

**STABILITY ANALYSIS IN BARLEY (*Hordeum vulgare* L.) FOR
YIELD AND CONTRIBUTING TRAITS UNDER VARIED
CONDITIONS**

by

Neha Manhas

(J-19-M-664)

**A Thesis submitted to
Faculty of Agriculture
in partial fulfillment of the requirements
for the degree of**

**MASTER OF SCIENCE IN AGRICULTURE
GENETICS AND PLANT BREEDING**



Division of Plant Breeding and Genetics

**Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu
Main Campus, Chatha, Jammu-180009**

2021

CERTIFICATE-I

This is to certify that the thesis entitled “Stability analysis in Barley (*Hordeum vulgare* L.) for yield and contributing traits under varied conditions” submitted in partial fulfillment of the requirements for the degree of **Master of Science in Agriculture (Genetics and Plant Breeding)** to the Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, is original work and has similarities with published work not more than minor similarities as per UGC norms of 2018 adopted by the University. Further the level of minor similarities has been declared after checking the manuscript with **URKUND** software provided by the University.

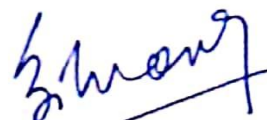
The work has been carried out by **Miss Neha Manhas** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma. It is further certified that help and assistance received during the course of thesis investigation have been duly acknowledged.



Major Advisor
Dr. Subhash Chander
Asstt. Professor (PBG)
SKUAST-Jammu

Place: Jammu

Date: 20/10/21



Head of the Division



Dean, FoA

CERTIFICATE-II

We, the members of Advisory committee of **Miss Neha Manhas**, Registration No. **J-19-M-664**, a candidate for the degree of **Master of Science in Agriculture (Genetics and Plant Breeding)**, have gone through the manuscript of the thesis entitled "**Stability analysis in Barley (*Hordeum Vulgare* L.) for yield and contributing traits under varied conditions**" and recommend that it may be submitted by the student in partial fulfillment of the requirements for the degree.



Dr. Subhash Chander
Assistant Professor
SKUAST-Jammu
(Major Advisor &
Chairman Advisory Committee)

Place: Jammu

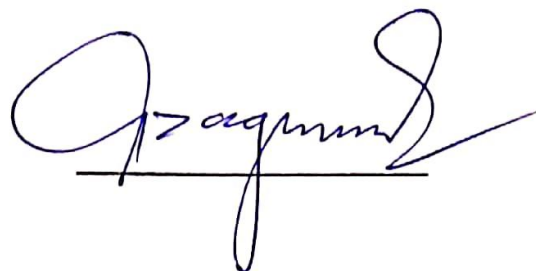
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Advisory Committee Members

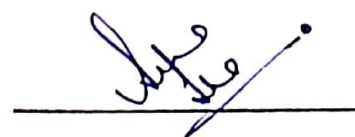
1. Dr. Tuhina Dey
Professor
Division of Plant Breeding & Genetics
(Member from Major Subject)



2. Dr. Gurdev Chand
Assistant Professor
Division of Plant Physiology
(Member from Minor Subject)




3. Dr. Susheel Sharma
Assistant Professor
School of Biotechnology
(Dean's Nominee)




CERTIFICATE-III

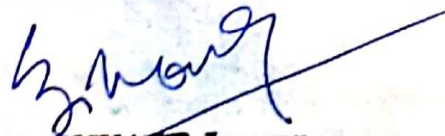
This is to certify that the thesis entitled "Stability analysis in Barley (*Hordeum vulgare* L.) for yield and contributing traits under varied conditions" submitted by Miss Neha Manhas, Registration No. J-19-M-664 to the Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu in partial fulfillment of the requirements for the degree of Master of Science in Agriculture (Genetics and Plant Breeding) was examined and approved by the advisory committee and external examiner(s) on 30-11-2021




Dr. Subhash Chander
Asstt. Professor (PBG)
Major Advisor



Head
Division of Plant Breeding & Genetics



Dean, FoA, SKUAST-Jammu



External Examiner
Dr. Farooq A. Sheikh
Prof. and Head,
Div. of EPB
FoA, SKUAST-K
Wadwara.



Acknowledgement

ACKNOWLEDGEMENTS

First and foremost, I would like to thank God Almighty, the author of knowledge and wisdom, for his countless love, for giving me the strength, knowledge, ability and opportunity to undertake this research study and to persevere and complete it satisfactorily. Without his blessings, this achievement would not have been possible.

I am very thankful for being a part of Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu (SKUAST-J, Chatha).

With respect I wish to express my heart full thanks to my Major Advisor, Dr. Subhash Chander Assistant Professor, Division of Plant Breeding and Genetics, SKUAST-Jammu for his valuable guidance, expert suggestions, motivation, enthusiasm, kind cooperation, supervision, constant encouragement, untiring help throughout the different phases of planning, commencement until ultimate completion of this study, constant encouragement during the course of the present investigation and all other considerations throughout the research work. Learning from him is an honour which I will cherish all my life. Without his able guidance this thesis would not have been possible and I shall eternally be grateful to him for his assistance.

I express my special gratitude towards worthy members of my advisory committee, Dr. Tuhina Dey, Professor (Division of Plant Breeding and Genetics), Dr. Gurdev Chand, Assistant professor (Division of Plant Physiology) and Dr. Susheel Sharma, Assistant Professor (School of Biotechnology) for their constant support, valuable suggestions, generous help and encouragement throughout the course of study.

I extend my sincere and profound thanks to Professor Bikram Singh, Dean Faculty of Agriculture and Head, Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu for being so kind, helpful and encouraging. His insightful guidance, constructive suggestions and continuous support has really inspired me to pursue my research work with precision.

I take pride in acknowledging the faculty members Dr. Bupesh Kumar, Assistant Professor, Dr. Sanjeev Kumar, Dr. R.S Sudan, Dr. Praveen Singh, and Dr. S.K Rai who taught me the science of Genetics and Plant Breeding. I am also thankful to Dr. M.K Pandey and Dr. V.B. Singh for always guiding me where ever possible. Thank you for all your kind motivation, guidance and support.

I express my sincere gratitude to Dr. Brinder Singh Jr. Scientist ACRA, Dhiansar for his timely help during my research work. Thank you for all your kind motivation, dedicated help and wise suggestions. I would like to convey my sincere thanks to Mr. Dalip Panotra for his timely cooperation during my data collection.

My sincere thanks are due to all technical and non-technical staff of Division of Plant Breeding and Genetics, especially Mr. Naresh Choudhary, Mr. Darshan Lal, Mr. Paramjit Singh, Mr. Rampal, Mr. Anoop Kumar and Mr. Vijay Kumar for their co-operation and timely help during my research work.

I am greatly indebted to my seniors Monika Sharma, Sapalika Dogra for their valuable support and constant encouragement.

I will never forget cheerful company, unbond affection, sincere cooperation and constant help of my colleagues Danish Mushtaq, Hilal Ahmed Pir, Kundan Veer Singh.

My acknowledgement would be incomplete without thanking the biggest source of my strength, my family. Without their unbounded love, unfailing prayers, blessing, uncountable sacrifices, unbarred assistance, faith and patience of my parents none of this would have been possible. I owe this success to my parents Smt. Kamlesh Rani and Sh. Ramesh Kumar. I have no words to express my heartfelt sense of gratitude towards them. I owe my thanks to my brother Love Manhas and Sister-in-law Risha Rajput for their encouragement, moral support, incessant love, care and affection.

My acknowledgement would be incomplete without the special mention of my friends Mr. Nesar Ahmad, Ms. Aman, Ms. Shilpa, for their never-ending support for me and for being with me in ups and downs of life during last two years. Without their help, cooperation and understanding throughout, the ambition of completing this task would not have been fulfilled.

I am also thankful to them who helped me in one or other way towards the completion of my thesis and deeply apologize for not being able to mention their name individually.

Neha
Neha Manhas

Date: 27/12/21

Place: Jammu

ABSTRACT

Title of Thesis : **Stability analysis in barley (*Hordeum vulgare* L.) for yield and contributing traits under varied conditions.**

Name of the Student : Neha Manhas

Registration Number : J-19-M-664

Major Subject : Genetics and plant Breeding

Name and Designation of Major Advisor : Dr. Subhash Chander, Assistant Professor, Plant Breeding and Genetics

Degree to be awarded : M.Sc. (Ag.) Genetics and Plant Breeding

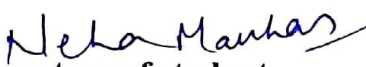
Year of award of Degree : 2021

Name of University : Sher-e- Kashmir University of Agricultural Sciences and Technology of Jammu, UT

The current study, titled “**Stability analysis in barley (*Hordeum vulgare* L.) for yield and contributing traits under varied conditions**” was conducted during Rabi 2019-20 and 2020-21 at two locations viz., Advance Centre for Rainfed Agriculture SKUAST-J, Dhiansar and Research Farm, Chatha to study the G×E interaction for stability of grain yield and component traits in barley to identify the stable genotypes and to assess the character association of yield and component traits. Analysis of variance (ANOVA) for thirteen characters of all the seventeen genotypes for individual environments *i.e.*, E1, E2, E3, E4 has shown maximum significant results for most of the traits, which suggested the desired variability among different barley genotypes. Significant and positive correlation of grain yield per plant was observed with harvest index, number of grains per spike, plant height and flag leaf width at both genotypic and phenotypic levels. Positive and direct effect on grain yield was observed through harvest index, number of tillers per plant, plant height, SPAD values, days to 50% flowering at both genotypic and phenotypic levels in pooled environment. G x E interaction was found significant for all the characters except flag leaf width and number of tillers per plant. In stability analysis for grain yield /plant, the genotype RD-2035 was found most stable and suitable followed by RD-2849 and BH-902. These genotypes recorded high means than general mean values and with regression coefficient close to unity $bi=1$ and $S^2di=0$. The genotypes RD-2035, RD-2849 and BH-902 were found stable for grain yield and other yield contributing characters namely SPAD values, flag leaf length, spike length and biological yield per plant therefore, while developing varieties for stable performance across environments such traits should be given priority. The stable genotypes can be used for future breeding programmes as well as for cultivation under varied environment for higher yield.

Keywords: Barley, stability, variability, G x E interaction, regression coefficient.


Signature of Major Advisor


Signature of student

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Abbreviation used	Terminology
%	Per cent
*	Significant at 5% level
**	Significant at 1% level
ANOVA	Analysis of variance
bi	Regression coefficient
C. D.	Critical difference
C.V.	Coefficient of variation
cm	Centimeter
d. f.	Degree of freedom
E	Environment
<i>et al.</i> ,	And others
g	Gram
<i>i.e.</i> ,	That is
kg	Kilogram
m	Meter
MS	Mean square
q/ha	Quintals per hectare
S. No.	Serial number
S. Em.	Standard error of mean
S. Ed.	Standard error of difference
<i>viz.</i> ,	Namely
<i>via.</i> ,	By the means of
S^2_{di}	Mean square deviation from linear regression
\bar{X}	Mean

Chapter-I

Introduction

CHAPTER-1

INTRODUCTION

Barley (*Hordeum vulgare* L. $2n=2x=14$) belongs to the grass family *Poaceae*. It is the fourth most important cereal crop of the world after rice, wheat and maize with a share of about 7% of global cereal production. In India barley is grown in rabi season mainly in states of Uttar Pradesh, Rajasthan, Bihar, M.P., Haryana and Punjab that constitute about 80% of total barley area of the country. In India total area occupied by barley is 600 thousand hectares with a total production of 1.69 million tons (Anonymous 2021). In J&K, barley occupies an area of about six thousand hectares with production of 4.4 thousand tonnes and average productivity of 5.76 q/ha which is significantly very low as compared to national production and productivity (Singh, 2018).

Barley can be grown in a wide range of environments than any other cereal crop, including extremes of latitude, longitude, and high altitude (Vangool and Vernon, 2006), it is therefore, frequently called as cosmopolitan crop. It is also known as poor man's crop because it needs low inputs and possess better adaptability to dry and marginal lands. In Jammu region of J&K, barley assumes greater importance in dry and kandi belts because of its usage as feed and fodder.

Barley grains are used as a protein and energy source in mulching cattle diets although it is most commonly used as malt source for alcoholic beverages in beer industries. It is commonly used in bread, soups, stews and health products (Badea and Wijekoon 2021). Nutritional value of barley has much importance as its grain have high protein, fiber, vitamins and natural bioactive antioxidants like phenolics and lipids. The whole barley grain contains about 65-68% starch, 10-17% protein, 4-9% β -glucan, 2-3% free lipids and 1.5-2.5% minerals (Quinde *et al.*, 2004). Grain germination speed and consistency of endosperm cell wall breakdown into fermentable sugars makes it a primary raw material for the production of alcoholic beverages or biofuels. Barley straw has a high level of lignocellulose, which could also be used as a form of renewable energy. Barley grain are used as animal feed as well as fodder as vegetative stage. It has advantages over oats, because of faster growth and dual utility. Dual purposes barley cultivation provides nutrition to the livestock through its green fodder and grains

can be harvested from the regenerated crop. Barley can be utilized solely as green fodder crop under limited water supply or under less rainfall (Kumar *et al.*, 2014).

Despite being a crucial crop rich in proteins, minerals and carbohydrates, barley has been neglected in most of the area because of dominance of wheat, rice, and other cash crops, as a result of which its area, production and productivity is decreasing year after year. Development of new barley cultivars with tolerance to abiotic and biotic stresses and improved yield is a prime objective of any breeding programme. To make this possible, a good knowledge of variability present in the available germplasm, wild and cultivated barley is pre-requisite. The rate of success, however, will depend on the occurrence of desirable genetic variation and the availability of precise methods of identification, selection and, transfer of superior genes (Ellis. *et. al.*, 2000).

Grain yield in barley is a complex trait and is measured by means of association of number of components which are under polygenic control. Thus, the identification of important traits and their correlation with yield will be very useful for the development of an effective breeding method for the development of better genotypes. The method of correlation coefficient analysis is a most appropriate, which gives the degree and extent of relationship among specific plant characters and it reflects the mutual relationship between the variables and provides basic idea for selection. The analysis of genetic association along with phenotypic correlation indicate the amount of phenotypically expressed correlation affected by the environment. The information on association of characters with yield and among themselves can be useful for planning a successful breeding programme because in most of the breeding programme, yield is the prime objective.

Path coefficient analysis is a statistical method specifically designed to assess the interrelationship of different traits and their effects on grain yield. It is a standardized partial regression coefficient and measures the direct impact of one variable upon some other and helps in the separation of the correlation coefficient into additives of direct and indirect results. The application of path coefficient analysis in plant breeding substantiated by Dewey and Lu (1959).

If correlation between dependent and independent variable is due to the direct effects of the latter, it shows a true relationship between them and selection can be performed for such a character, so as to intensify the dependent variable. But if the association is through indirect effects of the characters *via* another component character, the breeder has to choose the latter one by which the indirect effect is applied on the dependent character such as yield. The study of correlation along with path analysis is extremely crucial to understand the cause and impact relationship between different pairs of characters.

