84.86**	0.90**	8.06**	17.99**	5.35**	-2.04**	1.09**
σ^2GCA	1.29**	0.92**	3.34**	-0.01**	7.93**	0.04**	0.59**	1.99**	-0.03**	0.20**	0.57**
σ^2SCA	4.11**	12.62**	34.03**	4.45**	86.83**	0.50**	1.82**	78.93**	168.15**	33.85**	6.30**
σ^2E	5.78	4.92	52.93	3.76	10.64	1.07	17.38	5.42	104.0	11.50	7.06
Variance ratio (σ^2GCA/σ^2SCA)	0.31	0.07	1.0	0.00	0.09	0.08	0.32	0.03	0.00	0.00	0.09
Additive variance (σ^2_A)	2.57	1.83	6.68	-0.03	15.86	0.08	1.18	3.99	-0.05	0.39	1.14
Dominance variance (σ^2_D)	4.11	12.62	34.03	4.45	86.83	0.50	1.82	78.94	168.15	32.16	6.30
Degree of dominance (σ^2A/ σ^2D)$^{1/2}$	0.79	0.38	0.44	0.08	0.43	0.42	0.81	0.22	0.02	0.11	0.43
Heritability (h^2ns) (%)	20.68	9.44	7.13	0.36	14.00	4.84	5.78	4.51	0.02	0.89	7.86

**Significance at $P \leq 0.01$

4.6.4.1 Estimates of general combining ability (GCA)

Various estimates of general combining ability for seed yield and its component traits are presented in Table 4.7.

i) Days to 50% flowering

Among seven lines, four lines exhibited significant and positive GCA effects, whereas one line showed significant negative effects. As negative significant effects are desirable for early flowering, parent HBL 738 (-9.11) was negatively significant for GCA effect. Among the testers, negative significant GCA effects were observed for Atahualpa (-2.74). Therefore, among lines and testers, line HBL 738 and tester Atahualpa were identified as the best general combiners for days to 50% flowering.

ii) Days to maturity

Significantly negative GCA effects were exhibited by three lines, namely HBL 748 (-5.81), HBL 713 (-4.23) and HBL 738 (-4.06). These lines were found good general combiner for days to maturity. None of the testers showed significant GCA effects.

iii) Plant height

GCA effects were significant and positive for lines HBL 751 (7.31) followed by Local Sudhrani (6.31), HBL 713 (5.56) and tester Atahualpa (4.75), which were the best general combiners for increased plant height. Significantly negative GCA effects were exhibited by two lines, namely HBL 723 (-12.69) and HBL 722 (-5.94) and tester DWRUB 64 (-6.44), which were good general combiners for reduced plant height.

iv) Number of tillers per plant

Significantly positive GCA effects were exhibited by two lines which were Local Sudhrani (1.71) and HBL 738 (1.63), and negatively significant GCA was observed for lines HBL 751 (-1.29) and HBL 748 (-1.29). Line Local Sudhrani and HBL 738 were good general combiners for this trait.

v) Number of grains per spike

Highly significant and positive GCA effects were recorded for lines HBL 751 (9.32), Local Sudhrani (6.82), HBL 713 (6.32) and HBL 748 (6.32), whereas testers HBL 276 (11.14) and DWRUB 64 (5.24) also showed positive GCA effects and were regarded as good general combiners.

vi) Spike length

None of the lines showed significant positive GCA for this trait. Among the testers HBL 113 (0.97) recorded positively significant GCA and was considered good general combiner for spike length.

vii) Peduncle length

Highly significant positive GCA effects were exhibited by line HBL 738 (3.00) and testers Atahualpa (3.17) and HBL 276 (1.97) which proved as good general combiners, whereas line HBL 723 (-3.59) and testers HBL 113 (-2.74) and DWRUB 64 (-2.40) exhibited negatively significant GCA effects and acted as poor general combiners.

viii) 1000 grain weight

Lines HBL 722 (7.32) followed by HBL 738 (6.15) and HBL 723 (5.40) were positively significant for GCA effects, while testers Atahualpa (4.57) and HBL 113 (3.76) also showed similar response and were good general combiners for 1000 grain weight.

ix) Biological yield per plant

Significantly positive GCA effects were exhibited only by one line i.e. Local Sudhrani (12.58) and one tester HBL 276 (4.86) which were found to be the best general combiners for this trait.

x) Seed yield per plant

Line Local Sudhrani (6.37) and tester HBL 276 (1.81) were the only genotypes which showed positive significant GCA effects and were found to be the best general combiners for seed yield/plant. However, lines HBL 723 (-5.46), HBL 722 (-2.00), HBL 751 (-2.20) and tester Atahualpa (-2.25) were poor general combiners for this trait.

xi) Harvest index

Four lines *viz*., HBL 713 (4.13), Local Sudhrani (2.39), HBL 748 (1.86) and HBL 738 (1.80) exhibited significantly positive GCA effects and were found to be a good general combiners. Tester HBL 113 (1.09) also proved to be a good general combiner for this trait.

4.6.4.2 Estimates of specific combining ability (SCA) effects

Specific combining ability (SCA) was used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved. Specific combining ability is due to dominance and epistasis. Trait-wise description of specific combining ability (SCA) effects are presented for grain yield and related traits in Table 4.8.

i) Days to 50 per cent flowering

Out of 28 crosses, three crosses exhibited the desired significant negative SCA effects. These were HBL 722 × HBL 113, HBL 723 × HBL 276 and Local Sudhrani × DWRUB 64 which were also good specific cross combinations for this trait.

ii) Days to maturity

Six crosses *viz*., HBL 722 × HBL 113, HBL 723 × DWRUB 64, HBL 722 × Atahualpa, HBL 748 × DWRUB 64, Local Sudhrani × HBL 113 and HBL 723 × HBL 276 exhibited the desired significant negative SCA effects.

iii) Plant height

Two crosses, HBL 723 x Atahualpa (-11.83) and HBL 723 x HBL 113 (-11.74) recorded negative SCA effects. These crosses were found to be good specific cross combinations for reduced plant height.

Table 4.7 Estimates of general combining ability (GCA) for different traits in barley

Trait	Days to flowering	Days to maturity	Plant height (cm)	No. of tillers/ plant	No. of grains/ spike	Spike length (cm)	Peduncle length (cm)	1000 grain weight (g)	Biological yield/plant (g)	Seed yield/ plant (g)	Harvest index (%)
Lines											
HBL 713	-0.86	-4.23**	5.56**	-0.54	6.32**	-0.08	1.25	-5.93**	-0.91	1.64	4.13**
HBL 722	2.06**	3.27**	-5.94**	0.21	-8.85**	0.44	-1.90	7.32**	1.05	-2.00*	-3.70**
HBL 723	1.48*	4.94**	-12.69**	-0.45	-10.85**	-0.39	-3.59**	5.40**	-10.20**	-5.46**	-3.65**
HBL 738	-9.11**	-4.06**	-3.02	1.63**	-9.10**	-0.52	3.00**	6.15**	1.12	1.43	1.80*
HBL 748	-0.27	-5.81**	2.48	-1.29*	6.32**	0.06	0.62	-2.01**	-1.73	0.20	1.86*
HBL 751	2.48**	1.86**	7.31**	-1.29*	9.32**	0.09	-0.12	-7.60**	-1.91	-2.20*	-2.82**
Local Sudhrani	4.23**	4.02**	6.31**	1.71**	6.82**	0.41	0.74	-3.35**	12.58**	6.37**	2.39**
SE (gi) ±	0.72	0.61	1.99	0.53	0.84	0.30	1.13	0.71	2.90	0.94	0.71
SE (gi-gj) ±	1.02	0.86	2.81	0.75	1.19	0.43	1.60	1.00	4.11	1.34	1.01
Testers											
Atahualpa	-2.74**	-0.63	4.75**	0.23	-10.10**	0.05	3.17**	4.57**	-8.37**	-2.25**	1.06
DWRUB 64	-1.02	0.56	-6.44**	-0.54	5.24**	-1.41**	-2.40**	-1.10*	2.92	-0.41	-2.13**
HBL 113	2.74**	0.37	0.65	0.70	-6.29**	0.97**	-2.74**	3.76**	0.59	0.85	1.09*
HBL 276	1.02	-0.30	1.04	-0.39	11.14**	0.39	1.97*	-7.24**	4.86*	1.81*	-0.01
SE (gi) ±	0.55	0.46	1.50	0.40	0.64	0.23	0.85	0.53	2.19	0.71	0.54
SE (gi-gj) ±	0.77	0.65	2.12	0.57	0.90	0.32	1.21	0.75	3.10	1.01	0.76

*Significance at $P \leq 0.05$; **Significance at $P \leq 0.01$

Table 4.8 Estimates of specific combining ability (SCA) for different traits in barley