The use of stable cultivars over various environments for high seed yield and quality characters is crucial for many crops. It is obvious from the various experiments that when cultivars are used in varied environments for seed yield and component traits, differences would be expected. This differential yield response of cultivars from one environment to another is called genotype \times environment (G \times E) interaction (Vargas *et al.*, 1998). The stability of genotypes over environments is the major factor, hence, Genotype \times Environment (GE) interactions are exceptionally important in the development and evaluation of plant varieties because they reduce the genotypic-stability values under diverse environments.

In any crop improvement programme for improving production, genetic variability and genotype \times environment interaction is exploited. Genotype \times environment cannot be measured at once; however, it needs to be inferred from measurements on phenotypes. This is a complex measure because all the genotypes do not react in the same way due to change in the environment. Different genotypes show differential performances in various environments due to the occurrence of genotype \times environment interactions. This affects the relative ranking of varieties in a range of varying environmental conditions. The multi-environmental testing has been an important part of nearly all the breeding programs. Genotype \times Environment interactions are normally taken into consideration as hinderance in plant breeding.

Stability analysis is a technique for estimating the adaptability of different crop varieties in diverse environments and to increase the efficiency of the selection of the superior cultivars by changing their comparative effectiveness in different environments (Biswas *et al.*, 2012). A precise approach to measure stability was first proposed by Finlay and Wilkinson (1963) and later progressed by Eberhart and Russell (1966). Linear Regression version of Eberhart and Russell (1966) is typically used for

evaluation of G×E interaction, in which the b-values (regression) give, information about adaptability and S^2_{di} (deviation from regression) are used as measures of stability of performance. The stability of varieties has been described through excessive implicit yield and regression coefficient ($b_i=1$) and deviations from regression as small as possible ($S^2_{di}=0$). Knowledge and study of the effect of environmental factors on crop production of field crops would enhance identity and choice of stable genotypes that can help in increased production of yield lower in numerous environments. Keeping in view the climatic condition of Jammu and Kashmir and scope of barley crop grown in marginal and rainfed regions the present experiment is devised to test the barley genotypes in different environments *viz.* irrigated and rainfed in two seasons accordingly forming four environments for stability analysis of grain yield and its component traits.

Therefore, present investigation entitled “**Stability analysis in Barley (*Hordeum vulgare* L.) for yield and contributing traits under varied conditions**” was carried out at two locations *i.e.*, Research Farm Chatha, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, and ACRA, Dhiansar, during *Rabi* season 2019-20 and 2020-21 constituting a total four environments. The aim of present investigation was to:

- To study the G×E interaction for stability of grain yield and component traits in barley genotypes.
- To study character association for yield and component traits in barley genotypes.
- To identify the stable genotypes in barley for different component traits.

Chapter-II

Review of Literature

REVIEW OF LITERATURE

Stability and G x E interaction

Bains and Gupta (1972) evaluated six bread wheat genotypes along with parental lines for stability by using Eberhart and Russell (1966) model. They concluded that variances among the means of the genotypes and environments and linear components of environments were highly significant for different characters.

Gill and Bhullar (1977) studied the overall performance and stability analysis of wheat. Three varieties WL 711, HD 2009 and HD 2122 were tested in comparison to 3 check varieties, namely WG 357, Sonalika and Kalayansona at 8 locations in Punjab. The stability analysis for grain yield was carried out as per model of Eberhart and Russell (1966) and reported significant variation in most of the varieties for all the characters.

Lai and Pomeranz (1977) carried out an experiment to study stability of new and old barley cultivars for malt properties for three years. Stability for kernel weight was significantly higher in the new than in the old cultivars. The stability of total extract and fine-coarse grind extract for six-rowed was greater and more consistent than for the two-rowed barley malts. Stability of α -amylase in some of the newer two-rowed and six-rowed barley malts was superior to that in the older cultivars.

Sayed and Ghandorah (1987) studied the performance and stability of 16 barley genotypes. The genotypes CI 13575 and Cr.259/36 with b-values of <1.0 showed relatively small deviation from mean square and better adapted to unfavourable environments. CI 13520 had the highest deviation from mean square of 1.387 making it the most unpredictable genotype across environment of this study.

Kolar *et al.*, (1991) carried out an experiment to show that winter barley genotypes can be improved for survival in cold tolerance in spite of fluctuations in air and soil temperature. They reported 'Norstar' winter wheat as cold tolerant than the barley genotypes, and little variation among winter barley genotypes for cold tolerance. They also concluded that winter barley cultivars were more, cold tolerant than facultative cultivars.

Josephides (1992) calculated the regression coefficient (b) of crop mean on the environmental index (I) and the mean square deviation from regression (Sd^2) for wheat, barley and triticale. The study showed that triticale had a similar mean grain yield (3,842 kg/ha) to that of bread wheat, but was significantly higher yielding than barley and durum wheat (5 and 7% respectively).

Nissila (1992) conducted a study on yield stability of barley and reported the effect of variation between locations and years on the yield stability of barley. He concluded that the genotype \times location interaction was highly significant and became an important factor than genotype \times year interaction in barley breeding for Finnish conditions in two experimental years.

Ishag and Mohamed (1996) evaluated five wheat (*Triticum aestivum* L.) cultivars for stability as per the model suggested by Eberhart and Russell (1966). The Genotype \times Environment interaction was significant for grains per ear, test weight and yield. G \times E (linear) interaction was significant for number of ears per m², productive tillers per plant, ears per m² and grain per ear. The stability parameters for other characters confirmed that the five cultivars were different in their response to varying environments.

Mehta *et al.*, (2000) studied stability of six wheat genotypes grown in artificially created fertility gradient for two years by using model proposed by Eberhart and Russell (1996). The linear component (bi) for individual genotype was significant for all genotypes while the non-linear component ($\sigma^2\delta_i$) was significant for only two genotypes viz., DL 802-3 and HD 2329. The significant and the highest $\sigma^2\delta_i$ values of grain yielding variety HD-2189 ($\sigma^2\delta_i=0.28$), indicated that the variety is for high fertility environments. The variety Kundan showed the lowest value ($\sigma^2\delta_i$) (0.07) and confirmed better performance even at lower fertility levels.

Madariya *et al.*, (2001) studied fifty bread wheat genotypes with three simulated environments for stability parameters in respect of grain yield and its components. Their results showed significant G \times E interaction for most of the characters viz. grain yield, test weight, no. spikelets/spike, no. of grains/spike. They also reported that no. of effective tillers/plant, no. of spikelets/spike, no. of grains/spike and test grain weight are the major component of yield and varied in compensatory fashion to impart stability to yield.

Costa and Bollero (2006) in their experiment in stability on barley reported significant differences among released and advanced lines for the traits of days to heading, plant height and grain yield. Most of the barley genotypes tested possessed regression slopes for grain yield that did not differ from 1.0 revealed good potential for yield response under varied environmental conditions.

Pilania (2007) conducted experiment on thirty-five genotypes of barley (*H. vulgare* L.). He reported that pooled analysis of variance for all the traits showed large variations among the genotypes and environments. Stability analysis was performed as per the method proposed by Eberhart and Russell (1966). Seven genotypes were found stable for grain yield, ten for 1000 grain weight, six for number of seeds/spike, four for number of tillers/ plant, seven for malt and four for starch percentage under different environmental conditions.

Anisuzzaman *et al.*, (2007) evaluated performance of six promising barley genotypes and reported that, for eleven yield related characters the genotype BSH-2 showed stable performance for plant height under different irrigation period. The genotype BSH-2 for number of tillers and BB-1 for the fertile tiller number were not suitable for excess moisture content soils. The results confirmed that genotype BSH-2 as an ideal genotype for developing improved barely cultivars.

Debebe *et al.*, (2008) evaluated ten genotypes of barley including one local variety to examine G×E interactions in low-moisture areas over ten environments. The statistical analysis was done by different stability models and AMMI analysis to study the performance of the genotypes and to identify stable one. This study concluded that in the low-moisture areas, the rainfall was important for yield performance and was the cause of G×E interactions and for early seedling formation and grain filling.

Soluki *et al.*, (2008) evaluated the stability, the adaptation and the highest yield for the 20 hulless barley genotypes. Based on the results, they reported ICN93-328 and Aleli/4/mola2 as stable genotypes and Gloria was found stable for low yielding areas.

Chand (2008) conducted an experiment to evaluate thirty diverse elite lines of barley along with six checks for stability and reported significant genotypes x environment (G x E) interactions for all the traits. The four genotypes viz., RD2634, RD2689, JB47 and RD2620 having high yield mean performance, $b_i=1$ and $S^2 d_i=0$ reflected better phenotypic stability. Two genotypes DWR51 and K792 associated with

$b_i < 1$ and $S^2 d_i = 0$ was found stable for poor environments. He also reported that on the basis of mean performance and stability parameters DWR51, JB42, NDB1401, NDB1289, RD2677, JB40, RD2670, NDB1276, BH65, NDB1280, NDB1281, JB47, RD2552, RD2689, JB47 and RD2634 were found as stable for most of the traits studied and these promising genotypes may be used as a donor in barley improvement programme for desired ecosystems.

Kavitha *et al.*, (2009) conducted experiment on stability performance of 20 malt barley genotypes including commercial cultivars and elite lines by Eberhart and Russell (1966). They reported that the genotypes BL 53 was found to be stable for days to flowering, VJM531, VJM540, DWRUB52, PL796 and RD2503 for plant height, VJM201, PL796, BL71 and DWR28 for tillers per plant, DWRUB52 and VJM531 for grains per spike, and BL73 and BL61 for 1000-grain weight and VJM531, VJM540 and DWRUB52 were found to be relatively stable for these characters respectively.

Muluken (2009) conducted an experiment to evaluate the yield performance and stability of twenty malting barley genotypes. Spearman rank correlation showed that b_j , R_i^2 , S_j^2 , CV_j and $IPCA_1$ of environments were positively correlated, which concluded that any of these five parameters can be used as a good alternative for stability evaluation. The mean of genotype yields was positively correlated with stability parameters of b_i and R_i^2 ($P < 0.01$), but were negatively correlated with $IPCA_1$, Wi_2 , P_i ($P < 0.01$) and $ASVi$. They concluded that the high yielding genotype G12 was not stable and genotypes G1 and G13 were stable for grain yield.

Rohman *et al.*, (2010) conducted an experiment on eight genotypes of hull-less barley to study genotype and environment ($G \times E$) interaction and to identify stable genotypes with high yield potential using Eberhart and Russell's (1966) model. They reported that in respect to plant height genotypes BHL-18 and BB-6 were stable for poor environment. BHL-3 and BHL-12 showed an unpredictable performance for number of grains/plant. Genotype BHL-1 was highly responsive for 1000-grain weight, while, BHL-3 found to be appropriate for poor environments. The genotype BHL-19 showed unit regression coefficient (b_i) value with small deviation from regression ($S^2 d_i$) value and higher mean of yield per plant in terms of stability which showed that this genotype had stable performance for yield across environments.

Hanifi *et al.*, (2011) carried out an experiment to assess the genotype \times environment interaction and to identify barley (*Hordeum vulgare* L.) genotypes with high stability for grain yield and yield components. They reported that significant differences between the environments for all the traits and between the genotypes for thousand-grain weight, days to heading and ear length. The analysis of correlations between traits showed the importance of selecting for earliness, number of grains/ear, plant height and ear length to obtain desirable grain yields under drought-stressed conditions.

Sabaghnia *et al.*, (2012) evaluated fourteen new breeding lines obtained from the barley breeding programs and cultivar Izeh as one local check genotype for yield stability at eleven environments and reported that Genotypes G1, G6 and G8 as more stable and had specific adaptability to favorable environments. Genotypes G4 (3,393 kg ha⁻¹) G12 (3 440 kg ha⁻¹) can be considered as the most stable genotype with respect to both stability and yield. The high values of DI (desirability index) were associated with high mean yield, but the other stability methods were not positively correlated with mean yield. The results from principal component analysis and correlation analysis indicated that EV (environmental index), CV (coefficient of variation), ER (regression parameters of Eberhart and Russel 1966), and DI (desirability index) stability parameters would be useful for selection for high yield and stability.

Bantayehu (2013) investigated malting barley genotypes under diverse agro-ecologies of north western Ethiopia to determine the magnitude effect of genotype, environment and their interaction on economically important traits and identify stable malt barley (*Hordeum distichon* L.) genotypes. The study revealed that genotype G1 was more stable whereas G13 showed specific adaptation in low potential environments. Further results showed that G9 and G11 in protein content and G1 and G11 in seed size, were stable in performance across environments.

Saad *et al.*, (2013) conducted an experiment to evaluate twelve genotypes of barley. Six parametric stability statistics were calculated (b_i , S^2_{di} , R_i^2 , W_i^2 , S^2_i and CV_i) to determine yield stability. The results concluded that genotypes Giza 123, Giza 129, Giza 127, G4, G2, G6 and G8 were more stable genotypes. These genotypes could be considered as donor parents for stability in barley improvement programs, and could be considered as stable high yielding cultivars. The results showed that high-yielding

genotypes can vary in yield stability, and concluded that yield stability and high grain yield are not mutually exclusive.

Welu (2014) conducted an experiment to estimate genotype \times environment on grain yield and yield related traits. The outcomes of ANOVA for grain yield confirmed highly significant ($p \leq 0.01$) variations amongst genotypes evaluated for grain yield at Maychew and significant ($p \leq 0.05$) variations in Korem, Alage and Mugulat. The ANOVA over places showed highly significant ($p \leq 0.01$) variation for the genotype effect, environment effects, genotype \times environment interaction (GEI) effect and significant ($p \leq 0.05$) variation for GEI effect of yield and for maximum of the yield related traits of food barley genotypes. Haftysene, Yidogit, Estayish and Basso genotypes showed relatively high mean grain yield in all places. Korem showed highest mean yield as it was best suited environment for all the genotypes while Mugulat is not suited one.

Verma *et al.*, (2015) conducted an experiment on 17 wheat genotypes, evaluated at 8 locations in the central zone of the country using AMMI model and found that highest positive score was found in genotype G8 followed by G11 and G10 and environments E4 and E8 recorded maximum yield while lowest yield was realized in environment E₁ and GGE biplot analysis indicated that G13 was found to perform better in environment E₆ whereas G1 was found better in environments E₇ and E₈.

Lodhi *et al.*, (2015) conducted experiment on 105 barley genotypes for stability performance by using regression on environmental means for grain yield and its components. Some of the genotypes did not satisfy the stability criteria as they showed the presence of non-linear component of $G \times E$ instead of the linear component for most of the traits studied. The genotypes RD-2618, PL-760 and NDB-1229 were found to be stable for days to heading, Lakhan, Clipper, JB-57, PL-760 and Maria for short duration; BH-688, BC-112, K-603, RD-2624 and BH-548 for dwarf stature; CIHO3510 for tiller number; JB-16 for peduncle length, DL-88, BCU-IC-437851, Karan-15, RD-2660, Lakhan and JB-15 for spike length; BCU-550, EIBGN-04-14 and RS-6 for flag leaf length; Manjula and EIBGN-04-14 for grains per ear; EIBGN-2-1 and Jyoti were found to be stable for grain yield per plant. These promising genotypes could be considered as donors in barley improvement program for desired environments.

Kashte *et al.*, (2015) conducted stability analysis for yield traits in wheat (*Triticum* species) genotypes. The experimental material comprised of thirteen genotypes and four checks. The stability analysis was done as recommended by Eberhart and Russel (1966). The genotypes MP 3302, K 0820, MP 4080 and RAJ 4210 were found to be more stable genotypes for grain yield. The genotypes NIAW 1548, NIAW 301 and HD 2189 recorded above average stability. These genotypes likely to perform well under unfavourable conditions.

Jat *et al.*, (2015) conducted an experiment for identifying the performance of bread wheat genotypes under different environmental conditions. Stability analysis was done using Eberhart and Russel model (1966). Results revealed non- significant deviation from regression ($S_2 d_i$) shown by two genotypes PBW 373 and Raj 3765 for grain yield per plant. However, three crosses viz., HD 2687 x Raj 3077, DBW 17 x PBW 373 and PBW 373 x Raj 4037 showed high performance with below average response ($b_i > 1$) making them stable for favourable environment. Hence, these genotypes and crosses could be considered in wheat improvement programmes for different cropping system.

Creissen *et.al.*, (2016) investigated ecological methods in genetically diverse crops by conducting field trials with winter barley varieties (*Hordeum vulgare*), grown as monocultures or as three-way mixtures in fungicide treated and untreated plots at three sites. Mixtures accomplished yields comparable to the best performing monocultures whilst improving yield stability despite being subjected to multiple predicted and unpredicted abiotic and biotic stresses consisting of brown rust (*Puccinia hordei*) and lodging. This study showed that crop varietal mixtures can stabilize productivity even when environmental conditions and stresses are not predicted in advance.

Ramla *et al.*, (2016) conducted an experiment on barley for stable grain yield. The outcomes from the experiment, revealed that twenty-eight genotypes had shown wide adaptability ($b_i=1$) and only a single line (DH40) had confirmed a specific adoption ($b_i<1$) and 10 genotypes confirmed yield stability over the environment studies. They additionally reported that the lines DH65, DH26 and DH2 were unstable in terms of yield performance.

Saleh *et al.*, (2016) investigated forty barley lines for Genotype x Environment interaction with 8 different environments and phenotypic stability for grain yield and its components. The results showed significant mean squares because of variations among barley lines, environments and their interactions for all traits. The environments; E5 and E6 reflected higher mean values for grain yield and its component traits than other environments. Two lines *viz*; genotype 37 and genotype 40 were recommended as the stable lines for grain yield and its components for different environments. The two lines genotype 32 and genotype 34 were considered as the most desirable based on the results of phenotypic stability and stable for grain yield / plant and its components under a wide range of environments.

Singh *et al.*, (2017) conducted experiment to assess the stability of these genotypes for yield and its contributing traits. Stability analysis was done as per Eberhart and Russell model (1966). They reported highly significant mean differences between genotypes in the analysis of variance for individual as well as over pooled environments for grain yield and components which reflects abundance of genetic variability among the genotypes. The genotypes like T-4037, T-4045, T-4047, T-4049, T-4050 and six *Triticum aestivum* genotypes namely RAJ-3765, RAJ-4079, RAJ-4083, WH-1105, RAJ-3077 and RAJ – 3777 showed average response for seed yield to change in environmental conditions as indicated by their unit regression and non-significant deviations which showed average stability and wider adaptability of these genotypes.

Ahmed *et al.*, (2018) carried out experiment to evaluate variation, mean performance and stability parameters of 12 diverse barley genotypes including the three check varieties Giza 123, Giza 126 and Giza 2000. Genotypes L2 and L4 showed highest stability across different environments and showed value of b_i below average stability. These two genotypes performed well for grain yield and its components and could be recommended to be grown in unfavourable environments as new genotypes or could be used as parental lines in barley breeding programs for desired environments.

Elsayed *et al.*, (2018) carried out an experiment to evaluate stability of barley (*Hordeum vulgare* L.) for grain yield, and its relationship to the duration of the growth cycle under 13 Mediterranean conditions in Egypt. Genotypes with high yields across environments were found very stable (G4, G21 G5), intermediate and stable (G1, G9) and highly responsive (G18, G19).

Shawy *et al.*, (2018) conducted an experiment to evaluate twenty barley genotypes under different environments for the stability of their performance. Giza 130, Line 4, Line 5 and Line 8 had the lowest (bi) values which were more adapted to unfavorable environments whereas, Giza 132, Line 3 and Line 6 were input sensitive and adapted to high potential environments.

Fatma (2018) evaluated eighteen barley genotypes differed in their genetic makeup under six varied environments. This study showed that, the three stability methods, *i.e.*, phenotypic stability, genotypic stability and AMMI, the most desired and stable genotypes were Line 9 and Line 11 for days to 50% heading; Line 6 and Line 5 for plant height; Line 11 and Giza 126 for flag leaf area; Line 1, Giza 123 and Line 11 for 1000-grain weight; Line 9, Line 7 and Line 2 for biological yield (ton / fad.) and Line 6, Line 9 and Line 3 for grain yield. These genotypes could be of great value in barley breeding programs for improving these traits under water stress in newly reclaimed sandy soils.

Taherian *et al.*, (2019) conducted experiment to identify salinity tolerant genotypes with stable yield and also evaluated genotype (G), environments (E) and G x E interactions using various stability parameters. According to Eberhart and Russell stability parameters, genotypes Fajre30, Nik and MBS82-4 had stable adaptation. Genotypes Fajre30, Nik, Rihan, Valfajr, MBS82-5 and Mbs87-12 were selected by simultaneous selection for yield and yield stability (YSi) method. According to the AMMI analysis, genotypes MBS87-12 and Fajre30 with seed yield greater than grand mean, were the most stable genotypes and with high salinity tolerance.

Pujer *et al.*, (2020) conducted an experiment where two stability parameters *i.e.*, regression coefficient (bi) and deviations from regression ($s^2 di$) were worked out and tested by using t-test and F-test separately from the pooled analysis. The genotypes NIAW 34, HW 1098 and BMZ 15- 16-2 showed higher grain yield (2965.7, 3131.5 and 3037.7kg/ha respectively), average responsiveness ($bi = 1$) and non-significant $S^2 di$ value suggesting suitability of these genotypes for different dates of sowing. The genotype HW 1098 exhibited superior performance for yield contributed by high number of tillers under early sown conditions. The results concluded that genotypes NIAW 34, HW 1098 and BMZ 15-16-2 were suitable for all the three dates of sowing condition. It was also found that early sowing is the most preferred time for high yield of wheat crop.

Askari *et al.*, (2020 a) carried out an experiment to test different salinity levels on yield of barley genotypes. The effects of salinity treatments studied by using stability based on Shukla stability variance, Wricke ecovalance and Eberhart and Russell regression model (1966), the STW82153, MBS8715 and Valfajr were found most stable and based on Romero environmental variance the genotype MBS8712 was found most stable. The genotypes STW82153, MBS8712, ESBYTM8910 and Valfajr performed better in all salinity levels, genotypes MBS8715 and WB7910 had the highest production capacity. The results indicated that the stability parameters would be useful for simultaneous selection for high yield and stability under salinity conditions.

Askari *et al.*, (2020 b) conducted a study to check indices for identifying barley genotypes at early growth stage with stable performance in salinity conditions. The effect of salinity treatments was studied through an analysis of the dry matter production, effects confirmed large differences among genotypes. The majority of the tolerance indices showed that ESBYTM8910, 4 Shori and MBS8715 have been the excellent barley genotypes showing the highest stress resistance for the finest NaCl concentration. Based on stability parameters the genotypes MBS8712 and Jo torsh were found phenotypically stable. The study concluded that the tolerant genotypes established the least stability according to stability parameters.

Choi *et al.*, (2020) investigated $G \times E$ interactions for β -glucan content of diverse barley genotypes across dryland environments in eastern Washington and determined the range and stability of β -glucan content across precipitation zones. The range of β -glucan was from 1.81 to 7.18 (% w/w), with a mean of 4.01 (% w/w). Genotype \times year (Y), $G \times$ location (L), $L \times Y$, and $G \times E$ ($G \times L \times Y$) interactions were found for β -glucan. The data obtained from this research gave a good understanding of, which cultivars, the farmers can grow in their area that will meet industry targets and standards for both food and malt barley.

Suresh *et al.*, (2020) investigated thirty wheat genotypes for yield stability under two dates of sowing *i.e.*, late and very late for two consecutive years. Stability was measured based on regression (bi) and stability parameter ($S^2 di$). According to these parameters, four varieties (HD 3059, WH 1105, HTW 66 and WH 1124) for late sown conditions and three varieties (HTW 11, WH 730 and BWL 5186) for very late sown conditions were recommended as good with their yield stability. The genotypes HD

3059, WH 1105, HTW 66 and WH 1124 with value of b_i significantly greater than 1 and higher average productivity than overall mean, were considered for late sown condition. Genotypes HTW 11, WH 730 and BWL 5186 with value of b_i less than unity and higher mean yield were recommended for very late sown condition.

Correlation, path coefficient analysis:

Najeeb and Wani, (2004) conducted experiment on 10 barley cultivars to study the relationship of important characters and their relative contribution towards yield. Path analysis revealed that high and positive direct effect of number of tillers per plant, plant height, grains per spike, days to flowering and 1000 grain weight on grain yield per plant. High direct negative effect on grain yield per plant was observed by spike length and yield per plant.

Bhutta *et al.*, (2005) obtained data on 10 yield-related traits for Correlation in six- rowed barley genotypes. They reported significant positive correlation between grain yield and test grain weight and no. of spikelets/spike. The grain yield was negatively correlated with days to heading. Path coefficient analysis revealed positive maximum association between peduncle length and no of spikelets with grain yield. The results showed extrusion length and spike density had negative association with grain yield.

Ali *et al.* (2008) evaluated seventy local and exotic wheat genotypes for variability parameters, correlations and path coefficients for eight metric traits *i.e.*, plant height, number of productive tillers/plants, no. of spikelets/spike, spike length, no. of grains/spike, thousand grain weight and yield/plant. Significant and positive correlation was observed with no. of tillers/plant, no. of grains/spike and spike length.

Mittal *et al.*, (2009) conducted an experiment to study phenotypic and genotypic correlations and to partition phenotypic correlation coefficients into direct and indirect contributions of different component traits for grain yield in barley. Path coefficient analysis showed that grains per spike had maximum positive direct effect followed by 100 grain weight and plant height over grain yield whereas spike length showed negative direct effect on grain yield. The study confirmed that grain yield in barley could be improved by selection of early flowering/maturing, tall genotypes with a greater number of grains per spike in the segregating populations.

Mohammad *et al.*, (2011) conducted an experiment on 22 hulless barley genotypes. The results of correlation analysis for the overall performance of the genetic traits showed that the maximum direct impact of number of seeds per main spike was more. The most direct impact of this trait through fertile tillers was implemented in phenotypic correlation. The most direct negative effect on performance was shown by days to heading.

Budakli and Celik (2012) conducted an experiment comprising of ten varieties of two-rowed barley to test the correlation among grain yield and yield components and to measure the direct and indirect effects of yield components on grain yield in barley by using correlation coefficient and path analysis methods. Path analysis results indicated that harvest index had the highest direct impact on grain yield followed by spike/per m² and kernel number per spike.

Shrivastava *et al.*, (2012) conducted experiment to study the correlation and path analysis for grain yield and contributing characters in twentyfive diverse malt barley genotypes. A significant and positive correlation was observed for grain yield per plot with harvest index, thousand grain weight, tillers number and spikelets/spike. Whereas, a positive and direct effect of spikelets per spike, tillers per running meter, plant height, grains per spike, harvest index, 1000-grain weight, days to 75 per cent maturity and days to 50 per cent heading with grain yield per plot in path analysis. They also observed low residual effect hence, all the essential yield contributing attributes should be taken in to account while selection.

Nasri *et al.*, (2013) investigated the cause-and-effect relationship in some traits and yield component in barley in drought conditions. The results of stress treatment showed a significant decrease in yield components. Path analysis showed the highest direct effect and positive spike weight ($P=1.343$) on grain yield. Harvest index (0.356) showed positive effect and dry weight (-0.935) showed negative indirect effect on grain yield.

Shekhawat and Kumar (2013) evaluated twenty barley genotypes for yield and associated morphological characters. Number of tillers per meter row length and flag leaf length showed the highest positive direct effects on green fodder yield. A positive direct effect on grain yield was shown by spike length, no. of spikelets/spike, no. of grains per spike, no. of tillers per meter row length, leaf width, test weight, peduncle

length and leaf length. Therefore, these traits could be used as selection indices for green fodder and grain yield.

Kumar *et al.*, (2013) studied the association among yield related traits and their direct and indirect influence on grain yield of 42 wheat genotypes in a randomized complete block design. Grain yield was significantly correlated with its component characters; day to heading, effective tillers/plant, number of tillers/plant & harvest index. Highest direct effect on seed yield/plant was shown by harvest index

Rahman *et al.*, (2013) conducted an experiment with 12 wheat genotypes for assessing variability and to select genotypes for improvement of wheat. They reported significant variation for all the 13 characters studied indicating the presence of considerable variations for selection. Heading days (HD), plant/ m² (PPM), spikelet per spike (SPS) and 1000 grains weight (TGW) exhibited high heritability coupled with moderate genetic advance. These characters had also medium to high genotypic coefficient of variation and phenotypic coefficient of variation coupled with high to moderate heritability and genetic advance. Grain yield had positive and highly significant association with heading days, maturity days and 1000 grains weight at both genotypic and phenotypic levels.

Yadav *et al.*, (2014) conducted experiment on fifty-two genotypes of barley for variability, correlation and path analysis for grain yield and contributing traits. Perusal of results revealed that highest value of positive direct effect was observed in days to 50% flowering, biological yield per plant and lowest for days to maturity on grain yield.

Mohtashami (2015) conducted an experiment to study the correlation between the agronomic traits and path analysis in four barley cultivars. Analysis of variance and covariance were used for the correlation coefficient analysis and path analysis of direct and indirect effects. At 5% level there was no significant difference between yield treatments. Treatments 2 and 4 (cultivar Valfajr) showed increased yield with average yield 6.520 and 6 490 t/ha based on analysis and comparison of treatments with good results including grain yield, plant height and grain weight.

Mohammadi (2015) conducted an experiment comprising of 16 barley genotypes to find the correlations and partition coefficient of correlation between grain yield with its primary components, into direct and indirect effects. Path analysis results in three growing seasons indicated that barley grain yield was affected by grain filling

period, thousand kernel weight and the number of tillers per square meter. The effect of 1000 kernel weight on grain yield in three environments showed that grain yield in barley is limited by source proficiency and it was recommended as a promising trait for increasing barley grain yield in specific water stress conditions.