Trait **Cross**	Days to flowering	Days to maturity	Plant height (cm)	No of tillers/plant	No. of grains/ spike	Spike length (cm)	Peduncle length (cm)	1000 grain weight (g)	Biological yield/plant (g)	Seed yield/ plant (g)	Harvest index (%)
HBL 713 X Atahualpa	-2.10	0.46	1.92	2.11	-4.99**	0.17	2.80	-1.74	4.00	2.29	1.87
HBL 713 X DWRUB 64	1.19	0.27	-1.56	-0.13	1.01	-0.04	0.37	5.93**	5.16	1.58	-1.00
HBL 713 X HBL 113	0.10	0.80	0.01	0.30	-6.80**	0.05	0.04	-1.60	-6.93	-1.91	1.15
HBL 713 X HBL 276	0.81	-1.54	-0.37	-2.27*	10.77**	-0.17	-3.20	-2.60	-2.23	-1.96	-2.02
HBL 722 X Atahualpa	-0.68	-3.70**	3.42	0.69	9.51**	-0.04	-0.47	-10.99**	-0.19	1.36	3.00*
HBL 722 X DWRUB 64	2.27	5.77**	2.94	4.12**	-6.15**	0.57	1.91	6.35**	26.33**	9.48**	2.27
HBL 722 X HBL 113	-4.15**	-6.70**	-4.15	-2.45*	7.04**	-1.27*	-1.42	-6.18**	-10.15	-4.15*	-2.02
HBL 722 X HBL 276	2.56	4.63**	-2.20	-2.36*	-10.39**	0.74	-0.02	10.82**	-15.99**	-6.69**	-3.25*
HBL 723 X Atahualpa	2.24	2.30	-11.83**	0.36	4.18*	-1.58**	-4.40	0.93	-1.44	-0.89	-1.30
HBL 723 X DWRUB 64	0.52	-4.56**	10.69**	1.45	-7.49**	0.35	2.00	-1.40	-8.63	-1.09	2.94
HBL 723 X HBL 113	0.10	5.30**	-11.74**	-2.79*	8.37**	-0.16	-0.69	2.74	4.28	-0.71	-3.70*
HBL 723 X HBL 276	-2.86**	-3.04*	12.88**	0.98	-5.06**	1.39*	3.08	-2.26	5.79	2.68	2.05
HBL 738 X Atahualpa	-0.51	-1.04	-1.50	0.27	9.76**	-0.15	-2.08	-7.15**	4.87	1.97	1.15
HBL 738 X DWRUB 64	-1.23	0.11	-4.31	-2.30*	-8.57**	0.27	-3.58	4.85**	-15.25*	-6.85**	-3.23*
HBL 738 X HBL 113	4.35**	1.96	1.26	1.80	10.95**	0.01	1.15	-11.35**	5.44	2.27	0.48
HBL 738X HBL 276	-2.61	-1.04	4.55	0.23	-12.14**	-0.13	4.51*	13.65**	4.94	2.62	1.60
HBL 748 X Atahualpa	0.32	-1.95	6.67	-1.14	-5.65**	0.86	1.75	6.35**	0.14	-0.74	-1.27
HBL 748 X DWRUB 64	0.94	-3.48**	-5.48	1.29	8.01**	-1.13	-1.97	2.35	15.46**	6.36**	1.04
HBL 748 X HBL 113	-1.15	2.05	2.76	-0.62	-6.80**	0.78	-0.54	5.15**	0.67	0.50	0.26
HBL 748 X HBL 276	-0.11	3.38**	-3.95	0.48	4.44**	-0.51	0.76	-13.85**	-16.26**	-6.11**	-0.03
HBL 751 X Atahualpa	1.90	2.38	-1.17	-2.81**	-10.32**	-0.27	0.30	3.93**	-16.49**	-6.96**	-3.88**
HBL 751 X DWRUB 64	-0.48	-1.48	-0.64	-1.05	9.01**	0.46	0.87	-4.40**	1.14	2.01	2.87*
HBL 751 X HBL 113	0.10	0.05	5.26	3.38**	-6.13**	-0.45	0.94	7.74**	12.02*	5.41**	2.35
HBL 751 X HBL 276	-1.52	-0.95	-3.45	0.48	7.44**	0.26	-2.10	-7.26**	3.33	-0.46	-1.34
Local Sudhrani X Atahualpa	-1.18	1.55	2.50	0.52	-2.49	1.01	2.11	8.68**	9.11	2.97	0.42
Local Sudhrani x DWRUB 64	-3.23*	3.36**	-1.64	-3.38**	4.18*	-0.47	0.41	-13.65**	-24.21**	-11.49**	-4.90**
Local Sudhrani x HBL 113	0.68	-3.45**	6.60	0.38	-6.63**	1.05	0.52	3.49*	-5.33	-1.41	1.49
Local Sudhrani x HBL 276	3.73*	-1.45	-7.45	2.48*	4.94**	-1.59**	-3.03	1.49	20.42**	9.92**	2.99*
S.E. ± (Sij)	1.44	1.22	3.97	1.07	1.69	0.60	2.26	1.41	5.81	1.89	1.43
S.E. ± (Sij-Skl)	2.04	1.73	5.62	1.51	2.39	0.85	3.19	1.99	8.21	2.67	2.02

*Significance at $P \leq 0.05$; **Significance at $P \leq 0.01$

iv) Number of tillers per plant

Three crosses *viz.* HBL 722 × DWRUB 64 (4.12), HBL 751 × HBL 113 (3.38) and Local Sudhrani × HBL 276 (2.48) showed positive and significant SCA effects for number of tillers/plant..

v) Number of grains per spike

Thirteen crosses showed positive and significant SCA effects for number of grains per spike. These were HBL 738 × HBL 113, HBL 713 × HBL 276, HBL 738 × Atahualpa, HBL 722 × Atahualpa, HBL 751 × DWRUB 64, HBL 723 × HBL 113, HBL 748 × DWRUB 64, HBL 751 × HBL 276, HBL 722 × HBL 113, Local Sudhrani × HBL 276, HBL 748 × HBL 276, HBL 723 × Atahualpa and Local Sudhrani × DWRUB 64. The SCA effects ranged from 10.95 (HBL 738 × HBL 113) to -12.14 (HBL 738 × HBL 276) for this trait.

vi) Spike length

Only one cross i.e. HBL 723 × HBL 276 (1.39) showed positive and significant SCA effect for spike length and also proved to be a good specific cross combination for this trait.

vii) Peduncle length

Only a single cross i.e. HBL 738 × HBL 276 (4.51) showed positive significant SCA effect and also found good for specific cross combination.

viii) 1000 grain weight

Significantly positive SCA effects were exhibited by eleven crosses for 1000 grain weight. Out of these, crosses HBL 738 × HBL 276, HBL 722 × HBL 276, Local Sudhrani × Atahualpa, HBL 751 × HBL 113, HBL 722 × DWRUB 64, HBL 748 × Atahualpa, HBL 713 × DWRUB 64, HBL 748 × HBL 113, HBL 738 × DWRUB 64, HBL 751 × Atahualpa and Local Sudhrani × HBL 113 were the top ranking ones and the SCA effects ranged from 13.65 (HBL 738 HBL × 276) to -13.65 (Local Sudhrani × DWRUB 64).

ix) Biological yield per plant

Four crosses, namely HBL 722 × DWRUB 64 (26.33), Local Sudhrani × HBL 276 (20.42), HBL 748 × DWRUB 64 (15.46) and HBL 751 × HBL 113 (12.02) were found to be good specific cross combinations as exhibited by the positive and significant SCA effects.

x) Seed yield per plant

Four crosses out of twenty eight recorded significantly positive SCA effects for seed yield/plant. These were Local Sudhrani × HBL 276 (9.92), HBL 722 × DWRUB 64 (9.48), HBL 748 × DWRUB 64 (6.36) and HBL 751 × HBL113 (5.41) and were found good specific cross combinations. The SCA effects ranged from 9.92 (Local Sudhrani × HBL 276) to -11.49 (Local Sudhrani × DWRUB 64).

xi) Harvest index

Three crosses, namely HBL 722 × Atahualpa (3.00), Local Sudhrani × HBL 276 (2.99) and HBL 751 × DWRUB 64 (2.87) showed positive and significant SCA effects and were found good specific cross combinations for harvest index.

4.6.4.3 Top ranking parents

Table 4.9 shows the best good general combiners (parents) based on significant GCA effects and three best parents on *per se* performance for different traits. Parents HBL 738 (118 days) and Atahualpa (121 days) were the best general combiners coupled with desirable (negative) mean values for days to 50% flowering. Similarly, parents HBL 723, DWRUB 64 and HBL 722 for plant height; HBL 276, HBL 713 and DWRUB 64 for number of grains/spike; HBL 113 for spike length; HBL 738 for peduncle length; HBL 722 and HBL 723 for 1000 grain weight; HBL 713 for harvest index and HBL 276 for seed yield/plant showed significant GCA effects alongwith high *per se* performance. Hence, these parents being good general combiners having high mean performance can directly be used in the crossing programme for getting substantial increase for the respective traits.

4.6.4.4 Top ranking specific cross combinations

Table 4.10 shows the top ranking cross combinations based on significant SCA effects, three best crosses on *per se* performance and the type of combiners

(High/Low/Average) involved on the basis of GCA effects. As evident from the perusal of Table 4.10, most of the cross combinations involved Low x Low (10) followed by Low x Average (8), High x Low (7) and High x High (5) type of combiners. The cross HBL 748 x DWRUB 64 (High x Average) showed significant SCA effects and high *per se* performance for days to maturity. Similarly, crosses HBL 723 x HBL 113 (High x Low) and HBL 723 x Atahualpa (High x Low) for plant height; HBL 722 x DWRUB 64 (Average x Low) and Local Sudhrani x HBL 276 (High x Low) for number of tillers/plant; HBL 751 x DWRUB 64 (High x High) for number of grains/spike; HBL 738 x HBL 276 (High x High) for peduncle length; HBL 722 x DWRUB 64 (High x Low) and HBL 738 x HBL 276 (High x Low) for 1000 grain weight were the best cross combinations for obtaining higher performance for the respective traits.