Sharma *et al.* (2018) used one hundred and seventy advanced homozygous lines for estimates of mutual correlations *vis-a-vis* path analysis for grain yield with ten morphological traits. Coefficient of variation was in the range of 1.40- 8.34 indicated adequacy of material and the traits studied for further estimation of genetic variability parameters. Highly significant values of mean squares due to genotypes were observed for all the characters, which indicating the presence of adequate genetic variability for all the characters. They also reported that improvement can be realized to the extent from 66 to 30 per cent for grain yield per plant, tillers per plant, hundred grain weight, and grain weight per spike. Highly significant and positive association was observed between grain weight per spike and spike weight

Choudhary *et al.*, (2020) reported highly significant positive correlation in wheat grain yield with biological yield, tillers per plant and number of grains per spike followed by spike length, awn length, plant height and 100 grain weight. These traits also showed positive direct effect on grain yield at genotypic level in path coefficient analysis. WP710/17, HD3189, WP708/17 TALL-1 and PBW343 were considered as most promising donors which could be used for further breeding programme to improve the yield potential of the targeted variety.

Chapter-III

Materials and Methods

CHAPTER-3

MATERIALS AND METHODS

The present investigation “**Stability analysis in Barley (*Hordeum vulgare* L.) for yield and contributing traits under varied conditions**” was conducted at two locations *viz.*, Advance Centre for Rainfed Agriculture SKUAST-J, Dhiansar, and Research Farm Chatha, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu during *Rabi* 2019-20 and 2020-21. The details of experimental materials, methods and techniques used during course of investigation are described here under:

3.1 Experimental material and cultural practices:

Experimental material for the present study comprising of 17 genotypes of barley genotypes obtained from Rajasthan Agricultural Research Institute (RARI), Durgapura, and some maintained in the Division of PBG, SKUAST- Jammu. Two separate experimental trials were grown during *rabi* 2019-20 and 2020-21 under rainfed and irrigated conditions at two different locations. All the recommended packages and practices were followed during the growth period.

Table 3.1 List of the barley genotypes used in this study.

S. No.	Variety	Source	Year of release	Pedigree
1.	RD-2035	RARI, Durgapura	1994	RD137/PL101
2.	RD-2052	RARI, Durgapura	1987	Api-CM-67/SO-727//PL101
3.	RD-2552	RARI, Durgapura	1999	RD2035/DL472
4.	RD-2592	RARI, Durgapura	2004	RD2035/UBL9
5.	RD-2715	RARI, Durgapura	2008	RD387/BH602//RD2035
6.	RD-2794	RARI, Durgapura	2014	RD2035/RD2683
7.	RD-2849	RARI, Durgapura	2014	DWRUB52/PL705
8.	RD-2899	RARI, Durgapura	2017	RD2592/RD2035//RD2715

9.	RD-2907	RARI, Durgapura	2017	RD103/RD2518//RD2592
10.	LOCAL	From local farmer		
11.	BH-902	CCSHAU- Hisar	2010	BH495/RD2552
12.	BH-946	CCSHAU- Hisar	2012	BHM 522A/BH949//RD2552
13.	BHS-352	IARI, Shimla	2003	HBL240/BHS504//VLB12 9
14.	BHS-400	IARI, Shimla	2014	34 th IBON-9009
15.	VLB-118	VPKAS, Almora	2014	14 th EMBSN-9313
16.	BHS-380	IARI, Shimla	2010	VOILET/MJA/7/ABN- B6/BA/GAL//FZA- B/5/DG/DC-B/PT- BAR/3/RA- B/BA/3/4/TRYIGAL
17.	BH-959	CCSHAU- Hisar	2015	BH-393/BH-331

3.1.1 Experimental details:

The details of the field experiment are given in Table 3.3. All other recommended practices were carried out as and when required so as to maintain good stand of the crop.

Table 3.2 Experiment details

Design	RBD
Genotypes	17
Replication	Three (for each experiment)
Plot size	2m ² (2m×1m)
Spacing	25cm, row to row
Season	<i>Rabi</i> 2019-20 and 2020-21

Table 3.3 Description of environments during Rabi 2019-20 and Rabi 2020-21.

Environment	Date of sowing	Location
E1	10th December 2019	Advance Centre for Rainfed Agriculture, SKUAST-J, Dhiansar.
E2	30th December 2019	Research Farm, Chatha, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu.
E3	10th December 2020	Advance Centre for Rainfed Agriculture, SKUAST-J, Dhiansar.
E4	30th December 2020	Research Farm, Chatha, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu.

3.1.2 Recording of observations:

Five plants were selected randomly from each plot for recording the observations on following characters.

- I. Plant height (cm)
- II. Number of tillers per plant
- III. Spike length (cm)
- IV. Number of spikelets per spike
- V. Number of grains per spike
- VI. Chlorophyll content of leaf (SPAD chlorophyll meter)
- VII. Flag leaf length (cm)
- VIII. Flag leaf width (cm)
- IX. Biological yield/plant (g)
- X. Grain yield/plant (g)

For the characters given below, observations were recorded on whole plot basis

- I. Days to 50 % flowering (heading)
- II. Test weight (g)
- III. Harvest index (%)

3.1.3 Methods of recording of the observations:

1. **Days to fifty percent flowering:** The observations were recorded as number of days taken to 50% flowering in a plot from the date of sowing.
2. **Plant height(cm):** Height of the main tiller of each of five selected plants was recorded in cm from base to tip of spike and average was worked out.
3. **Chlorophyll content of leaf (SPAD chlorophyll meter):** Nitrogen content of flag leaf was measured with SPAD chlorophyll meter using calibration method of five randomly selected plants.
4. **Flag leaf length(cm):** Flag leaf of main tiller was considered and length was recorded from base to tip with the help of metered scale.
5. **Flag leaf width(cm):** Width of flag leaf was recorded using metered scale, considering the main tiller
6. **Number of tillers per plant:** Total no of effective tillers was recorded for each selected plants and average was worked out.
7. **Spike length(cm):** Length of five spikes emerging from the main tiller from the base of the spike to its tip of five randomly selected plants was recorded in cm and average was worked out.
8. **Number of spikelets per plant:** Total no of matured spikelets was counted for each selected plant and average was worked out.
9. **Number of grains per spike:** No of grains were counted from the five spikes selected and average was worked out.
10. **Biological yield per plant(g):** The bundle weight was taken with the help of spring balance.
11. **Grain yield per plant(g):** The threshed grains obtained from individual plants after harvest were weighed in grams.
12. **Test weight (g):** Random sample of thousand grains was taken from the threshed produce and weight was recorded in grams.
13. **Harvest index (%):** The harvest index was calculated in percent using following formula:

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



Plate 3.1 Field experiment at ACRA, SKUAST-Jammu, Dhiansar



Plate 3.2 Two-row and six-row Barley spike



**Plate 3.3 Recording of morphological data at Research Farm, Chatha
Division of Plant Breeding & Genetics, SKUAST-Jammu**



Plate 3.4 Recording of chlorophyll content by SPAD meter

3.2 Statistical analysis:

3.2.1 Analysis of variance

The analysis of variance for Randomized Complete Block Design was carried out to test the differences among genotypes by F-test for individual characters for the different environments. It was carried out according to the procedure of Randomized Complete Block Design as per methodology given by Panse and Sukharne (1967). ANOVA helps in partitioning the total variance into three components *viz.*, replication, treatment and error.

Analysis of variance was done under the fixed effect model given below:

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

Where, Y_{ij} = phenotypic effect of i^{th} genotype in the j^{th} replication

μ = General mean of population

g_i = Effect of i^{th} genotype

r_j = Effect of j^{th} replication

e_{ij} = random error associated with the i^{th} genotype in the j^{th} replication.

Table 3.4 Analysis of variance

Sources	d.f	MSS	Expected MS	F. Ratio
Replications	(r-1)	Mr	$\sigma e^2 + g\sigma^2 r$	Mr/Me
Genotype	(g-1)	Mg	$\sigma e^2 + r\sigma^2 g$	Mg/Me
Error	(r-1) (g-1)	Me	$\sigma^2 e$	

Where,

r = number of replications,

g = number of treatments or genotypes,

σ^2_r = Variance due to the replications,

σ^2_g = Variance due to genotypes, and

σ^2_e = error variance

The standard error of mean [S.E. (m)], standard error of differences [S.E. (d)] and critical differences (C.D.) for comparing any two genotypes were calculated as below:

$$\text{S.E. (m)} \pm = (\text{Me/r})^{1/2} \text{ or } \sqrt{(\text{Me/r})}$$

$$\text{S.E. (d)} \pm = (2\text{Me/r})^{1/2} \text{ or } \sqrt{(2\text{Me/r})}$$

$$\text{C.D. (0.05)} = \text{S.E. (d)} \times t \text{ value (0.05) at error degree of freedom}$$

3.2.2 Combined analysis of variance over environments:

The combined analysis of variance over environments was performed as per Verma *et al.* (1987) and was based on the following model.

$$Y_{ijk} = \mu + g_i + I_j + (gI)_{ij} + r_k + e_{ijk}$$

Where,

Y_{ijk} = phenotypic effect of i^{th} genotype in the j^{th} environment and k^{th} replication,

μ = General mean,

g_i = Effect of i^{th} genotype,

I_j = Effect of j^{th} environment,

$(gI)_{ij}$ = effect of interaction between g^{th} genotype and j^{th} environment,

r_k = effect of the k^{th} replication and

e_{ijk} = random error

Table 3.5 Pooled analysis of variance over environments

Sources	d.f	M.S.S.	Expected M.S.
Replications within environments	n (r-1)	Mr	$\sigma^2_e + g\sigma^2_r$
Environment	(n-1)	Mn	$\sigma^2_e + r\sigma^2_n$
Genotype	(g-1)	Mg	$\sigma^2_e + r\sigma^2_{gn} + rn\sigma^2_g$
Genotype × environment	(n-1) (g-1)	Mg × Mn	$\sigma^2_e + r\sigma^2_{gn}$
Pooled Error	n (r-1) (g-1)	Me	σ_e^2

Where,

n = number of environments

g = number of genotypes and

r = number of replications in each environment

3.3 Correlation coefficient analysis:

The correlations between all the characters under study at genotypic and phenotypic levels were estimated according to the method given by Searle (1961) using the following formula:

1. Genotypic correlation between traits X and Y:

$$r_{xy}(g) = \frac{\text{Cov. XY}(g)}{\sqrt{\text{Var. X}(g) \times \text{Var. Y}(g)}}$$

2. Phenotypic correlation between traits X and Y.

$$r_{xy}(p) = \frac{\text{Cov. XY}(p)}{\sqrt{\text{Var. X}(p) \times \text{Var. Y}(p)}}$$

Where,

Cov. XY (p) and Cov. XY (g) denote phenotypic and genotypic covariance between characters X and Y, respectively. Var X (p) and Var. X (g) denote variance for character X, while Var. Y (p) and Var. Y (g) denote phenotypic and genotypic variance for character Y, respectively.

Test statistics

$$t_c = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}; (n-2) \text{ df.}$$

3.4 Path Coefficient Analysis:

Path coefficient analysis was worked out using phenotypic and genotypic correlation values of yield components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). Standard path coefficients, which are the standardized partial regression coefficients, were calculated. These values were obtained by solving the following set of 'p' simultaneous equation using above package.

$$\begin{array}{c} P_{01} + P_{02} r_{12} + \dots + P_{0p} r_{1p} = r_{01} \quad P_{01} + P_{12} r_{02} + \dots + P_{0p} r_{2p} = r_{02} \\ \downarrow \\ P_{01} + r_{1p} + P_{02} r_{2p} + \dots + P_{0p} = r_{0p} \end{array}$$

Where, $P_{01}, P_{02}, \dots, P_{0p}$ are the direct effects of variables 1, 2, 3, ..., p on the dependent variable 0 and $r_{12}, r_{13}, \dots, r_{1p}, \dots, r_{p(p-1)}$ are the possible correlation coefficients between various independent variables and $r_{01}, r_{02}, r_{03}, \dots, r_{0p}$ are the correlation between dependent and independent variables.

The indirect effects of the i^{th} variable via j^{th} variable is attained as $(P_{0j} \times r_{ij})$. The contribution of remaining unknown factor is measured as the residual factor, which is calculated and given below.

$$P^2_{ox} = 1 - (P^2_{01} + 2P_{01}P_{02}r_{12} + 2P_{01}P_{03}r_{13} + \dots + P^2_{02} + 2P_{02}P_{03}r_{23} + \dots + P^2_{0p})$$

$$\text{Residual factor} = \sqrt{P^2_{ox}}.$$

3.5 Stability Analysis

The performance of a genotype mostly depends on the environmental interaction. The estimation of phenotypic stability which involves regression analysis has proved to be an effective technique for assessing the response of various genotypes under diverse environmental conditions. The evaluation of genotypes x environment interaction gives an idea of the buffering quantity of the population under study. The low magnitude of the genotype environmental interactions predicts consonant performance of a population over diverse environmental conditions. Hence, it shows high buffering ability of the population (Gupta *et al.*, 1977). Eberhart and Russell Model is used to find the stable genotypes in the present investigation.

3.5.1 Eberhart and Russell Model (1966)

The stability model proposed by Eberhart and Russell (1966) was adopted to analyze the data over four environments. The model involves the estimation of three stability parameters like mean (\bar{X}), regression coefficient (b_i) and deviation from the regression (S^2d), which are defined by the following mathematical formula:

$$Y_{ij} = a_i + b_i I_j + d_{ij} \quad (i = 1, g; j = 1, n),$$

Where,

Y_{ij} = Mean of i^{th} genotype in j^{th} environment ($i = 1 \dots 10, j = 1 \dots 9$)

a_i = Mean of i^{th} genotype over all the environments.

b_i = The regression coefficient which is a measures of response of i^{th} genotype to varying environment.

d_{ij} = Deviation from regression of the i^{th} genotype of j^{th} environment and

I_j = j^{th} environmental index obtained by subtracting the regression of the i^{th} genotype

grand mean from the mean of all the genotype at j^{th} environment.

$$\text{i.e., } d_{ij} = Y_{ij} - \hat{Y}_{ij}$$

The regression coefficient 'b' was estimated as:

$$b_i = \frac{\sum Y_{ij} I_j}{I_j^2}$$

In this model, the total variance is first divided into two components, *i.e.*, (i) genotype and (ii) environment plus interaction [E + (G×E)]. The second component is further sub-divided into three components, viz., (a) environment linear, (b) genotype × environment (liner) and (c) pooled deviations. The variance due to pooled deviations is further divided into variance due to individual genotype.

The stability parameter, measuring deviation from regression was estimated as follows:

$$S_{di}^2 = \frac{\sum d_{ij}^2}{n-2} - \frac{S_e^2}{r}$$

Where,

$$\sum d_{ij}^2 = [\sum_j Y_{ij}^2 - \frac{Y_i^2}{n}] - \frac{(\sum Y_{ij} I_j)^2}{\sum I_j^2}$$

S_e^2 = pooled error mean square,

r = number of replications and

n = number of environments.