Cross combinations Local Sudhrani x HBL 276 and HBL 722 x DWRUB 64 involved High x High and Low x Low combiners for seed yield/plant, respectively, whereas for biological yield/plant, the same set of crosses involved High x High and Average x Average combiners with significant SCA effects and high *per se* performance.

The occurrence of High/Low or Average/Low gene interactions in the crosses indicate the operation of non-additive gene action. However, High x Low good performance may be attributed to the interaction between dominance alleles from good combiners and recessive alleles from poor combiners. Such cross combinations involving at least one low general combiner suggests both additive and non-additive gene action which allows for the exploitation of heterosis in F_1 generation. It was also observed that involvement of poor combiners (Low x Low) also produced most number of superior specific combining hybrids and this involvement of combiners with low GCA has been attributed to dominance x dominance interaction.

The High x High cross combinations show interaction between positive alleles which can be fixed in subsequent generations for effective selection with the assumption that no repulsion phase linkages are involved and can be advanced to the next generation to derive superior segregants.

Table 4.9 Best good general combiners (parents) on the basis of GCA and *per se* performance for different traits in barley

Trait	GCA effects of parents		Parents *per se* performance	
Days to flowering	HBL 738 (118)	-9.11	HBL 738	118
	Atahualpa (121)	-2.74	Atahualpa	121
			DWRUB 64	125
Days to maturity	HBL 748 (166)	-5.81	Local Sudhrani	154
	HBL 713 (168)	-4.23	Atahualpa	155
	HBL 738 (155)	-4.06	DWRUB 64	159
Plant height (cm)	HBL 723 (84)	-	HBL 723	84
	DWRUB 64 (94)	12.69	HBL 722	88
	HBL 722 (88)	-6.44	DWRUB 64	94
		-5.94		
Number of tillers/plant	Local Sudhrani (10)	1.71	HBL 113	14
	HBL 738 (9)	1.63	HBL 276	13
			HBL 722	13
Number of grains/spike	HBL 276 (66)	11.14	HBL 276	66
	HBL 751 (62)	9.32	DWRUB 64	64
	Local Sudhrani (58)	6.82	HBL 713	63
	HBL 713 (63)	6.32		
	HBL 748 (60)	6.32		
	DWRUB 64 (64)	5.32		
Spike length (cm)	HBL 113 (11.07)	0.97	HBL 113	11.07
			HBL 722	9.32
			HBL 276	9.00
Peduncle length (cm)	Atahualpa (30.40)	3.17	HBL 276	35.73
	HBL 738 (33.65)	3.00	HBL 738	33.65
	HBL 276 (35.73)	1.97	HBL 751	32.47
1000 grain weight (g)	HBL 722 (58)	7.32	HBL 748	68
	HBL 738 (46)	6.15	HBL 722	58
	HBL 723 (56)	5.40	HBL 723	56
	Atahualpa (51)	4.57		
	HBL 113 (40)	3.76		
Biological yield/plant (g)	Local Sudhrani (65.61)	12.58	HBL 723	115.64
	HBL 276 (84.05)	4.86	HBL 748	95.16
			HBL 713	93.68
Seed yield/plant (g)	Local Sudhrani (22.60)	6.37	HBL 723	36.83
	HBL 276 (32.34)	1.81	HBL 713	34.75
			HBL 276	32.34
Harvest Index (%)	HBL 713 (37.0)	4.13	Atahualpa	42.00
	Local Sudhrani (34.79)	2.39	HBL 276	38.39
	HBL 748 (32.0)	1.86	HBL 713	37.00
	HBL 738 (32.48)	1.80		
	HBL 113 (33.83)	1.09		

Note: Values in the parenthesis are the mean values

Table 4.10 Top ranking of specific cross combinations for different traits on the basis of SCA, *per se* performance and GCA effects involved in barley

Trait	***per se* performance**	**Significant SCA effects**	**GCA effects of parents**
Days to flowering	HBL 738 x Atahualpa (117)	HBL 722 x HBL 113	Low x Low
	HBL 738 x DWRUB 64 (118)	Local Sudhrani x DWRUB 64	Low x Average
	HBL 738 HBL 276 (119)	HBL 723 x HBL 276	Low x Low
Days to maturity	HBL 748 x Atahualpa (156)	HBL 722 x HBL 113	Low x Low
	HBL 748 x DWRUB 64 (156)	HBL 723 x DWRUB 64	Low x Low
	HBL 713 x HBK 276 (158)	HBL 722 x Atahualpa	Low x Average
		HBL 748 x DWRUB 64	High x Average
		Local Sudhrani x HBL 113	Low x Low
Plant height (cm)	HBL 723 x HBL 113 (86)	HBL 723 x Atahualpa	High x Low
	HBL 723 x Atahualpa (90)	HBL 723 x HBL 113	High x Low
	HBL 738 x DWRUB 64 (96)		
Number of tillers/plant	HBL 738 x HBL 113 (14)	HBL 722 x DWRUB 64	Average x Low
	HBL 722 x DWRUB 64 (14)	HBL 751 x HBL 113	Low x Average
	Local Sudhrani x HBL 276 (13)	Local Sudhrani x HBL 276	High x Low
Number of grains/spike	HBL 113 x HBL 276 (67)	HBL 738 x HBL 113	Low x Low
	HBL 751 x HBL 276 (67)	HBL 713 x HBL 276	High x High
	HBL 751 x DWRUB 64 (63)	HBL 738 x Atahualpa	Low x Low
		HBL 722 x Atahualpa	Low x Low
		HBL 751 x DWRUB 64	High x High
Spike length (cm)	Local Sudhrani x HBL 113 (11.55)	HBL 723 x HBL 276	Low x Average
	HBL 748 x HBL 113 (10.93)		
	HBL 722 x HBL 276 (10.7)		
Peduncle length (cm)	HBL 738 x HBL 276 (42.4)	HBL 738 x HBL 276	High x High
	HBL 113 x Atahualpa (40.13)		
	Local Sudhrani x Atahualpa (38.93)		
1000 grain weight (g)	HBL 722 x DWRUB 64 (68)	HBL 738 x HBL 276	High x Low
	HBL 738 x HBL 276 (68)	HBL 722 x HBL 276	High x Low
	HBL 723 x HBL 113 (67)	Local Sudhrani x Atahualpa	Low x High
		HBL 751 x HBL 113	Low x High
		HBL 722 x DWRUB 64	High x Low
Biological yield/plant (g)	Local Sudhrani x HBL 276 (95.92)	HBL 722 x DWRUB 64	Average x Average
	HBL 722 x DWRUB 64 (88.34)	Local Sudhrani x HBL 276	High x High
	HBL 748 x DWRUB 64 (74.69)	HBL 748 x DWRUB 64	Low x Average
		HBL 751 x HBL 113	Low x Average
Harvest Index (%)	HBL 713 x Atahualpa (41.7)	HBL 722 x Atahualpa	Low x Average
	HBL 713 x HBL 113 (41.0)	Local Sudhrani x HBL 276	High x Low
	Local Sudhrani x HBL 276 (40.0)	HBL 751 x DWRUB 64	Low x Low
Seed yield/plant (g)	Local Sudhrani x HBL 276 (38.36)	Local Sudhrani x HBL 276	High x High
	Local Sudhrani x Atahualpa (27.36)	HBL 722 x DWRUB 64	Low x Low
	HBL 722 x DWRUB 64 (27.34)	HBL 748 x DWRUB 64	Average x Low
		HBL 751 x HBL 113	Low x Average

Note: Values in the parenthesis are the mean values

4.7 Heterosis

The aim of estimation of heterosis in the present investigation was to find out the superior cross combinations giving high degree of useful heterosis and characters of parents for their prospectus for future use in breeding programme. For successful heterosis breeding programme in any crop, there must be presence of significant heterotic effect in the cross combinations that can be exploited easily.

The magnitude of heterosis for grain yield and component characters have been cited below with significant values shown in Table 4.11.

i) Days to 50 % flowering

Three crosses showed negative significant heterosis which was desirable for early flowering. These were HBL 713 × Atahualpa (-3.57%) followed by HBL 713 × HBL 113 (-2.84%) and HBL 738 × DWRUB 64 (-2.61%).

ii) Days to maturity: Seven crosses *viz*., HBL 713 x HBL 276 followed by HBL 713 x HBL 113, HBL 748 x HBL 113, HBL 748 x DWRUB 64, HBL 748 HBL 276, HBL 751 x HBL 276, HBL 751 x HBL 113 and HBL 748 x Atahualpa exhibited significant negative heterosis desirable for early maturity.

iii) Plant height: Negative heterosis is desirable for plant height. Though, significantly positive heterosis was observed for fifteen crosses, none of the crosses showed significant negative heterosis for plant height.

iv) Number of tillers per plant

Four crosses *viz*., HBL 722 × DWRUB 64 (60.0%) followed by HBL 723 × DWRUB 64 (53.85%), HBL 748 × DWRUB 64 (45.95%) and HBL 751 × HBL 113 (34.55%) showed positive significant heterosis.

v) Number of grains per spike

Only one cross i.e. HBL 738 x HBL 113 (15.56%) exhibited significant positive heterosis, whereas eighteen crosses were negatively significant. The negatively significant heterosis ranged from Local Sudhrani × DWRUB 64 (-9.54%) to HBL 723 × DWRUB 64 (-57.84%).

vi) Spike length

Seven crosses observed positive significant heterosis. These were Local Sudhrani × Atahualpa (30.17%) followed by HBL 723 × HBL 276 (27.9%), HBL 748 × Atahualpa (27.71%), HBL 751 × HBL 276 (20.82%), Local Sudhrani × HBL 276 (20.64%), HBL 748 × HBL 113 (17.04%) and HBL 722 × HBL 276 (16.83%).

vii) Peduncle length

Eight crosses showed positive significant heterosis for crosses HBL 713 × HBL 113 (45.23%) followed by HBL 713 × Atahualpa (44.36%), HBL 748 × HBL 113 (39.69%), HBL 748 × Atahualpa (38.31%), HBL 738 × HBL 113 (32.60%), Local Sudhrani × HBL 113 (29.46%), Local Sudhrani × Atahualpa (27.98%) and HBL 738 x HBL 276 (22.22%).

viii) 1000 grain weight

Twenty one crosses recorded positive significant heterosis and two crosses were negatively significant for heterosis. The significant heterosis for this trait ranged from 73.50% for cross HBL 738 × HBL 276) to -20.43% for cross Local Sudhrani × DWRUB 64.

ix) Biological yield per plant

Out of twenty eight crosses, five crosses showed positive significant mid parent heterosis. The highest positive significant heterosis was exhibited by cross HBL 722 × DWRUB 64 (73.39%) followed by HBL 751 × DWRUB 64 (52.90%), HBL 751 × HBL 113 (52.32%), HBL 738 × HBL 113 (29.51%) and Local Sudhrani × HBL 276 (28.18%).

x) Seed yield per plant

The most important trait of a plant from agronomic point of view is its yielding ability. In the present study, the significant positive heterosis is desirable for this character as it indicates increased yield. Five crosses recorded positively significant heterosis over the mid parent value, and 11 crosses were showed significantly negative heterosis. Positive significant heterosis was observed for crosses HBL 722 × DWRUB 64 (81.86%) followed by HBL 751 × DWRUB 64 (59.55 %), HBL 751 × HBL 113 (52.32 %), HBL 738 × HBL 113 (48.64 %) and Local Sudhrani x HBL 276 (39.64%). The negatively significant heterosis ranged from HBL 713 × HBL 113 (-24.55%) to HBL 723 × Atahualpa (-61.70%).

Table 4.11 Estimation of heterosis over mid parent for seed yield and related traits in barley

Traits Cross	Days to flowering	Days to maturity	Plant height (cm)	No of tillers/ plant	No. of grains/ Spike	Spike length (cm)	Peduncle length (cm)	1000 grain weight (g)	Biological yield/plant (g)	Seed yield/ plant (g)	Harvest index (%)
HBL 713 x Atahualpa	-3.51**	-1.03	14.38**	-11.69	-33.33**	10.32	44.36**	7.22*	-30.19**	-25.44**	5.56
HBL 713 x DWRUB 64	-1.15	-1.63	9.71	2.04	-18.42**	-9.61	19.90	12.50**	-5.99	-3.80	7.38
HBL 713 x HBL 113	-2.84*	-4.91**	13.91**	-23.08*	-33.10**	2.37	45.23**	19.38**	-34.29**	-24.55**	15.76**
HBL 713 x HBL 276	-0.64	-5.94**	11.18*	-50.00**	4.66	5.30	8.10	0.85	-32.73**	-35.14**	-2.56
HBL 722 x Atahualpa	1.45	4.59**	12.19*	-17.95	7.23	9.42	14.26	2.44	-11.62	-15.16	-2.63
HBL 722 x DWRUB 64	3.51**	10.01**	10.26	60.00**	-35.53**	-0.38	7.10	24.92**	73.39**	81.86**	4.86
HBL 722 x HBL 113	-2.38	-1.73	5.61	-39.24**	1.64	-9.08	14.94	22.03**	-15.87	-19.85	-5.85
HBL 722 x HBL 276	4.52**	5.63**	5.30	-45.45**	-33.33**	16.83*	2.46	46.13**	-31.89**	-45.58**	-18.94**
HBL 723 x Atahualpa	4.69**	9.62**	-8.01	-13.43	-49.05**	-8.44	2.50	23.36**	-56.07**	-61.70**	-17.05**
HBL 723 x DWRUB 64	3.03*	4.64**	13.86*	53.85*	-57.84**	-2.49	9.53	9.43**	-47.56**	-46.85**	3.36
HBL 723 x HBL 113	1.65	6.71**	-7.53	-38.24**	-35.00**	2.63	21.74	39.58**	-40.29**	-47.87**	-13.98*
HBL 723 x HBL 276	1.18	2.05*	16.23**	-12.12	-45.21**	27.09**	14.29	15.91**	-41.40**	-44.21**	-6.34
HBL 738 x Atahualpa	-1.82	2.15*	6.97	4.48	9.20	14.48	15.53	20.96**	14.47	15.78	3.75
HBL 738 x DWRUB 64	-2.61*	2.33*	2.13	28.21	-40.74**	0.34	-3.52	35.42**	10.45	10.57	0.47
HBL 738 x HBL 113	0.92	-0.41	10.88*	20.59	15.56*	8.08	32.60**	24.81**	29.51*	48.64**	14.60*
HBL 738 x HBL 276	-2.86	-1.85	11.77*	0.00	-36.96**	13.19	22.22*	73.50**	11.45	15.51	7.31
HBL 748 x Atahualpa	1.06	-2.90**	18.72**	-32.31*	-32.58**	27.71**	38.31**	7.56**	-37.01**	-36.12**	-1.93
HBL 748 x DWRUB 64	1.31	-4.30**	5.24	45.95*	-5.12	-16.00	8.83	-7.91**	6.52	20.60	15.37*
HBL 748 x HBL 113	-1.26	-4.55**	16.44**	-24.24	-30.96**	17.04*	39.69**	14.81**	-26.23**	-14.63	14.97*
HBL 748 x HBL 276	1.30	-3.39**	7.36	-21.88	-2.92	9.13	19.04	-36.00**	-49.86**	-48.65**	3.60
HBL 751 x Atahualpa	1.68	2.65**	12.95**	-37.04*	-37.78**	15.88	15.38	25.84**	-31.41*	-50.17**	-23.63**
HBL 751 x DWRUB 64	-0.38	-0.20	12.24*	53.85	-0.27	6.32	2.74	-4.55	52.90**	59.55**	2.83
HBL 751 x HBL 113	-0.86	-2.91**	20.59**	34.55*	-24.74**	5.80	22.53	51.28**	45.31**	52.32**	4.06
HBL 751 x HBL 276	-0.38	-3.13**	9.73	-5.66	4.96	20.82*	-4.20	-5.71	9.30	-11.29	-15.75**
Local Sudhrani x Atahualpa	0.00	9.48**	15.09**	4.35	-23.08**	30.17**	27.98**	38.30**	15.91	17.15	0.30
Local Sudhrani x DWRUB 64	-1.77	10.00**	9.83	7.32	-9.54*	-5.95	7.63	-20.43**	-10.86	-17.70	-6.50
Local Sudhrani x HBL 113	0.24	1.64	20.52**	5.71	-28.52**	20.64**	29.46*	42.17**	4.11	21.00	15.42**
Local Sudhrani x HBL 276	4.27**	3.31**	4.61	17.65	-0.27	-2.46	-1.48	22.67**	28.18**	39.64**	9.33

*Significance at $P \leq 0.05$; **Significance at $P \leq 0.01$

xi) Harvest index

Five crosses showed the positive and significant heterosis over the mid parent value. These were HBL 713 x HBL 113 (15.76%) followed by Local Sudhrani x HBL 113 (15.42%), HBL 748 x DWRUB 64 (15.37%), HBL 748 x HBL 113 (14.97%) and HBL 738 x HBL 113 (14.60%).

Table 4.12 shows that crosses HBL 722 x DWRUB 64, HBL 751 x DWRUB 64, HBL 751 x HBL 113, HBL 738 x HBL 113 and Local Sudhrani x HBL 276 were the most promising crosses exhibiting significant mid-parent heterosis for seed yield/plant and other characters associated with seed yield.