Table 3.6 Analysis of variance for stability (Eberhart and Russell model, 1966)

Source	d.f.	S.S.	MSS
Genotype	(g-1)	$\frac{1}{e} \sum_i Y_i^2 - C. F$	M_1
Environments	(e-1)	$\frac{1}{g} \sum_j Y_j^2 - C. F$	
G × E	(g-1) (e-1)	$\sum_i \sum_j Y_{ij}^2 - \frac{\sum Y_i^2}{e} - Env. SS.$	
E+(G × E)	g (e-1)	$\sum_i \sum_j Y_{ij}^2 - \frac{\sum Y_i^2}{e}$	
Environment (Linear)	1	$\frac{1}{g} (\sum_j Y_j I_j)^2 / \sum_j I_j^2$	

G × E (Linear)	g-1	$\sum_i [(\sum_j Y_{ij} I_j)^2 / \sum_j I_j^2] - \text{Env. (linear) S.S}$	M ₂
Pooled deviation	g (e-2)	$\sum_i \sum_j \delta_{ij}^2$	M ₃
Genotype 1	e-2	$[\sum_j Y_{1j}^2 - (Y_1)^2/e] - (\sum_j Y_{1j} I_j)^2 / \sum_j I_j^2$	
-	-		
-	-		
-	-		
Genotype g	e-2	$[\sum_j Y_{gj}^2 - (Y_g)^2/n] - (\sum_j Y_{gj} I_j)^2 / \sum_j I_j^2$	
Pooled error	e (r-1) (g-1)	Pooled replication × genotypes SS over environment	

Where,

g= No. of genotypes

e= No. of environments

r= replications

According to this model, a stable variety is the one which has regression coefficient (*b*) equal to unity (*b*=1) and deviation from regression is as small as possible ($S^2 di = 0$). A genotype with significant *b* value (*b*>1) is said to be a highly responsive-suitable for favourable environments and with *b* value (*b*<1) is said to be low responsive-suitable for unfavourable environments.

1. **Range:** It was expressed as the difference between the lowest value and the highest value present in the observation for each trait.
2. **Standard deviation (σ):** Expressed in terms of square root of variance.

$$SD = \sqrt{Var} = \sqrt{\sigma^2} = \sigma$$

3. **Variance:** Expressed as the average of squared deviation of all the individual observation from the mean. Mathematically

$$\text{Variance (var.) or } \sigma^2 = \frac{\sum (x - \bar{x})^2}{N - 1}$$

4. **Standard error (SE):** Expressed as the mean difference between sample estimates of mean and the population parameter μ *i.e.*, it is the measure of uncontrolled variation present in a sample. Mathematically:

$$\text{Standard error} = \frac{\text{Standard deviation}}{\sqrt{N}}$$

Where,

X_i = i^{th} observation of a given character.

N = Total number of observations

Var/σ^2 = Variance of sample

In fact, S.E is the SD of means and is expressed as SE_m

5. **Coefficient of variation (CV):**

$$\text{CV (\%)} = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

3.5.2 Stability parameters

The mean (a_i), the regression coefficient (b_i) and mean square deviation from linear regression line ($S^2 d_i$) are the three stability parameters proposed by Eberhart and Russell (1966) in their stability model. These parameters were computed by using the following formula.

$$a_i (\text{mean}) = \frac{\sum_i Y_{ij}}{n}$$

$$b_i (\text{regression coefficient}) = \frac{\sum Y_{ij} I_j}{\sum I_j^2}$$

$$\text{where, } I_j = \sum Y_{ij}/g - \sum \sum Y_{ij}/ge$$

S² di (deviation from the regression coefficient)

$$S^2_d = \frac{S_e^2}{r} - \frac{\sum \delta_{ij}^2}{e-2}$$

S_e^2 = estimate of pooled error

F test

- (a) For testing significance of the differences between genotypic means 'F' test was calculated by following formula

$$F = \frac{MS_1}{MS_3}$$

- (b) Testing of the varieties differ for their response for regression on the environmental index

$$F = MS_2/MS_3$$

- (c) To test individual deviation from linear regression

$$F = \left[\frac{\sum \delta_{ij}^2}{e-2} \right] / \text{Pooled error}$$

- (d) To test whether varieties do not differ for their regression on the environmental index, the appropriate 't' test was calculated by

$$t = \frac{b-1}{SE(b_i)} \sim \text{t-distribution with 1 df}$$

$$SE_{bi} = \sqrt{MS \text{ due to pooled deviation of } i^{\text{th}} \text{ genotype} / \sum I_j^2}$$

A joint consideration of the three parameters is,

1. The mean performance of the genotype over the environment (\bar{X})
2. The regression coefficient (b_i) and
3. The deviation from linear regression ($S^2 d$) is used to define stability of a genotype.

The estimate of deviations from regression ($S^2 d$) suggests the degree of dependance that should have to put to linear regression for interpretation of the data. If their values are significantly deviating from zero, the performance of desired phenotype cannot be predicted satisfactorily. When the deviations ($S^2 d$) are not significant the conclusion can be obtained by the joint analysis of mean yield and the regression coefficient (b_i) values as below:

Regression coefficient	Mean yield	Stability	Remarks
$\hat{b}_i = 1$	High	Average	Well adapted to all environments
$\hat{b}_i = 1$	Low	Average	Poorly adapted to all environments
$\hat{b}_i = 1$	High	Below average	Specially adapted to favorable environments
$\hat{b}_i = 1$	High	Below average	Specially adapted to unfavorable environments

Based on the data recorded and analyzed or discussed above results were tabulated and interpretations made as detailed in the following chapters.

Chapter-IV

Results

RESULTS

The present investigation “**Stability analysis in Barley (*Hordeum vulgare* L.) for yield and contributing traits under varied conditions**” comprising of 17 genotypes was conducted at two locations *viz.*, Advance centre for rainfed agriculture SKUAST-J, Dhiansar, and Research Farm Chatha, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu during *Rabi* 2019-20 and 2020-21. and observations on 13 characters *viz.*, days to 50 per cent flowering, plant height (cm), chlorophyll content of leaf (SPAD values), flag leaf length, flag leaf width, number of tillers/plant, Spike length, number of spikelets per spike, number of grains/spike, biological yield per plant, grain yield per plant, test weight, harvest index was recorded. The data collected was subjected to statistical analysis and the results obtained are presented character-wise here under:

1. Analysis of variance.
2. Mean performance.
3. Correlation studies.
4. Path coefficient analysis.
5. Stability analysis.

4.1 ANALYSIS OF VARIANCE

The results obtained from Analysis of Variance (ANOVA) for all the characters of seventeen barley genotypes in all the four environments *i.e.*, E1, E2, E3 and E4 (table 4.1) revealed significant differences between the genotypes for all the characters that reflected the presence of enough variability among the genotypes.

The results of pooled analysis of variance for all the characters (Table 4.2) revealed mean square due to genotypes as significant for all the characters except flag leaf length and grains per spike. Similarly, Genotype x Environment interaction was significant for all the characters except flag leaf width. Significant differences were also observed between the environments.

4.2 Mean Performance

The results of mean performance of all thirteen characters are given in appendix-1, the perusal of which is given under following headings

Days to 50% flowering:

The mean performance for days to 50% flowering in environment E1 ranged from 72-83 days with overall mean of 77 days. Genotype RD-2907 was found to be earliest with mean of (72 days) followed by BHS-380 (74.33 days) and BH-959 (74.33 days).

The mean performance for days to 50% flowering in environment E2 ranged from 72-85 days with overall mean of 80 days. Genotype BH-959 was found to be earliest with mean of (72 days) followed by BHS-380 (75 days) and RD-2907 (76 days).

The mean performance for days to 50% flowering in environment E3 ranged from 74-84 days with overall mean of 80 days. Genotype BHS-380 was found to be earliest with mean of (74 days) followed by BH-959 (75 days) and VLB-118 (75 days).

The mean performance for days to 50% flowering in environment E4 ranged from 71-86 days with overall mean of 78 days. Genotype RD-2794 was found to be earliest with mean of (71 days) followed by RD-2907 (73 days) and BH-946 (73 days).

The different genotypes showed significant differences in their pooled mean performances viz. Days to 50 % flowering ranged from 74-83 days with overall mean of 79 days. Genotype BH-959 found to be earliest with a mean of (74 days) followed by BHS-380 (75) and RD-2907(76).

Plant height(cm)

The mean performance for plant height in environment E1 ranged from 70.53-86.87 cm with overall mean of 80.16 cm. Genotype BHS-352 (86.87 cm) found to have maximum plant height followed by RD-2035 (86.37 cm) and RD-2592 (85.53 cm).

The mean performance for plant height in environment E2 ranged from 70.33-89.90 cm with overall mean of 83.34 cm. Genotype BHS-380 (89.90) found to have maximum plant height followed by RD-2794 (88.33 cm) and RD-2907 (87.63 cm).

Table 4.1. Analysis of variance of yield and contributing traits in *Hordeum vulgare* L. in four environments

Source of variation	Environment	DF	Days to 50% flowering	Plant height (cm)	SPAD values	Flag leaf length (cm)	Flag leaf width (cm)	Tillers/plant	Spike length (cm)	No. of Spikelet/spike	No. of Grains/spike	Biological yield/plant (g)	Grain yield/plant (cm)	Test weight(g)	Harvest index (%)
Replication	E1	2	11.314	9.591	9.078	0.841	0.008	1.196	0.558	2.373	15.549	0.0002	0.001	8.074	8.713
Treatment		16	20.740*	55.773*	31.110*	11.614**	0.025**	3.708**	0.856**	12.074**	63.255*	0.014**	0.009**	134.967**	81.443**
Error		32	10.064	24.096	12.673	3.241	0.009	0.488	0.269	4.331	27.737	0.003	0.001	6.830	10.307
Replication	E2	2	9.176	41.984	15.007	1.432	0.025	2.29	0.004	0.137	32.373	0.022	0.004	4.930	21.969
Treatment		16	32.956*	85.673*	15.883*	12.869*	0.040**	3.99*	1.021*	8.895*	44.926*	0.234**	0.055**	64.612**	166.092**
Error		32	13.801	37.127	8.121	5.689	0.015	1.65	0.426	3.575	21.956	0.014	0.004	9.725	11.010
Replication	E3	2	1.647	15.808	39.512	8.567	0.043	0.706	0.222	0.961	23.353	0.036	0.002	9.451	17.697
Treatment		16	35.537**	84.848**	28.009*	17.903**	0.053**	3.797*	1.504**	8.615*	65.203*	0.462**	0.037**	64.555**	69.483**
Error		32	10.522	29.853	12.698	3.474	0.019	1.914	0.522	4.023	32.270	0.101	0.009	7.312	8.859
Replication	E4	2	4.294	10.185	21.154	1.838	0.006	0.529	0.060	0.549	44.176	0.038	0.002	12.567	0.417
Treatment		16	72.186**	75.897*	13.501*	6.902**	0.039*	4.314**	0.694*	7.324**	33.895*	0.594**	0.009**	70.328**	10.943**
Error		32	11.440	30.226	6.057	2.556	0.016	0.884	0.274	2.695	17.218	0.028	0.001	6.459	0.861

*, ** significant at 5% and 1% level, respectively

Table 4.2. Pooled analysis of variance for yield and contributing traits in *Hordeum vulgare* L. in four environments

Source of variation	d.f.	Days to 50% flowering	Plant height (cm)	SPAD values	Flag leaf length (cm)	Flag leaf width (cm)	Tillers/ plant	Spike length (cm)	No. of Spikelet / spike	No. of Grains/ spike	Biological yield/ plant (g)	Grain yield/ plant (cm)	Test weight (cm)	Harvest index (%)
Genotypes	16	32.15*	49.24*	29.43*	8.67	0.04*	4.97*	1.42*	8.07**	21.21	0.63*	0.10**	58.85	22.88
Environments	3	124.98**	2933.4**	52.65*	504.7**	0.08*	312.25**	9.50**	57.82**	110.78	85.49**	2.47**	1284.30**	65552.63**
G X E	48	17.12**	26.24**	15.23**	7.33**	0.02	2.67	0.75**	3.16*	47.52**	0.28*	0.02*	53.97**	89.98**
Pooled error	136	3.59	9.51	3.10	1.17	0.02	1.31	0.11	1.15	8.18	0.05	0.02	2.47	1.88

*, ** significant at 5% and 1% level, respectively

The mean performance for plant height in environment E3 ranged from 87.87-105.43 cm with overall mean of 97.55 cm. Genotype BHS-400 (105.43 cm) found to have maximum plant height followed by RD-2907 (103.87 cm) and BHS-352 (103.67 cm).

The mean performance for plant height in environment E4 ranged from 75.33-92.70 cm with overall mean of 86.57 cm. Genotype VLB- (92.70 cm) found to have maximum plant height followed by RD- BHS-400 (92.37 cm) and LOCAL (91.27 cm).

All the genotypes showed significant differences in their pooled mean performances for plant height which ranged from 78.01cm to 91.05cm with an overall mean of 86.91 cm. The genotype BHS-400 found to have maximum plant height (91.05cm) followed by BHS-352 (90.59cm) and VLB-118 (90.48cm).

SPAD values

The mean performance for SPAD values in environment E1 ranged from 32.33-52.20 with overall mean of 39.71. The genotype BHS-352 (52.90) showed maximum SPAD value followed by RD-2035 (52.20) and RD-2592 (45.27)

The mean performance for SPAD values in environment E2 ranged from 35.83-50.53 with overall mean of 41.05. The genotype RD-2035 (50.53) showed maximum SPAD value followed by BHS-352 (50.37) and BHS-400 (42.07).

The mean performance for SPAD values in environment E3 ranged from 35.33-51.80 with overall mean of 40.53. The genotype RD-2035 (50.53) showed maximum SPAD value followed by BHS-352 (49.53) and RD-2849 (44.03).

The mean performance for SPAD values in environment E4 ranged from 34.87-49.70 with overall mean of 39.14. The genotype RD-2035 (49.70) showed maximum SPAD value followed by BHS-352 (48.27) and RD-2052 (41.77).

Most of the genotypes showed significant differences in their pooled mean performances for SPAD values ranged from (37.38-51.06) with an average mean of (40.11). The genotype RD-2035 showed maximum SPAD value (51.06) followed by BHS-352 (50.27) and RD-2849 (40.24).

Flag leaf length(cm)

The mean performance for flag leaf length in environment E1 ranged from 17.00-24.73 cm with overall mean of 21.55 cm. The genotype RD-2035 (24.73 cm) showed highest flag leaf length followed by BHS-352 (24.60 cm) and RD-2552 (22.93cm).

The mean performance for flag leaf length in environment E2 ranged from 16.93-23.83 cm with overall mean of 20.77 cm. The genotype BHS-352 (23.83 cm) showed highest flag leaf length followed by RD-2035 (23 cm) and BHS-400 (23cm).

The mean performance for flag leaf length in environment E3 ranged from 12.43-20.40 cm with overall mean of 15.83 cm. The genotype RD-2899 (20.40 cm) showed highest flag leaf length followed by RD-2035 (19.87cm) and BHS-352 (19.53cm).

The mean performance for flag leaf length in environment E4 ranged from 12.87-19.17 cm with overall mean of 15.69 cm. The genotype VLB-118 (19.17 cm) showed highest flag leaf length followed by RD-2035 (17.67 cm) and LOCAL (17.17cm).

Most of the genotypes showed significant differences in their pooled mean performances for flag leaf length. The average range of flag leaf length per plant was 16.32-21.32 cm with an overall mean of 18.46 cm. The genotype RD-2035 showed highest flag leaf length with average mean of (21.32cm) followed by BHS-352 (21.20cm) and RD-2899 (20.33cm).