The above results on heterosis studies are in line with the findings of Daya et al. (2009), Vishwakarma et al. (2011) Mansour (2016), Bernhart et al. (2017) and Madhukar et al. (2018)

Table 4.12 Promising crosses having significant mid parent heterosis for yield and related traits in barley

Cross	**Characters having significant heterosis**
HBL 722 x DWRUB 64	Seed yield/plant (27.34g), biological yield/plant (88.34g), No. of tillers/plant (14) and 1000 grain weight (68g)
HBL 751 x DWRUB 64	Seed yield/plant (19.67g) and biological yield/plant (60.20g)
HBL 751 x HBL 113	Seed yield/plant (24.32g), 1000 grain weight (59g), biological yield/plant (68.76g), No. of tillers/plant (12) and days to maturity (167 days)
HBL 738 x HBL 113	Seed yield/plant (24.81g), peduncle length (34.33cm), 1000 grain weight (54g), biological yield/plant (65.21g), No. of grains/spike (35) and harvest index (38%)
Local Sudhrani x HBL 276	Seed yield/plant (38.36g), biological yield/plant (95.92g) and 1000 grain weight (46g)

Note: Values in parenthesis are the mean values

5. SUMMARY AND CONCLUSIONS

The present investigation entitled, "Estimation of morphological and genetic aspects for yield and yield contributing traits in barley (*Hordeum vulgare* L.)" was undertaken at the Experimental Farm of Hill Agricultural Research and Extension Centre, Bajaura, Kullu, HP during *Rabi* season 2016-2017. The experimental material comprising of F_1 population of 28 crosses developed by crossing 7 lines/genotypes *viz.*, HBL 713, HBL 722, HBL 723, HBL 738, HBL 748, HBL 751 and Local Sudhrani with four testers *viz*., HBL 113, HBL 276, DWRUB 64 and Atahualpa were evaluated in randomized block design over three replications to assess the general and specific combining ability contributing to yield and related traits, association among different morphological traits and their direct and indirect effects on seed yield for effective selection**.** All the lines used as female parents were crossed to each of the testers by hand pollination using the standard procedure as per line x tester model. Data were recorded on eleven characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of effective tillers/plant, number of grains/spike, spike length (cm), peduncle length (cm), 1000 grain weight (g), biological yield/plant (g), seed yield/plant (g) and harvest index (%).The observations were recorded on five random competitive plants for parents (lines and testers) and individual plants were sampled for F_1s in each replication for all the traits, whereas days to 50% flowering and days to maturity were recorded on plot basis. Data analysis were done as per the standard procedures for parameters of genetic variability, correlation, path coefficient, line x tester and heterosis.

The analysis of variance revealed highly significant differences among the genotypes for all the traits studied. On the basis of mean performance, none of the parents/crosses were significantly better than the best check for days to maturity, number of tillers/plant, number of grains/spike, spike length, peduncle length, biological yield/plant and harvest index. However, two crosses, HBL 738 x Atahualpa (117 days) and HBL 738 x DWRUB 64 (118 days) and one parent HBL 738 (118 days) were significantly early in flowering than the best check, Atahualpa (121 days). Similarly, for 1000 grain weight, 16 crosses and one parent (HBL 748) were significantly higher than the best check, Atahualpa (68g). For seed yield/plant, only one cross Local Sudhrani x HBL 276 (38.36g) outyielded the best check, HBL 276 (32.34g)

The estimates of PCV and GCV indicated substantial variability and ensured ample scope for improvement for the studied traits. The traits, number of grain per spike and seed yield per plant showed high values of PCV and GCV. Moderate value of PCV and GCV were observed for 1000 grain weight which suggests cautioned approach while following direct selection for this trait. High PCV with moderate GCV were recorded for biological yield and number of tillers per plant. Low values of PCV and GCV were observed for days to flowering, days to maturity, plant height and harvest index.

High heritability coupled with high genetic advance was observed for number of grain per spike and seed yield per plant indicating the inheritance of these traits under the control of additive gene action and selection would be more effective for their improvement. High heritability coupled with moderate genetic advance was observed for 1000 grain weight, whereas moderate heritability coupled with high genetic advance was shown by biological yield/plant which indicated the preponderance of additive and non-additive gene effects in their inheritance.

Correlation studies revealed that seed yield per plant had a positive and significant correlation at both phenotypic and genotypic levels with biological yield/plant, number of effective tillers/plant, harvest index and number of grains/spike. It was also observed that none of the traits exhibited significant negative association with seed yield. This reflects that selection on the basis of the above traits can lead to higher yield in barley.

Path coefficient analysis indicated that biological yield/plant followed by harvest index, number of tillers/plant and number of grains/spike at both phenotypic and genotypic levels exerted maximum positive direct effects on seed yield/plant suggesting the importance of these traits towards seed yield. The traits biological yield/plant and harvest index also proved to be of high significance through which all the other traits exerted positive indirect effects on seed yield/plant. Besides, the traits plant height, spike length and harvest index also exhibited positive indirect effects on seed yield/plant via number of tillers/plant, whereas biological yield/plant showed positive indirect effects both via number of tillers/plant and number of grains/spike. However, negative indirect effects on seed yield/plant were also exerted by days to 50% flowering, days to maturity and 1000 grain weight via harvest index. 1000 grain weight and number of tillers/plant also exerted negative effects via grains/spike. This implies that these traits would be of great significance for indirect selection for achieving enhanced seed yield in barley.

Combining ability studies revealed that there was predominance of contribution of lines for days to flowering, days to maturity, plant height and harvest index. Testers also showed maximum contribution for number of grains/spike, spike length and peduncle length. Line x tester interaction was observed more for number of tillers/plant, biological yield/plant, seed yield/plant and 1000 grain weight than lines and testers indicating higher estimates of SCA variances for interaction.

The estimates of genetic variances exhibited larger values of dominance variance than additive variance for all characters indicating non-additive type of gene action. Higher values of variance due to SCA than the GCA and the ratio of GCA and SCA being less than one suggested the major role of non-additive effects in the manifestation of all the traits.

General combining ability for the parents revealed that among the lines, Local Sudhrani was good general combiner for most of the traits *viz.*, seed yield/plant, biological yield/plant, number of tillers per plant, number of grains/spike and harvest index. The other lines, namely HBL 722 and HBL 723 for plant height; HBL 751 for number of tillers/plant, number of grains/spike, biological yield/plant and harvest index; HBL 738 and HBL 713 for early maturity and HBL 738 also for peduncle length were recorded as good general combiners. Among the testers, HBL 276 was a good general combiner for seed yield/plant, biological yield/plant, number of grains/spike and peduncle length. Tester Atahualpa for peduncle length, 1000 grain weight and days to flowering, HBL113 for spike length and harvest index and DWRUB 64 for plant height showed desirable GCA effects and were good general combiners for the respective traits.

Specific combining ability among the parents exhibited that most of the cross combinations involved Low x Low (10) followed by Low x Average (8), High x Low (7) and High x High (5) type of combiners. Cross combinations Local Sudhrani x HBL 276 (High x High) followed by HBL 722 x DWRUB 64 (Low x Low), HBL 748 x DWRUB 64 (Average x Low) and HBL 751 x HBL 113 (low x Average) were highly significant for seed yield/plant and the first two cross combinations also showed high *per se* performance. Similarly, crosses HBL 748 x DWRUB 64 (High x Average) for days to maturity; HBL 723 x HBL 113 (High x Low) and HBL 723 x Atahualpa (High x Low) for plant height; HBL 722 x DWRUB 64 (Average x Low) and Local Sudhrani x HBL 276 (High x Low) for number of tillers/plant; HBL 751 x DWRUB 64 (High x High) for number of grains/spike; HBL 738 x HBL 276 (High x High) for peduncle length; HBL 722 x DWRUB 64 (High x Low) and HBL 738 x HBL 276 (High x Low) for 1000 grain weight were the best cross combinations for obtaining higher performance for the respective traits.

Heterosis breeding programme in any crop can only be successful with the presence of significant heterotic effects in the cross combinations which can be exploited easily. A wide range of mid parent heterosis was observed for grain yield and other traits in twenty eight crosses. Five crosses *viz.*, HBL 722 × DWRUB 64, Local Sudhrani × HBL 276, HBL 751 × DWRUB 64, HBL 751 × HBL 113 and HBL 738 × HBL 113 exhibited significant and positive heterosis for seed yield over the mid parent. The cross combinations HBL 713 x Atahualpa for days to 50% flowering, HBL 713 x HBL 276 for days to maturity, HBL 722 x DWRUB 64 for number of tillers/plant and biological yield/plant, HBL 738 x HBL 113 for number of grains/spike, Local Sudhrani x Atahualpa for spike length, HBL 713 x HBL 113 for peduncle length, HBL 738 x HBL 276 were the most heterotic for the respective traits.

Conclusions

- The analysis of variance revealed highly significant differences among the genotypes for all the traits studied.
- High values of PCV and GCV and high heritability coupled with high genetic advance was observed for number of grain per spike and seed yield per plant.