Flag leaf width(cm)

The mean performance for flag leaf width in environment E1 ranged from 0.90-1.30 cm with overall mean of 1.10 cm. The genotype RD-2035 (1.30 cm) showed highest flag leaf width followed by RD-2592 (1.20 cm) and RD-2849 (1.17 cm).

The mean performance for flag leaf width in environment E2 ranged from 0.73-1.20 cm with overall mean of 1.08 cm. The genotype RD-2592 (1.20 cm) showed highest flag leaf width followed by BH-946 (1.20 cm) and RD-2849 (1.17 cm).

The mean performance for flag leaf width in environment E3 ranged from 0.77-1.23 cm with overall mean of 1.04 cm. The genotype RD-2035 (1.23 cm) showed highest flag leaf width followed by BHS-352(1.23cm) and BH-946 (1.20 cm).

The mean performance for flag leaf width in environment E4 ranged from 0.80-1.20 cm with overall mean of 0.96 cm. The genotype BHS-352 (1.20cm) showed highest flag leaf width followed by BHS-400 (1.17 cm) and RD-2592 (1.07 cm).

Most of the genotypes showed significant difference in their pooled mean performance for flag leaf width which ranged from 0.81-1.17 cm. The overall mean performance of flag leaf width was 1.05 cm. The genotype with highest flag leaf width was RD-2035(1.17cm) followed by BHS-352 (1.16cm) and RD-2592 (1.11cm) and BH-946 (1.11cm).

Number of tillers/plant

The mean value of no of tillers/ plant in environment E1 was ranged from 5-9 with overall mean of 7. The genotype BHS-352 (9) showed highest number of tillers per plant followed by BHS-400 (8) and RD-2035 (8).

The mean of number of tillers per plant in environment E2 ranged from 10-15 with overall mean of 12. The genotype BHS-352 (15) showed highest number of tillers per plant followed by VLB-118 (14) and BHS-400 (13).

The mean of number of tillers per plant in environment E3 ranged from 6-10 with overall mean of 7. The genotype RD-2035 (10) showed highest number of tillers per plant followed by RD-2899 (9) and VLB-118 (8).

The mean of number of tillers per plant in environment E4 ranged from 7-11 with overall mean of 8. The genotype RD-2035 (11) showed highest number of tillers per plant followed by RD-2052 (10) and RD-2794 (9).

All genotypes showed significant differences in their pooled mean values for number of tillers per plants per plant. The average range of number of tillers per plant was (8.08-11) with an overall mean of (9.25). The genotype BHS-352 possessed highest average number of tillers per plants (11) followed by RD-2035 (10.75), RD-2052 (9.92) and RD-2592 (9.92).

Spike Length(cm)

The mean performance for spike length in environment E1 ranged from 6.47-8.40 cm with overall mean of 7.49. The genotype BHS-400 (8.40 cm) showed highest spike length followed by RD-2849 (8.33 cm) and BHS-352 (8.30 cm).

The mean performance for spike length in environment E2 ranged from 6.13-8.43 cm with overall mean of 7.06. The genotype BH-946 (8.43 cm) showed highest spike length followed by RD-2035 (7.77 cm) and RD-2849 (7.43 cm).

The mean performance for spike length in environment E3 ranged from 5.67-8.33 cm with overall mean of 6.49. The genotype RD-2035 (8.33 cm) showed highest spike length followed by BH-959 (7.40 cm) and VLB-118 (7.17 cm).

The mean performance for spike length in environment E4 ranged from 6.13-7.87 cm with overall mean of 6.49 cm. The genotype BHS-352 (7.87 cm) showed highest spike length followed by BHS-352(7.87 cm) and RD-2035 (7.77 cm).

The pooled mean data showed that most of the genotypes were found to be significant for the spike length with mean performances ranged from 6.58-7.91cm with an overall mean of 7.00cm. Genotype RD-2035 recorded the highest spike length of (1.17cm) followed by BHS-352 (7.50cm) and BHS-400(7.12cm).

Number of spikelets per spike

The mean performance for no. of spikelet per spike in environment E1 ranged from 15-22 with overall mean of 19. The genotype RD-2035 (22) showed highest spikelet per spike followed by BHS-352 (21.67) and BHS-400 (21).

The mean performance for no. of spikelet per spike in environment E2 ranged from 16-21 with overall mean of 17. The genotype BHS-352 (21) showed highest spikelet per spike followed by RD-2035 (19) and BHS-946 (18).

The mean performance for spikelet per spike in environment E3 ranged from 16-21 with overall mean of 17. The genotype RD-2035 (21) showed highest spikelet per spike followed by RD-2552 (20) and BHS-400 (19).

The mean performance for no. of spikelet per spike in environment E4 ranged from 14-20 with overall mean of 16. The genotype BHS-352 (20) showed highest spikelet per spike followed by RD-2035 (19) and RD-2899 (17).

Data showed significant differences in their pooled mean performances for number of spikelets per spike under different dates of sowing conditions which ranged

from 15.42-20.50 and average overall mean was 17.69. The genotype BHS-352(20.50) recorded the highest average mean followed by RD-2035(20.42) and BHS-400(19.09).

Number of grains per spike

The mean performance for number of grains per spike in environment E1 ranged from 41-57 with overall mean of 52. The genotype RD-2035 (57) showed highest number of grains per spike followed by RD-2899 (56) and RD-2592 (55).

The mean performance for number of grains per spike in environment E2 ranged from 41-55 with overall mean of 51. The genotype RD-2899 (55) showed highest number of grains per spike followed by LOCAL (54) and RD-2035 (53).

The mean performance for number of grains per spike in environment E3 ranged from 45-64 with overall mean of 53. The genotype RD-2035 (64) showed highest number of grains per spike followed by RD-2592 (57) and BH-946 (56).

The mean performance for number of grains per spike in environment E4 ranged from 44-53 with overall mean of 49. The genotype RD-2899 (54) showed highest number of grains per spike followed by RD-2035 (53) and BHS-352 (52).

Most of the Genotypes showed significant differences in their pooled mean performances for number of grains per spike under different dates of sowing conditions ranged from 47.08-56.92 with average overall mean was (51.71). The genotype RD-2035 (56.92) with highest average mean followed by RD-2899 (54.58) and BHS-352 (54.17).

Biological yield per plant(g)

The mean performance for biological yield per plant in environment E1 ranged from 52.88-88.91g with overall mean of 62.31g. The genotype RD-2035 (88.91g) showed highest biological yield per plant followed by RD-2052 (74.69g) and BHS-352 (74.35g).

The mean performance for biological yield per plant in environment E2 ranged from 54.27-97.11g with overall mean of 83.48g. The genotype RD-2035 (97.11g)

showed highest biological yield per plant followed by RD-2899 (96.26g) and LOCAL (93.43g).

The mean performance for biological yield per plant in environment E3 ranged from 49.96-82.33g with overall mean of 60.17g. The genotype RD-2035 (82.33g) showed highest biological yield per plant followed by BHS-352 (68.77g) and RD-2794 (68.68g).

The mean performance for biological yield per plant in environment E4 ranged from 47.29g with overall mean of 67.05g. The genotype RD-2035 (91.30g) showed highest biological yield per plant followed by RD-2052 (83.45g) and LOCAL (82.34g).

Data recorded showed that most of the genotypes were significant in their pooled mean performances for biological yield per plant under different dates of sowing conditions ranged from 51.1-89.913g with average overall mean was 68.25g. The genotype RD-2035 (89.91g) recorded highest spike weight followed by RD-2052 (78.91g) and BHS-946 (72.17g).

Grain yield per plant(g)

The mean performance for grain yield per plant in environment E1 ranged from 11.01-30.32g with overall mean of 18.99g. The genotype RD-2035 (30.32g) showed highest grain yield per plant followed by RD-2052 (24.85g) and BHS-352 (23.26g).

The mean performance for grain yield per plant in environment E2 ranged from 23.95-RD-2899g with overall mean of 30.85g. The genotype RD-2899 (38.63g) showed highest grain yield per plant followed by BHS-400 (35.91g) and RD-2052 (35.11g).

The mean performance for grain yield per plant in environment E3 ranged from 12.36-32.28g with overall mean of 18.29g. The genotype RD-2035 (32.28g) showed highest grain yield per plant followed by BHS-352 (24.54g) and RD-2849 (22.73g).

The mean performance for grain yield per plant in environment E4 ranged from 011.16-29.40g with overall mean of 17.57g. The genotype RD-2035 (29.40g) showed highest grain yield per plant followed by RD-2052 (24.11g) and BHS-352 (21.32g).

Most of the genotypes showed significant differences in their pooled mean performances for Grain yield per plant ranged from 15.60-30.32g with average overall mean 21.43g. The genotype RD-2035(30.32g) recorded highest grain yield per plant followed by RD-2052 (26.35g) and BHS-352 (24.99g).

Test weight(g)

The mean performance for test weight in environment E1 ranged from 37.40-60.53g with overall mean of 49.90g. The genotype BHS-352 (60.53) showed highest test weight followed by RD-2035 (59.30g) and RD-2052 (57.53g).

The mean performance for test weight in environment E2 ranged from 38.93-56.97g with overall mean of 51.11g. The genotype RD-2899 (56.97g) showed highest test weight followed by RD-2552 (56.23g) and BHS-352 (56g).

The mean performance for test weight in environment E3 ranged from 36.67-50.63g with overall mean of 43.23g. The genotype RD-2052 (50.63g) showed highest test weight followed by RD-2849 (49.57g) and RD-2794 (48.30g).

The mean performance for test weight in environment E4 ranged from 31.23-50.13g with overall mean of 40.78g. The genotype RD-2035 (50.13g) showed highest test weight followed by RD-2052 (46.67g) and BHS-380 (46.57g).

Most of the genotypes showed significant differences in pooled mean performances of different genotypes for test weight with range of 40.78-52.40g and average overall mean 46.26g. The genotype RD-2035(52.40g) recorded highest test weight followed by BHS-352(51.80g) and RD-2052 (51.29g).

Harvest index (%)

The mean performance of harvest index in environment E1 ranged from 21.55-44.74 with overall mean of 31.96. The genotype BHS-352 (44.74) showed highest harvest index followed by RD-2592 (39.80) and RD-2849 (38.40)

The mean performance of harvest index in environment E2 ranged from 30.13-44.13 with overall mean of 37.34. The genotype BH-959 (44.13) showed highest harvest index followed by BHS-380 (43.77) and BH-902 (40.77).

The mean performance of harvest index in environment E3 ranged from 23.80-41.52 with overall mean of 29.40. The genotype RD-2899 (41.52) showed highest harvest index followed by RD-2035 (39.21) and VLB-118 (31.94).

The mean performance of harvest index in environment E4 ranged from 19.66-35.09 with overall mean of 27.08. The genotype BHS-352 (35.09) showed highest harvest index followed by VLB-118 (33.34) and BHS-380 (33).

The results revealed that the genotypes have significant differences in their pooled mean performances for harvest index ranged from (25.93-38.99) with average overall mean of (31.44). The genotype BHS-352 (38.99) recorded highest harvest index followed by RD-2899 (35.36g) and RD-2035 (33.91).

4.3 CORRELATION STUDIES

In present investigation, phenotypic and genotypic correlation between grain yield and contributing characters in barley were estimated for E1, E2, E3, E4 and pooled environment and presented in Tables 4.3, 4.3.1, 4.3.2, 4.3.3 and 4.3.4 respectively.

Days to 50% flowering

In first environment E1, this trait showed positive and significant association with SPAD values (0.963***, 0.355*), flag leaf length (0.926**, 0.334*), flag leaf width (0.912**, 0.284*), number of tillers per plant (0.487**, 0.449**), no. of spikelet per spike (0.841**, 0.465**) and test weight (0.734**, 0.348*) at both phenotypic and genotypic levels, whereas, this trait showed positive and significant association with no. of grains per spike (0.999**), grain yield per plant (0.526*) and harvest index (0.743**) at genotypic level only and it showed positive and significant association with plant height (0.343*) at phenotypic level only.

In second environment E2, this trait showed positive and significant association with flag leaf length (0.961**, 0.283*), spike length (0.567**, 0.305*) and biological yield per plant (0.707**, 0.427**), whereas, it showed positive and significant association with SPAD values. (0.131**), flag leaf width (0.765**), no. of spikelet per spike (0.488*), no. of grains per spike (0.726**) and test weight (0.719**) only at genotypic level. It showed negative significant association with harvest index (-0.821**, -0.578**) both at genotypic and phenotypic level.

Table 4.3. Phenotypic (P) and Genotypic (G) correlation coefficient analysis of grain yield per plant with other characters in environment 1

Characters		Plant height(cm)	SPAD values	Flag leaf length(cm)	Flag leaf width(cm)	No. of tiller/plant	Spike length(cm)	No. of Spikelet/spike	No. of Grains/spike	Biological yield/plant (g)	Test weight(g)	Harvest Index (%)	Grain yield/plant (g)
Days to 50% flowering	G	0.390	0.963**	0.926**	0.912**	0.487**	0.401	0.841**	0.999**	-0.474	0.734**	0.743**	0.526*
	P	0.343*	0.355*	0.334*	0.284*	0.449**	0.082	0.465**	0.213	-0.165	0.348*	0.251	0.194
Plant height(cm)	G		0.106	0.911**	0.441	0.591*	0.642**	1.000**	0.947**	-0.101	0.559*	0.787**	0.777**
	P		0.340*	0.396**	0.282*	0.288*	0.283*	0.302*	0.265	-0.021	0.345*	0.374**	0.383**
SPAD values	G			0.877**	0.797**	0.593*	-0.371	0.563*	0.748**	-0.422	0.454	0.273	0.120
	P			0.227	0.238	0.407**	-0.088	0.117	0.125	-0.225	0.302*	0.151	0.071
Flag leaf length(cm)	G				0.932**	0.503*	0.771**	0.376**	0.765**	-0.290	0.853**	0.952**	0.849**
	P				0.461**	0.313*	0.241	0.539**	0.463**	-0.237	0.563**	0.500**	0.463**
Flag leaf width(cm)	G					0.394	0.413	0.911**	0.967**	-0.403	0.306	0.852**	0.699**
	P					0.046	0.187	0.243	0.362**	-0.268	0.222	0.473**	0.391**
No. of tillers/plant	G						0.551*	0.718**	0.457	0.3073	0.299	0.324	0.432
	P						0.249	0.395**	0.315*	0.226	0.207	0.169	0.257
Spike length(cm)	G							0.823**	0.646**	0.144	0.280	0.712**	0.780**
	P							0.390**	0.376**	0.309*	0.199	0.305*	0.465**
No. of Spikelet/spike	G								0.582*	-0.159	0.765**	0.686**	0.622**
	P								0.623**	-0.002	0.383**	0.328*	0.389**
No. of Grains/spike	G									-0.322	0.779**	0.962**	0.854**
	P									0.005	0.319*	0.449**	0.490**
Biological yield/plant(g)	G										-0.255	-0.211	0.159
	P										-0.188	-0.314*	0.127
Test weight(g)	G											0.478	0.390
	P											0.351*	0.288*
Harvest index(%)	G												0.936**
	P												0.887**

*, ** significant at 5% and 1% level, respectively

Table 4.3.1 Phenotypic (P) and Genotypic (G) correlation coefficient analysis of grain yield/plant with other characters in environment 2