- Seed yield per plant had a positive and significant correlation with biological yield/plant, number of effective tillers/plant, harvest index and number of grains/spike. The traits biological yield/plant, harvest index, number of tillers/plant and number of grains/spike directly or indirectly influenced seed yield/plant and these may be selected for further improvement in seed yield of barley.
- Combining ability analysis revealed significant differences for lines, testers and lines x testers indicating wide genetic variability among the genotypes and prevalence of additive variance for the significant traits.
- Predominance of contribution of lines was observed for days to flowering, days to maturity, plant height and harvest index, whereas testers showed maximum contribution for number of grains/spike, spike length and peduncle length. Line x tester contribution was more for number of tillers/plant, biological yield/plant, seed yield/plant and 1000 grain weight than lines and testers indicating higher estimates of SCA variances for interaction.
- The estimates of genetic variances exhibited the major role of non-additive effects in the manifestation of all the traits as suggested by larger values of dominance variance than additive variance; higher values of variance due to SCA than the GCA and ratio of GCA and SCA being less than one.
- Line Local Sudhrani for seed yield/plant alongwith HBL 713, HBL 738 were good general combiners for most number of yield contributing characters. Tester HBL 276 was a good general combiner for seed yield and associated traits.
- Four cross combinations *viz.,* Local Sudhrani × HBL 276, HBL 722 × DWRUB 64, HBL 748 × DWRUB 64 and HBL 751 x HBL 113 were identified as the best on the basis of seed yield and component traits.
- On the basis of mid parent heterosis five crosses viz., HBL 722 x DWRUB 64, HBL 751 x DWRUB 64, HBL 751 x HBL 113, HBL 738 x HBL 113 and Local Sudhrani x HBL 276 were identified as promising for seed yield and related traits.

LITERATURE CITED

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

ABd El-Aty M, Amer K, Eldegwy I and El-Akhdar A. 2011. Genetic studies on yield and its components in some barley crosses. *Journal Plant Prod* 11: 1537-1550

Abdulamonov, K. 1984. Combining ability of spring barley varieties in the Pamirs. *Ahboroti Akademijai Fanhoi RSS Tocikiston, Su"bai Fanhoi Biologija.* No. 3, 48-51

Al-Tabbal JA and Al-Fraihat AH. 2012. Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Science* 4(3):193-210

Ajmal S, Asif M and Muni M. 2004. Implication of combining ability: analysis of some characteristics of spring wheat. *Quarterly Science Vision* 9(1-2 & 3-4):1-5

Amiruzzaman MAY, Akond and Uddin M S. 2008. Line x tester analysis of combining ability in hulled and hulless crosses of barley (*Hordeum vulgare* L.). *Bangladesh Journal of Agriculture* 33: 15-20

Amer KhA, Eid AA, El Sayed MMA, El Akhdar AA. 2012. Estimation of some genetic parameters for yield and its components in some barley genotypes. *Egyptian Journal of Agricultural Research* 90:117-130

Anonymous. 2018. Annual Progress Report, Indian Institute of Wheat and Barley Research, Karnal.

Arabi MI, Sarrafi A, Barraault G and Albertini L.1992. Genetic variability for grain yield and protein content in barley and its modification in net blotch. *Plant Breeding* 108(4): 296-301

Ataei M. 2006. Path analysis of barley (*Hordeum vulgare* L.) yield. *Tarim Bilimleri Dergisi* 12(3): 227-232

Bhatnagar VK and Sharma SN. 1997. Genetic analysis of grain yield and its component in barley over environments. *Crop Improvement* 24 (2): 244-48

Bhatnagar VK and Sharma SN. 1998(ab). Diallel analysis for grain yield and harvest index in barley under diverse environments. *Rachis* 16: 22-27

Bhatta WM, Tahira B and Muhammad I. 2005. Path-coefficient analysis of some quantitative characters in barley. *Caderno de Pesquisa Serie Biologia* 17: 65-70

Bockelman HE, Valkoun J. 2010. Barley germplasm conservation and resources. *In: Ullrich SE, (ed) Barley: production, improvement and uses* Wiley-Blackwel, pp144-159

Bornare SS, Prasad LC, Lal JP and Singh J. 2013. Heterosis and combing ability for yield and its contributory traits in crosses of two row and six row barley under rainfed environment. *Crop Improvement* 40 (1): 81-86

Bornare SS, Prasad LC, Lal JP, Madakemohekar AH, Prasad R, Singh J and Kumar S. 2014. Exploitation of heterosis and combining ability for yield and its contributing traits in crosses of two-row and six-row barley (*Hordeum vulgare* L.) under rainfed environment. *International Journal of Plant Research* 27(3): 40-46

Bouzerzour H and Djakoune A. 1998. Inheritance of grain yield and grain yield component in barley. *Rachis* 16 (1-2): 9-16

Brockman DA, Chen X, Gallaher DD. 2013. Consumption of a high β-glucan barley flour improves glucose control and fatty liver and increases muscle acylcarnitines in the Zucker diabetic fatty rat. *European Journal of Clinical Nutrition* 52:1743-1753

Bruce AB. 1910. The Mendelion of heritability and augmentations of vigour. *Science* 32: 627-628

Burgazova I (Burgasova I) and Burgasova I. 1985. Inheritance of stem height and ear yield in intervarietal hybrids of winter forage barley. *Rasteniev"dni Nauki* 22(2):3-10

Carpc EB and Celk N. 2012. Correlation and path coefficient analyses of grain yield and yield components in two-rowed barley (*Hordeum vulgare*) varieties. *Notulae Scientia Biologicae* 4:128-131

Chauhan, BPS. 1985. Heterosis and combining ability in barley. *Acta Agronomica Academiae Scientiarum Hungaricae* 34 (3-4): 286- 293

Choudhary BD and Singh RK and Kakar SN. 1974. Estimation of genetic parameters in barley (*Hordeum vulgare* L.). *Theoretical and Applied Genetics* 45 (5): 192-196

Dadashi MR, Noorinia A, Askar M and Azizi S. 2010. Evaluation of crop and weed ecophysiology. *Journal of Agriculture Science* 4:29-40

Davis RL. 1927. Report of plant breeder. Ann. Report, Puerto Rico Agric. Exp. Station, pp 14-15

Derbew S, Urage E and Mohammed H. 2013. Genetic Variability in Barley (*Hordeum vulgare* L.) Landrace Collections from Southern Ethiopia. *International Journal of Science and Research* 2(12): 358-366

Dewey DR and Lu KH. 1959. A correlation and path coefficient analysis of crested wheat grass seed production. *Agronomy Journal* 51:515-518

Dhadhal BA, Dobariya` KL. 2006. Combining ability analysis over environments for grain yield and its components in bread wheat (*Triticum aestivum* L.). *National Journal of Plant Improvement* 8 (2): 172-173

Drikvand R, Samiei K and Hossinpur T. 2011. Path Coefficient analysis in hulless barley under rainfed condition. *Australian. Journal of Basic & applied Science* 5:12-27

El-Seidy ESH. 1997a. Inheritance of earliness and yield in some barley crosses. *Annals of Agricultural Science* 35 (2): 715-730

Eshghi R, Ojaghi J, Rahimi M and Salayeva S. 2010. Genetic characteristics of grain yield and its component in Barley (*Hordeum vulgare* L.) under normal and drought condition. *American-Eurasian Journal of Agricultural and Environmental Science* 9(5):519-528

Fedak G. 1985. Wide crosses in *Hordeum. Crop Science Society of America* pp 155-186

Garkavyi PF, Linchevskii AA and Khodzhakulov T. 1980. Study of quantitative characters in barley hybrids from crosses between varieties belonging to different ecotypes. Doklady Vsesoyuznoi Ordena, Lenina, I Ordena Trudovogo, Krasnogo, Znameni, Akademii, Sel'skokhozyaistvennikh, Nauk, Imeni V.I. Lenina. No. 5, 3-5

Grafius JE. 1959. Heterosis in barley. *Agronomy Journal* 51 (9): 551-554

Grifing B. 1956. Concept of general and specific combining ability in relation to diallel crossing system. *Australian Journal of Biological Science* 9 (4): 463- 493

Hayes JK. 1964. Development of heterosis concept in heterosis, Gowen, J.W. (Ed.) Heterosis. Hafner Publishing. New York. Chapter 33

Hayman BI. 1957. Interaction, heterosis and diallel crosses. *Genetics* 42: 336-355

Huang ZR. 1984. Studies on heterosis and combining ability in F_1 hybrids of six rowed barley. *Acta Agronomica Sinica.* 10: 123-131

Hull FH. 1945. Recurrent selection for specific combining ability in corn. *Journal of American Society of Agronomy* 37: 134-145

Irfan-ul-Haq SB and Khaliq WMR. 1997. Path-coefficient analysis of some quantitative characters in husked barley. *Pakistan Journal of Agricultural Sciences* 34:108-110

Jalal A and Ahmad A. 2012. Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Science* 4(3): 193-210

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: 44-52

Johnson HW, Robinson HF and Comstock RE. 1955b. Genotypic and phenotypic correlation in soybean and their implication in selection. *Agronomy Journal* 47: 477-482

Kakani RK, Sharma Y and Sharma SN. 2007. Combining ability analysis in barley (*Hordeum vulgare* L.). *SABRAO Journal Breed. Genet* 39 (2): 117-126

Kempthorne O. 1957. An Introduction to Genetical Statistics. John Wiley & Sons. Inc. New York.