Characters		Plant height(cm)	SPAD values	Flag leaf length(cm)	Flag leaf width(cm)	No. of tiller/plant	Spike length(cm)	No. of Spikelet / spike	No. of Grains/ spike	Biological yield/plant (g)	Test weight(g)	Harvest Index (%)	Grain yield/plant (g)
Days to 50% flowering	G	0.465	0.131**	0.961**	0.765**	0.433	0.567**	0.488*	0.726**	0.707**	0.719**	-0.821**	0.036
	P	0.077	0.228	0.283*	0.246	0.238	0.305*	0.176	0.249	0.427**	0.273	-0.578**	-0.131
Plant height(cm)	G		-0.303	0.458	0.928**	0.340**	0.396	-0.365	0.019	0.836**	0.089	-0.113	0.398
	P		0.022	0.196	0.232	0.064	0.100	-0.197	0.053	0.326*	0.050	-0.061	0.115
SPAD values	G			0.68**	0.629**	0.521*	0.983**	0.737**	0.523*	0.500*	0.229	-0.676**	0.253
	P			0.358**	0.202	0.166	0.313*	0.236	0.114	0.229	0.271	-0.150	0.217
Flag leaf length(cm)	G				0.107	0.535*	0.494**	0.315	0.038	0.779**	0.983**	-0.356	0.070
	P				0.243	0.262	0.294*	0.077	0.008	0.360**	0.428**	-0.133	-0.010
Flag leaf width(cm)	G					0.425	0.887**	0.156	0.077	0.841**	0.237	-0.248	0.858**
	P					0.274	0.223	0.295*	0.277*	0.404**	0.031	-0.133	0.473**
No. of tillers/plant	G						0.290	0.522*	0.365	0.729**	0.088	0.274	0.503*
	P						0.063	0.426**	0.208	0.332*	-0.114	0.067	0.194
Spike length(cm)	G							0.178**	0.756**	0.542*	0.615**	-0.274	0.307
	P							-0.022	0.001	0.238	0.376**	-0.177	0.114
No. of Spikelet/spike	G								0.596*	0.576*	0.158	0.109	0.465
	P								0.411**	0.357*	-0.091	0.040	0.311*
No. of Grains/spike	G									0.529	-0.055	-0.168	-0.101
	P									0.209	-0.253	-0.077	-0.037
Biological yield/plant(g)	G										0.116	-0.235	0.437
	P										0.078	-0.210	0.361**
Test weight(g)	G											-0.392	0.021
	P											-0.269	0.025
Harvest index(%)	G												0.328
	P												0.384**

*, ** significant at 5% and 1% level, respectively

Table 4.3.2 Phenotypic (P) and Genotypic (G) correlation coefficient analysis of grain yield per plant with other characters in environment 3

Characters		Plant height(cm)	SPAD values	Flag leaf length(cm)	Flag leaf width(cm)	No. of tiller/plant	Spike length(cm)	No. of Spikelet / spike	No. of Grains/ spike	Biological yield/plant (g)	Test weight(g)	Harvest Index (%)	Grain yield/plant (g)
Days to 50% flowering	G	0.474	-0.309	-0.038	0.660**	0.262	-0.251	0.696**	0.346	0.765**	0.213	-0.431	0.297
	P	0.299*	-0.151	0.056	0.407**	0.279*	0.013	0.187	0.002	0.331*	0.073	-0.233	0.069
Plant height(cm)	G		-0.272	0.273	0.520*	0.356	0.090	0.476	-0.436	0.194	0.059	-0.450	-0.386
	P		0.052	0.129	0.203	-0.052	-0.133	0.144	-0.032	0.172	-0.057	-0.257	-0.094
SPAD values	G			0.392	-0.317	0.334	-0.025	0.0762	-0.024	-0.290	0.604*	0.003	-0.596*
	P			0.122	-0.154	0.044	-0.228	0.130	-0.101	-0.115	0.129	0.050	-0.110
Flag leaf length(cm)	G				0.504*	0.878**	0.583*	0.701**	0.072	0.062	0.423	-0.407	-0.569*
	P				0.175	0.381**	0.227	0.236	-0.001	-0.073	0.264	-0.192	-0.366**
Flag leaf width(cm)	G					0.941**	0.288	0.492*	0.138	0.188	0.185	-0.290	-0.304
	P					0.137	0.208	0.232	0.066	0.27	0.113	-0.222	0.024
No. of tillers/plant	G						0.213	0.967**	0.564**	0.822**	0.65**	-0.473	0.487*
	P						0.244	0.259	0.112	0.006	0.424**	-0.079	-0.148
Spike length(cm)	G							0.106	0.568*	-0.136	-0.126	0.139	0.115
	P							0.208	0.044	0.010	0.038	-0.015	-0.012
No. of Spikelet/spike	G								0.477	0.797**	0.506*	-0.781**	-0.131
	P								0.444**	0.366**	0.235	-0.422**	-0.063
No. of Grains/spike	G									0.898**	0.274	-0.434	0.916**
	P									0.374**	0.145	-0.200	0.310*
Biological yield/plant(g)	G										0.473	-0.773**	0.288
	P										0.162	-0.712**	0.423**
Test weight(g)	G											-0.320	0.157
	P											-0.123	0.017
Harvest index (%)	G												0.347
	P												0.284*

*, ** significant at 5% and 1% level, respectively

Table 4.3.3 Phenotypic (P) and Genotypic (G) correlation coefficient analysis of grain yield per plant with other characters in environment 4

Characters		Plant height(cm)	SPAD values	Flag leaf length(cm)	Flag leaf width(cm)	No. of tiller/plant	Spike length(cm)	No. of Spikelet / spike	No. of Grains/ spike	Biological yield/plant (g)	Test weight(g)	Harvest Index (%)	Grain yield/plant (g)
Days to 50% flowering	G	-0.136	0.453	0.173	0.765**	0.223	0.377	0.249	0.336	0.203	0.338	0.174	0.408
	P	-0.010	0.144	0.024	0.328*	0.181	0.142	0.234	0.023	0.102	0.195	0.122	0.225
Plant height(cm)	G		-0.202	0.195	0.479	-0.390	-0.112	-0.236	0.200	0.484*	-0.205	-0.581*	-0.324
	P		-0.039	0.077	0.047	-0.285*	-0.194	0.099	0.002	0.221	-0.104	-0.256	-0.117
SPAD values	G			0.253**	0.811**	0.859**	0.501*	0.657**	0.519*	-0.170	0.788**	0.359	0.353
	P			0.235	0.149	0.305*	0.344*	0.049	0.256	-0.043	0.469**	0.194	0.228
Flag leaf length(cm)	G				0.49*	0.6278**	0.551*	0.679**	0.818**	0.230	0.600*	-0.214	-0.075
	P				0.171	0.178	0.228	0.168	0.089	0.215	0.400**	-0.077	0.068
Flag leaf width(cm)	G					0.828**	0.499**	0.893**	0.570*	0.597*	0.456	-0.154	0.380
	P					0.430**	0.179	0.288*	0.054	0.257	0.285*	0.046	0.276*
No. of tillers/plant	G						0.796**	0.794**	0.088	0.069	0.562*	0.142	0.313
	P						0.437**	0.303*	-0.029	0.058	0.388**	0.026	0.097
Spike length(cm)	G							0.353**	0.169	0.303	0.641**	0.227	0.628**
	P							0.239	0.158	0.189	0.320*	-0.070	0.083
No. of Spikelet/spike	G								0.743**	0.582*	0.692**	-0.214	0.278
	P								0.297*	0.206	0.447**	0.006	0.192
No. of Grains/spike	G									0.535*	0.534*	0.222	0.787**
	P									0.191	0.195	0.064	0.236
Biological yield/plant(g)	G										0.031	-0.688**	0.049
	P										0.032	-0.617**	0.046
Test weight(g)	G											0.196	0.337
	P											0.161	0.254
Harvest index (%)	G												0.722**
	P												0.753

*, ** significant at 5% and 1% level, respectively

Table 4.3.4 Phenotypic (P) and Genotypic (G) correlation coefficient analysis of grain yield per plant with other characters of pooled environment.

Characters		Plant height(cm)	SPAD values	Flag leaf length (cm)	Flag leaf width (cm)	No. of tiller/plant	Spike length(cm)	No. of Spikelet / spike	No. of Grains/ spike	Biological yield/plant (g)	Test weight(g)	Harvest Index (%)	Grain yield/plant (g)
Days to 50% flowering	G	0.311**	0.513**	0.081	0.622**	0.383**	0.049	0.262**	0.466**	0.131	0.296**	0.021	0.425**
	P	0.224**	0.174*	0.051	0.288**	0.293**	0.019	0.177*	0.107	0.086	0.169*	-0.016	0.250**
Plant height(cm)	G		0.003	-0.476**	0.092	-0.170*	-0.423**	-0.128	0.205**	0.495**	-0.318**	-0.090	0.660**
	P		0.116	-0.319**	0.030	-0.157*	-0.294**	-0.079	0.104	0.396**	-0.233**	-0.068	0.520**
SPAD values	G			0.444**	0.453**	0.461**	0.102	0.408**	0.480**	-0.194**	0.527**	0.224**	0.273**
	P			0.177**	0.095	0.238**	-0.018	0.122	0.082	-0.102	0.287**	0.148*	0.177*
Flag leaf length(cm)	G				0.602**	0.389**	0.734**	0.712**	0.319**	-0.742**	0.818**	0.525**	-0.289**
	P				0.377**	0.311**	0.408**	0.387**	0.126	-0.633**	0.649**	0.447**	-0.246**
Flag leaf width(cm)	G					0.319**	0.578**	0.679**	0.463**	-0.406**	0.510**	0.451**	0.179*
	P					0.176**	0.237**	0.334**	0.215**	-0.255**	0.303**	0.290**	0.149*
No. of tillers/plant	G						0.144*	0.133	0.072	-0.147*	0.408**	0.177*	0.243**
	P						0.118	0.111	0.019	-0.150*	0.340**	0.152*	0.172*
Spike length(cm)	G							0.725**	0.359**	-0.341**	0.439**	0.165*	-0.358**
	P							0.277**	0.105	-0.222**	0.322**	0.075	-0.267**
No. of Spikelet/spike	G								0.586**	-0.390**	0.638**	0.413**	-0.034
	P								0.470**	-0.251**	0.358**	0.251**	-0.005
No. of Grains/spike	G									-0.091	0.398**	0.365**	0.400**
	P									-0.057	0.141*	0.187**	0.205**
Biological yield/plant(g)	G										-0.588**	-0.819**	0.084
	P										-0.544**	-0.797**	0.097
Test weight(g)	G											0.479**	-0.010
	P											0.435**	-0.019
Harvest index (%)	G												0.382**
	P												0.385**

*, ** significant at 5% and 1% level, respectively

In third environment E3, this trait showed positive and significant association with flag leaf width (0.660**, 0.407**) and biological yield per plant (0.765**, 0.331*) at both genotypic and phenotypic levels while it showed positive and significant association with plant height (0.299*) and number of tillers per plant (0.279*) at phenotypic level only.

In fourth environment E4, days to 50% flowering showed positive and significant association with flag leaf width (0.765**, 0.328*) at both genotypic and phenotypic levels.

In pooled environment, days to 50% flowering showed positive and significant association with plant height (0.311**, 0.224*), SPAD values (0.513**, 0.174**), flag leaf width (0.622**, 0.288*), no. of tillers/ plant (0.383**, 0.293**), no. of spikelet/ spike (0.262**, 0.177*), test weight (0.296**, 0.169*) and grain yield/ plant (0.425**, 0.250**), at both genotypic and phenotypic level while, it showed positive and significant association with grains per spike (0.466**) at only genotypic level .

Plant height (cm)

In first environment E1, this trait showed positive and significant association with flag leaf length (0.911**, 0.396**), no of tillers/ plant (0.591*, 0.288*), spike length (0.642**, 0.283*), no. of spikelet/ spike (1.000**, 0.302*), grain yield (0.777**, 0.383**), test weight (0.559*, 0.345*) and harvest index (0.787**, 0.374**) both at phenotypic and genotypic levels although it showed positive and significant association with no. of grains per spike (0.947**) at genotypic level only whereas, it showed positive and significant association with SPAD values (0.340*) and flag leaf width (0.282*) at phenotypic level only.

In second environment E2, this trait showed positive and significant association with biological yield (0.836**, 0.326*) both at phenotypic and genotypic levels while, with flag leaf width (0.928**) and number of tillers per plant (0.340**) at genotypic level only.

In third environment E3, this trait showed positive and significant association with flag leaf width (0.520*) at genotypic level only.

In fourth environment E4, plant height showed positive and significant association with biological yield (0.484*) at genotypic level whereas, it showed negative and significant association with number of tillers per plant (-0.285*) at phenotypic level and negative and significant association with harvest index (-0.581*) at genotypic level.

In pooled environments, plant height showed positive and significant association with biological yield (0.495**, 0.396**) and grain yield per plant (0.660**, 0.520**) both at phenotypic and genotypic levels whereas, it showed negative and significant association with flag leaf length (-0.476**, -0.319**), number of tillers per plant (-0.170*, -0.157*), spike length (-0.423**, -0.294**) and test weight (-0.318**, -0.233**) both at phenotypic and genotypic levels.

SPAD values

In first environment E1, this trait showed positive and significant association with number of tillers per plant (0.288*, 0.593*) both at phenotypic and genotypic levels while, it showed positive and significant association with flag leaf length (0.877**), flag leaf width (0.797**), no. of spikelet per spike (0.563*), no. of grains per spike (0.748**) at genotypic level while positive and significant association with test weight (0.302*) at phenotypic level only.

In second environment E2, SPAD values showed positive and significant association with flag leaf length (0.680**, 0.358**) and spike length (0.983**, 0.313*) both at phenotypic and genotypic levels while, it showed positive and significant association with flag leaf width (0.629**), no. of tillers/ plant (0.521*), no. of spikelet/ spike (0.737**), no. of grains/spike (0.523*) and biological yield (0.500*) at genotypic level.

In third environment E3, SPAD values showed positive and significant association with test weight (0.604*) only at genotypic level. It showed negative significant association with grain yield (-0.596*) at genotypic level only.

In fourth environment E4, positive and significant correlation with no of tillers/ plant (0.859**, 0.305*), spike length (0.501*, 0.344*) and test weight (0.788**, 0.469**) were observed for SPAD value both at phenotypic and genotypic levels, however, flag leaf length (0.253**), flag leaf width (0.811**), no. of spikelet per spike

(0.657**), no. of grains per spike (0.519*) have shown a positive and significant association with SPAD values at genotypic level only.

In pooled environment, SPAD values showed positive and significant association with flag leaf length (0.444**, 0.177*), number of tillers per plant (0.461**, 0.238**), test weight (0.527**, 0.287**), harvest index (0.224**, 0.148*) and grain yield per plant (0.273**, 0.177*) both at phenotypic and genotypic levels while, positive and significant association with flag leaf width (0.453**), no. of spikelet per spike (0.408**), no. of grains per spike (0.480**) at genotypic level only. This trait showed negative and significant association with biological yield per plant (-0.194**) at genotypic level only.