Kaur S, Kaur H, Singh P, Cheema BS and Kumar V. 2016. Genetic variation and evaluation of exotic barley (*Hordeum vulgare* L.) genotypes for grain protein content, starch content and agronomic traits. *Electronic Journal of Plant Breeding* 7(4): 1114-1121

Kishore R, Pandey DD and Verma SK. 2000. Genetic variability and character association in hull-less barley. *Crop Research* 19:221-244

Kishore N, Kumar V and Verma RPS. 2016. Barley. In: Broadening the genetic base of grain cereals (M Singh, S Kumar eds.). Springer India. P 89-125

Kumar S and Prasad LC. 2002. Variability and Correlation studies in barley (*Hordeum vulgare* L.). *Research on Crops* 3:432-4326

Kumar M, Vishwakarma SR, Bhushan B, Kumar A. 2013. Estimation of genetic parameters and character association in barley (*Hordeum vulgare* L.) *Journal of Wheat Research* 5: 76-78

Kumar M and Shekhawat SS. 2013. Genetic variability in barley (*Hordeum vulgare* L.). *Journal of Plant Breeding* 4(4):1309-1312

Kumar M and Shekhawat SS. 2013b. Correlation and path coefficient studies in barley (*Hordeum vulgare* L.) under dual purpose condition. *Electronic Journal of Plant Breeding* 4(4):1313-1318

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

Koelreuter, JG. 1776. Dritte forsetzung der varlufigen Nachricht von einigen das Geschlecht der pflazen Betreftenden veruschen und Beobachtunger Leipzing.

Lodhi RD, Prasad LC, Bornare SS, Madakemohekar AH and Prasad R. 2015. Stability analysis of yield and its component traits of barley (*Hordeum vulgare* L.) genotypes in multi environment trials in the north eastern plains of India. *SABRAO Journal Breeding and Genetics* 47 (2): 143-159

Madic M. 1996. Inheritance of spike traits and grain yield in barley (*Hordeum vulgare* L.) hybrids. Review of res. work at the faculty of *Agri. Belgrade* 41 (1): 53-65

Madic M, Knezevic D, Paunovic A and Durovic D. 2012. Genetic analysis of spike traits in two-rowed and multi-rowed barley crosses. *Genetika* 44 (3): 475-482

Madhukar K, Prasad LC, Lal JP, Chandra K and Thakur P. 2018. Heterosis and mixing effects in barley (*Hordeum vulgare* L.) for yield and drought related traits. Journal of Pharmacognosy and Phytochemistry 7(2): 2882-2888

Manmohan S, Sohu VS and Mavi GS. 2003. Gene action for grain yield and its components under heat stress in bread wheat (*Triticum aestivum* L.). *Crop Science* 30: 189-197

Martinez JHE and Foster AE. 1998 a. Genetic analysis of heading date and other agronomic characters in barley (*Hordeum vulgare* L.). *Euphytica* 99(3): 145-53

Mansour M. 2016. Genetical analysis of some quantitative traits in barley under saline soil conditions. Proceedings: The sixth field crops conference, FCRI, ARC, Giza, Egypt, 22-23 Nov. 2016. pp. 99-107

Najeeb S and Wani SA. 2004. Correlation and path analysis studies in barley (*Hordeum vulgare* L.). *National Journal of Plant Improvement* 6:124-125

Nasr HG and Khayrallah W. 1976. Heterosis, inbreeding depression and combining abilities in a five-parent diallel of six-row barley. *The Journal Agriculture Science,* 86 (3): 537-542

Naik VR, Hanchinal RR, Maled BG and Patil BN. 1988. Correlation and path analysis in barley. *Karnataka Journal of Agricultural Science* 11: 230-232

Nanak C, Vishwakarma SR, Verma OP, Kumar M. 2008.Worth of genetic parameters to sort out new elite barley lines over heterogeneous environments. *Barley Genetics Newsletter* 38:10-13

Newton AC, Flavell AJ, George TS, Leat P, Mullholland BJ et al. 2011 Crops that feed the world. Barley: a resilient crop? Strengths and weaknesses in the context of food security. *Food Security* 3: 141-178

Pal S, Singh T and Ramesh B. 2010. Estimation of genetic parameters in barley (*Hordeum vulgare* L.). *Crop Improvement* 37: 52-56

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

Pesaraklu S, Soltanloo H, Ramezanpour SS, KalateArabi M, Nasrollah NejadGhomi AA. 2016(ab). An estimation of the combining ability of barley genotypes and heterosis for some quantitative traits**.** *Iran Agricultural Research* 35 (1): 73-80

Phogat DS, Singh D, Dahiya GS and Singh D. 1995. Genetics of yield and yield components in barley (*Hordeum vulgare* L.) *Crop Research* 9:3, 363-369

Potla KR, Bornare SS, Prasad LC, Prasad R and Madakemohekar AH. 2013. Study of heterosis and combining ability for yield and yield contributing traits in barley (*Hordeum vulgare* L.). *The Bioscan,* 8 (4): 1231-1235

Raikwar RS, Upadhyay AK, Gautam US and Singh VK. 2014. Genetic architecture of quantitative traits in barley (*Hordeum vulgare* L.). *Indian Journal of Genetics and Plant Breeding* 74: 93-97

Ram M. and Shekhawat AS. 2017c. Heterosis, inbreeding depression and combining ability analysis for yield and its component traits in barley (*Hordeum vulgare* L.). *Plant Archives*, **17 (2):** 851-860

Rathore RKS and 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 Science and Research* 16 (1): 56-63

Riggs TJ and Hayter AM. 1972. Diallel analysis of time to heading in spring barley. *Heredity* 29 (3) 341-357

Sethi SK, Paroda RS and Singh D. 1987. Combining ability for harvest index and grain yield in barley. *Crop Improvement* 14 (2): 157- 159

Sethi GS, Singh HB. 1971. Variability, correlation and regression analysis in hull less barley. *Plant Sciences* 3: 43

Sethi GS, Singh HB, Sharma KO. 1972. Variability and correlation in hulled barley (*Hordeum vulgare* L.). *The Indian Journal of Agricultural Science* 44: 585-590

Shahinnia F, Rezai AM and Tabatabaei BES. 2005. Variation and path coefficient analysis of important agronomic traits in two- and six-rowed recombinant inbred lines of barley (*Hordeum vulgare* L.). *Czech Journal of Genetics and Plant Breeding* 41: 246-250

Sharma RC. 1978. Combining ability in Barley (*Hordeum vulgare* L.). *Indian Journal of Heredity* 10 (3): 33-41

Shendy M Z. 2015(ab). Estimation of heterosis, inbreeding depression and combining ability in six barley genotypes in both F_1 and F_2 generations. *Egyptian Journal of Plant Breeding* 19 (4): 167-1182

Shull GH. 1914. Duplicate genes for capsule form in *Bursa Pastoris. Zeitscher Inducting Abstam*. U. V-ererhungslehare, **12**: 97-149

Singh SJ and Singh BD. 1990. Genetics of earliness in barley. *Crop Improvement* 17 (2): 174-178

Singh, A.K., Yadav, H.S. and Singh, SB. 1996. Comparative assessment of diallel mating designs for genetic analysis in hulless barley. *Crop Research* 12 (3): 327-335

Singh I, Dashora SL, Sharma SN, Sastry EVD. 1999. Inheritance of some quantitative characters in six-rowed barley. *Indian Journal of Genetics and Plant Breeding* 59(1) 99-101

Singh SC, Singh SK, Singh SK. 2002. Combining ability and heterosis in six rowed barley. *Progressive Agriculture* 2: 54-56

Singh G and Srivastava SBL. 2005. Combining ability analysis for yield and its components in barley (*Hordeum vulgare* L.). *Farm Science Journal* 14: 36-39

Singh HL, Singh SK, Singh P and Singh BC. 2006. Genetic variability and characters association in barley (*Hordeum vulgare* L.). *International Journal of Plant Sciences* 1: 256-258

Singh S, Dhindsa GS, Sharma A and Singh P. 2007. Combing ability for grain yield and its components in barley (*Hordeum Vulgare* L.). *Crop Improvement* 34 (2): 128-132

Singh SK, Anil S, Kerkhi SA and Singh RP. 2008. Genetic variability and components compensation for grain yield in barley (*Hordeum vulgare* L.*). Environment and Ecology* 26**:** 2379-2381

Singh AP. 2011. Genetic variability in two-rowed barley (*Hordeum vulgare* L.). *Indian Journal of Scientific Research* 2(3): 21-23

Singh K, Sharma SN, Sharma Y and Tyagi BS. 2012. Combining ability for high temperature tolerance and yield contributing traits in bread wheat. *Journal of Wheat Research* 4 (1): 29-37

Singh M. 2012. Genetic improvement through variability, heritability and genetic advance in barley crop (*Hordeum vulgare* L.). *Environment and Ecology* 30: 1343-1345

Singh J, Prasad LC, Madakemohekar AH and Bornare SS. 2014. Genetic variability and character association in diverse genotypes of barley (*Hordeum vulgare* L.). *The Bioiscan* 9(2): 759-761

Sprague, G.F. and Tatum, LA. 1942. General vs. specific combining ability in single cross of corn. *Journal of American Society of Agronomy* 34: 923-932

Spunar J. 1978. Heterosis for yield and grain size in six rowed winter x two rowed spring barley F_1 hybrids. *Barley Genetics Newsletter* 8: 94-96

Subhani GM, Chowdhary MA and Gilani SMM. 2000. Manifestation of heterosis in bread wheat under irrigated and drought stress conditions. *Pakistan Journal of Biological Science,* 3 (7): 971-974

Sullivan P, Arendt E, Gallagher E. 2013. The increasing use of barley and barley by-products in the production of healthier baked goods. *Trends in Food Science and Technology* 29: 124-134

Sultan MS, Abdel-Moneam MA and Haffez SH. 2016. Estimation of combining ability for yield and its components in barley under normal and stress drought condition. *Journal of Plant Production* 7 (6): 553-558

Ullrich SE. 2010. Significance, adaptation, production and trade of barley. In: Barley: production, improvement and uses (Ullrich SE, Eds.). Wiley-Blackwell, Chichester. P 3-13

Ulker M and Ozgen M. 1993. Hybrid vigour in winter in two rowed barley (*Hordeum vulgare L)* convar. distichon. Alef. Doga Turk Tarim ve Ormancilik Dergisi 17 (1): 307-313

Verma I, Verma SR. 2011. Genotypic variability and correlations among morpho-physiological traits affecting grain yield in barley (Hordeum vulgare L.) *Journal of Wheat Research* 3: 37-42

Vir OM and Sultan SM. 2013. Genetic variability and character association in the germplasm of barley under rainfed Condition of Himalaya. *Crop Research* 45:91-95

Vishwakarma SR, Shukla A, Rajbahadur and Singh N. 2011. Expression of heterosis for yield and chlorophyll content in barley. *Plant Archives* 11(2) : 894

Wright S. 1921. Correlation and causation. *Journal of Agricultural Research* 20: 557-585

Xinzhong Zhang, Liangjie Lv, Chao Lv, Baojian Guo., Rugen Xu 2015. Combining Ability of Different Agronomic Traits and Yield Components in Hybrid Barley. Meixue Zhou, University of Tasmania, Australia 10(6):e0126828

Yadav SK, Pawar KK, Baghel SS, Jarman M and Singh AK. 2014. Barley correlation, path analysis, heritability and genetic advance. *Journal of Wheat Research* 6(2): 56-60

Yadav VK, Ram L, Kumar R, Singh SP. 2002. Genetics of yield components and some malting attributes in barley (*Hordeum vulgare* L.) *Progressive Agriculture* 2: 14-18

Yang JH, Yu Y, Cheng LL, and JiaSheng 2008. Analysis of yield components and the effect on grain yield with different rowed type barley introduced from CIMMYT. *Southwest China Journal of Agricultural Sciences* 21: 920-924

Zaefizadeh M, Ghasemi M, Azimi J, Khayatnezhad M. and Ahadzadeh B. 2011. Correlation analysis and path analysis for yield and its components in hulless barley. *Advances in Environmental Biology* 5:123-126

Zhang X, Liangjie L, Chao L, Guo B, and Xu R. 2015. Combining ability of different agronomic traits and yield *c*omponents in hybrid barley. Meixue Zhou, Uni. of Tasmania, Aus 10 (6): e0126828

Appendix I

Mean values of parents and crosses for seed yield and related traits in barley

Trait	Days to flowering	Days to maturity	Plant height (cm)	No of tillers/ plant	No. of grains/ spike	Spike length (cm)	Peduncle length (cm)	1000 grain weight (g)	Biological yield/plant (g)	Seed yield/ plant (g)	Harvest index (%)
Line											
HBL 713	136	168	102	12	63	8.60	25.20	46	93.68	34.75	37.00
HBL 722	132	157	88	13	27	9.32	28.62	58	56.82	16.84	29.89
HBL 723	128	157	84	9	59	7.55	24.43	56	115.64	36.83	32.15
HBL 738	118	155	94	9	26	6.67	33.65	46	39.74	12.88	32.48
HBL 748	130	166	97	8	60	7.62	25.20	68	95.16	30.59	32.00
HBL 751	137	172	102	5	62	7.33	32.47	38	33.67	11.43	33.94
Local Sudhrani	139	154	103	10	58	8.09	30.44	43	65.61	22.60	34.79
Tester											
Atahualpa	121	155	111	13	28	8.20	30.40	51	57.54	24.11	42.00
DWRUB 64	125	159	94	4	64	8.22	28.40	50	45.08	13.22	29.38
HBL 113	135	171	102	14	34	11.07	18.13	40	60.97	20.50	33.83
HBL 276	127	169	107	13	66	9.00	35.73	32	84.05	32.34	38.39
Line x tester											
HBL 713 X Atahualpa	124	160	122	11	30	9.27	40.13	52	52.78	21.95	41.70
HBL 713 X DWRUB 64	129	161	107	8	52	7.60	32.13	54	65.22	23.08	35.64
HBL 713 X HBL 113	131	161	116	10	32	10.07	31.47	51	50.81	20.84	41.00
HBL 713 X HBL 276	130	158	116	6	67	9.27	32.93	39	59.78	21.76	36.73
HBL 722 X Atahualpa	128	163	112	11	30	9.58	33.72	56	50.54	17.37	35.00
HBL 722 X DWRUB 64	133	174	100	13	29	8.73	30.53	68	88.34	27.34	31.08
HBL 722 X HBL 113	130	161	100	8	31	9.27	26.87	60	49.55	14.96	30.00

	Days to flowering	Days to maturity	Plant height (cm)	No of tillers/ plant	No. of grains/ spike	Spike length (cm)	Peduncle length (cm)	1000 grain weight (g)	Biological yield/plant (g)	Seed yield/ plant (g)	Harvest index (%)
HBL 722 X HBL 276	135	172	103	7	31	10.70	32.97	66	47.97	13.38	27.67
HBL 723 X Atahualpa	130	171	90	10	22	7.21	28.10	66	38.04	11.67	30.75
HBL 723 X DWRUB 64	130	165	101	10	26	7.69	28.93	58	42.14	13.30	31.80
HBL 723 X HBL 113	134	175	86	7	30	9.55	25.91	67	52.72	14.94	28.38
HBL 723 X HBL 276	129	166	111	10	34	10.52	34.38	51	58.51	19.29	33.03
HBL 738 X Atahualpa	117	159	110	12	30	8.51	37.00	59	55.68	21.42	38.64
HBL 738 X DWRUB 64	118	161	96	8	27	7.47	29.93	65	46.84	14.43	31.08
HBL 738 X HBL 113	127	163	109	14	35	9.58	34.33	54	65.21	24.81	38.00
HBL 738X HBL 276	119	159	112	11	29	8.87	42.40	68	68.98	26.12	38.03
HBL 748 X Atahualpa	127	156	124	7	30	10.10	38.45	64	48.09	17.47	36.29
HBL 748 X DWRUB 64	129	156	100	9	59	6.65	29.17	54	74.69	26.42	35.41
HBL 748 X HBL 113	131	161	116	8	32	10.93	30.27	62	57.58	21.81	37.84
HBL 748 X HBL 276	130	162	109	8	61	9.07	36.27	32	44.92	16.16	36.46
HBL 751 X Atahualpa	131	168	121	6	28	9.00	36.27	56	31.28	8.86	29.00
HBL 751 X DWRUB 64	130	165	110	7	63	8.27	31.27	42	60.20	19.67	32.56
HBL 751 X HBL 113	135	167	123	12	36	9.73	31.00	59	68.76	24.32	35.26
HBL 751 X HBL 276	131	165	115	8	67	9.87	32.67	33	64.33	19.41	30.47
Local Sudhrani X Atahualpa	130	169	123	12	33	10.60	38.93	65	71.37	27.36	38.51
Local Sudhrani x DWRUB 64	129	172	108	7	55	7.67	31.67	37	49.34	14.74	30.00
Local Sudhrani x HBL 113	137	165	123	12	33	11.55	31.44	59	65.89	26.08	39.60
Local Sudhrani x HBL 276	138	167	109	13	62	8.33	32.60	46	95.92	38.36	40.00
Mean	**129.48**	**163.71**	**106.56**	**9.61**	**42.07**	**8.91**	**31.65**	**53.1**	**60.86**	**21.11**	**34.51**
C.V. (%)	**1.86**	**1.35**	**6.82**	**20.07**	**7.75**	**11.6**	**13.17**	**4.38**	**16.76**	**16.06**	**7.7**
C.D. @ 5%	**3.91**	**3.61**	**11.83**	**3.15**	**5.3**	**1.68**	**6.78**	**3.79**	**16.58**	**5.51**	**4.32**
S.E.	**1.39**	**1.28**	**4.20**	**1.12**	**1.88**	**0.60**	**2.41**	**1.34**	**5.89**	**1.96**	**1.53**

Brief biodata of student

Name : Ravinder Kumar

Mother's Name : Kamlesh Devi

Father's Name : Rajbir Singh

Date of Birth : 15 August, 1993

Permanent Address : Village Kamalpur Roran, P.O. Sangoha, Karnal,
Haryana-132001

Academic Qualification:

Qualification	**Year**	**School/Board/ University**	**Marks (%/ OGPA)**	**Division**	**Major Subjects**
10th	2008	Guru Nanak Sr. Sec. School, BSEH, Karnal	53.8	Second	English, Hindi, Mathematics, Social Science, Science &
10+2	2011	S D Sr Sec School BSEH, Karnal	64.2	First	English, Hindi, Mathematics, Physics, Chemistry
B.Sc. (Agri.)	2015	HNB Garhwal Central University, Srinagar, Uttrakhand	7.07	First	Agriculture and Allied subjects
M.Sc.(Agri.)	-	CSK HPKV, Palampur, HP (176 062)	6.52	First	Genetics and Plant Breeding