Flag leaf length (cm)

In first environment E1, flag leaf length showed positive and significant association with flag leaf width (0.932**, 0.461**), no. of tillers/ plant (0.503*, 0.313*), no of spikelet/ spike (0.376**, 0.539**), no. of grains/ spike (0.765**, 0.463**), grain yield (0.849**, 0.463**), test weight (0.853**, 0.563**) and harvest index (0.952**, 0.500**) both at phenotypic and genotypic levels while, positive and significant association with spike length (0.771**) at genotypic level only.

In second environment E2, this trait showed positive and significant association with spike length (0.494**, 0.294*), biological yield (0.779**, 0.360**) and test weight (0.983**, 0.428**) both at phenotypic and genotypic levels while, with number of tillers per plant (0.535*) it showed positive and significant association at genotypic level only.

In third environment E3, this trait showed positive and significant association with number of tillers per plant (0.878**, 0.381**) both at phenotypic and genotypic levels while this trait showed positive and significant association with flag leaf width (0.504*), spike length (0.583*) and no. of spikelet per spike (0.701**) at genotypic level only. This trait showed negative and significant association with grain yield per plant (-0.569*, -0.366**) both at phenotypic and genotypic levels.

In fourth environment E4, this trait recorded positive and significant association with test weight (0.600*, 0.400**) both at phenotypic and genotypic levels while it showed positive and significant association with flag leaf width (0.490*), no. of tillers/

plant (0.627**), spike length (0.551*), no. of spikelet/ spike (0.679**) and no. of grains/ spike (0.818**) at genotypic level only.

In pooled environments this trait showed positive and significant association with flag leaf width (0.602**, 0.377**), no. of tillers/ plant (0.389**, 0.311**), spike length (0.734**, 0.408**), no. of spikelet/ spike (0.712**, 0.387**), test weight (0.818**, 0.649**) and harvest index (0.525**, 0.447**) both at phenotypic and genotypic levels while, this trait showed positive and significant association with no. of grains per spike (0.319**) at genotypic level only. It showed negative and significant association with biological yield (-0.742**, -0.633**) and grain yield (-0.289**, -0.246**) both at phenotypic and genotypic levels.

Flag leaf width (cm)

In first environment E1, this trait showed positive and significant association with no. of grains per spike (0.0967**, 0.362**), grain yield (0.699**, 0.391**), harvest index (0.852**, 0.473**) both at phenotypic and genotypic levels while, this trait showed positive and significant association with no. of spikelet per spike (0.911**) at genotypic level only.

In second environment E2, this trait showed positive and significant association with biological yield (0.841**, 0.404**) and grain yield per plant (0.858**, 0.473**) both at phenotypic and genotypic levels, whereas, it showed positive and significant association with spike length (0.887**) at genotypic level only while, this trait showed positive and significant association with no. of spikelet per spike (0.295*) and no. of grains per spike (0.277*) at phenotypic level only.

In third environment E3, positive and significant association was shown with no. of tillers per plant (0.941**), number of spikelets/ spike (0.492*) at genotypic level only.

In fourth environment E4, it showed positive and significant association with number of tillers per plant (0.828**, 0.430**) and no. of spikelet per spike (0.893**, 0.288*) both at phenotypic and genotypic levels while, this trait showed positive and significant association with spike length (0.499**), no. of grains per spike (0.570*) and biological yield (0.597*) at genotypic level only and showed positive and significant association with grain yield (0.276*) and test weight (0.285*) at phenotypic level only.

In pooled environment this trait showed positive and significant association with number of tillers/ plant (0.319**, 0.176**), spike length (0.578**, 0.237**), number

of spikelet/ spike (0.679**, 0.334**), number of grains/ spike (0.463**, 0.215**), test weight (0.510**, 0.303**), harvest index (0.451**, 0.290**) and grain yield/ plant (0.179*, 0.149*) both at phenotypic and genotypic levels. It showed negative and significant association with biological yield per plant (-0.406**, -0.255**) both at phenotypic and genotypic levels.

Number of tillers per plant

In first environment E1, this trait showed positive and significant association with no. of spikelet per spike (0.718**, 0.395**) both at phenotypic and genotypic levels while, this trait showed positive and significant association with spike length (0.551*) at genotypic level and with no. of grains per spike (0.315*) at phenotypic level.

In second environment E2, this trait showed positive and significant association with spikelet per spike (0.522*, 0.426**) and biological yield (0.729**, 0.332*) both at phenotypic and genotypic levels while, this trait showed positive and significant association with grain yield (0.503*) at genotypic level only.

In third environment E3, it showed positive and significant association with test weight (0.650**, 0.424**) both at phenotypic and genotypic levels while, this trait showed positive and significant association with no. of spikelet per spike (0.967**), no. of grains per spike (0.564**) and biological yield (0.822**) at genotypic level.

In fourth environment E4, this trait showed positive and significant association with spike length (0.796**, 0.437**), no. of spikelet per spike (0.794**, 0.303*) and test weight (0.562*, 0.388**) both at phenotypic and genotypic levels.

In pooled environments it showed positive and significant association with test weight (0.408**, 0.340**), harvest index (0.177*, 0.152*) and grain yield (0.243**, 0.172*) both at phenotypic and genotypic levels while, this trait showed positive and significant association with spike length (0.144*) at genotypic level only. This trait showed negative and significant association with biological yield per plant (-0.147*, -0.150*).

Spike length (cm)

In first environment E1, this trait showed positive and significant association with no. of spikelet/ spike (0.823**, 0.390**), number of grains/ spike (0.646**, 0.376**), grain yield/ plant (0.780**, 0.465**) and harvest index (0.712**, 0.305*) both at

phenotypic and genotypic levels while, this trait showed positive and significant association with biological yield per plant (0.309*) at phenotypic level only.

In second environment E2, it showed positive and significant association with test weight (0.615**, 0.376**) both at phenotypic and genotypic levels while, positive and significant correlation of spike length, with no. of grains/ spike (0.756**) & biological yield/plant (0.542*) at genotypic level only.

In third environment E3, this trait showed positive and significant association with no. of grains per spike (0.568*) at genotypic level.

In fourth environment E4, it showed positive and significant association with test weight (0.641**, 0.320*) both at phenotypic and genotypic levels while, this trait showed positive and significant association with no. of spikelet per spike (0.353**) and grain yield per plant (0.628**) at genotypic level.

In pooled environment it showed positive and significant association with no. of spikelet per spike (0.725**, 0.277**), test weight (0.439**, 0.322**) both at phenotypic and genotypic level while, this trait showed positive and significant association with no. of grains per spike (0.359**) and harvest index (0.165*) at genotypic level only. It showed negative and significant association with biological yield per plant (-0.341**, -0.222**) and grain yield per plant (-0.358**, -0.267**).

Number of spikelets per spike

In first environment E1, this trait showed positive and significant association with no. of grains per spike (0.582*, 0.623**), grain yield (0.622**, 0.389**), test weight (0.765**, 0.383**) and harvest index (0.686**, 0.328*) both at phenotypic and genotypic levels.

In second environment E2, no. of spikelet per spike revealed positive and significant correlation with no. of grains/ spike, (0.596*, 0.411**) and biological yield/ plant (0.576*, 0.357*) both at phenotypic and genotypic levels while, this trait showed positive and significant association with grain yield (0.311*) at phenotypic level only.

In third environment E3, this trait showed positive and significant association with biological yield per plant (0.797**, 0.366**) both at phenotypic and genotypic levels while, this trait showed positive and significant association with no. of grains per spike (0.444**) at phenotypic level while, this trait showed positive and significant

association with test weight (0.506*) at genotypic level. It showed negative and significant association with harvest index (-0.781**, -0.422**) both at phenotypic and genotypic levels.

In fourth environment E4, it showed positive and significant association with no. of grains per spike (0.743**, 0.297*) and test weight (0.692**, 0.447**) both at phenotypic and genotypic levels while, this trait showed positive and significant association with biological yield per plant (0.582*) at genotypic level only.

In pooled environment it showed positive and significant association with no. of grains per spike (0.586**, 0.470**), test weight (0.638**, 0.358**), harvest index (0.413**, 0.251**), both at phenotypic and genotypic levels.

Number of grains per spike

In first environment E1, this trait showed positive and significant association with test weight (0.779**, 0.319*), harvest index (0.962**, 0.449**) and grain yield per plant (0.854**, 0.490**) both at phenotypic and genotypic levels.

In second environment E2, it showed positive and non-significant association with almost all the characters except test weight, harvest index and grain yield per plant that showed negative and non-significant association both at phenotypic and genotypic levels.

In third environment E3, it showed positive and significant association with biological yield per plant (0.898**, 0.374**) and grain yield per plant (0.916**, 0.310*) both at phenotypic and genotypic levels.

In fourth environment E4, this trait showed positive and significant association with biological yield per plant (0.535*), grain yield per plant (0.787*), test weight (0.534*) at genotypic level.

In pooled environment it showed positive and significant association with test weight (0.398**, 0.141*), harvest index (0.365**, 0.187**), grain yield per plant (0.400**, 0.205**) both at phenotypic and genotypic levels.

Biological yield per plant (g)

In first environment E1, this trait showed negative and significant association with harvest index (-0.314*) at phenotypic level.

In second environment E2, this trait showed positive and significant association with grain yield per plant (0.361**) at phenotypic level only.

In third environment E3, it showed positive and significant association with grain yield per plant (0.423**) at phenotypic level only.

In fourth environment E4, this trait showed negative and significant association with harvest index (-0.688**, -0.617**) both at phenotypic and genotypic levels.

In pooled environment it showed negative and significant association with test weight (-0.588**, -0.544**), harvest index (-0.819**, -0.797**) both at phenotypic and genotypic levels.

Test weight (g)

In first environment E1, this trait showed positive and significant association with grain yield per plant (0.288*) at genotypic level while, it showed positive and significant association with harvest index (0.351*) at phenotypic level only.

In second environment E2, this trait recorded non-significant association with most of the characters at both phenotypic and genotypic levels.

In third environment E3, this trait showed non-significant association with most of the characters at both phenotypic and genotypic levels.

In fourth environment E4, it showed non-significant association with most of the characters at both phenotypic and genotypic levels.

In pooled environment this trait showed positive and significant association with harvest index (0.479**, 0.435**) both at phenotypic and genotypic levels while it showed non-significant association with most of the characters at both phenotypic and genotypic levels.

Harvest index (%)

In first environment E1, this trait showed positive and significant association with grain yield per plant (0.936**, 0.887**) both at phenotypic and genotypic levels.

In second environment E2, this trait showed positive and significant association with grain yield per plant (0.384*) at phenotypic level.

In third environment E3, this trait showed positive and significant association with grain yield per plant (0.284*) at phenotypic level only.

In fourth environment E4, this trait showed positive and significant genotypic correlation with grain yield/ plant (0.722**))

In pooled environment it showed positive and significant correlation with grain yield/ plant (0.382**, 0.385**) at phenotypic and genotypic levels.

4.4 PATH COEFFICIENT ANALYSIS

In the present investigation of path coefficient analysis, direct and indirect effects of all the contributing traits on grain yield per plant of barley were assessed at phenotypic and genotypic levels for all the environments E1, E2, E3, E4 and are presented in tables 4.4, 4.4.1, 4.4.2, 4.4.3, 4.4.4.

Days to 50% flowering

In first environment E1, it showed positive and direct effect (0.011, 0.011) on grain yield at both genotypic and phenotypic levels. The indirect effects were positive *via* harvest index (0.677, 0.252) and flag leaf length (0.033, 0.022) at both genotypic and phenotypic levels. Whereas, the indirect effects were negative *via* number of tillers per plant (-0.039, -0.051), biological yield (-0.182, -0.097) and test weight (-0.038, -0.007) at both genotypic and phenotypic levels.

In second environment E2, it showed positive and direct effect (0.264) on grain yield at genotypic level and negative direct effect (-0.098) at phenotypic level. The indirect effects were positive *via* flag leaf width (0.795, 0.106), no. of spikelet per spike (0.355, 0.026), biological yield per plant (0.323, 0.158) and test weight (0.278, 0.049) at genotypic and phenotypic levels Whereas, indirect effects were negative *via* flag leaf length (-0.609, -0.091), no. of grains per spike (-0.485, -0.052) and harvest index (-0.208, -0.278) both at genotypic and phenotypic levels.

In third environment E3, it showed negative and direct effect (-0.441, -0.063) on grain yield at genotypic and phenotypic levels. The indirect effects were positive *via* plant height (0.066, 0.006), biological yield per plant (0.218, 0.414), SPAD values (0.128, 0.001) and no. of grains per spike (0.013, 0.001) at both genotypic and phenotypic levels. The indirect effects were negative *via* harvest index (-0.638, -0.269), spikelet per spike (-0.038, -0.010), flag leaf width (-0.037, -0.001), number of tillers per plant (-0.030, -0.008) and flag leaf length (-0.003, -0.002) at genotypic and phenotypic levels.

In fourth environment E4, it showed negative and direct effects (-0.090, -0.037) on grain yield at both genotypic and phenotypic levels. The indirect effects were positive *via* harvest index (0.245, 0.151), biological yield per plant (0.209, 0.080), and flag leaf width (0.033, 0.023), test weight (0.027, 0.005) and SPAD values (0.021, 0.002). The indirect effects were negative *via* flag leaf length (-0.014, -0.001), no. of grains per spike (-0.013, -0.001) and plant height (-0.004, -0.001) at both genotypic and phenotypic level.

In pooled environment, it showed positive and direct effects (0.453, 0.080) on grain yield at both genotypic and phenotypic levels. The indirect effects were positive *via* plant height (0.544, 0.050), SPAD values (0.520, 0.007), number of tillers per plant (0.302, 0.056), test weight (0.299, 0.015) at both genotypic and phenotypic level. The indirect effects were negative *via* flag leaf length (-0.321, -0.016) and no. of spikelet per plant (-0.004, -0.010) at both genotypic and phenotypic level.

Plant height (cm)

In first environment E1, it had positive and direct effect (0.058) at genotypic level, negative direct effect (-0.031) at phenotypic level on grain yield. The indirect effects were positive *via* harvest index (0.716, 0.377), flag leaf length (0.032, 0.026) and days to 50% flowering (0.004, 0.004) at both genotypic and phenotypic levels. The indirect effects were negative *via* biological yield/ plant (-0.039, -0.012), test weight (-0.029, -0.007), no. of tillers/plant (-0.021, -0.032) and spike length (-0.005, -0.004) at genotypic as well as at phenotypic levels.

In second environment E2, it showed negative and direct effect (-0.286) at genotypic level, positive and direct effect (0.059) at phenotypic level on grain yield. The indirect effects were positive *via* flag leaf width (0.698, 0.101), biological yield per plant (0.323, 0.121), test weight (0.278, 0.009) and SPAD values (0.084, 0.004). The indirect effects were negative *via* no. of grains per spike (-0.485, -0.011), flag leaf length (-0.290, -0.063), no. of spikelet per spike (-0.266, -0.029) and harvest index (-0.208, -0.029) at both genotypic and phenotypic levels.

In third environment E3, this trait showed positive and direct effect (0.138, 0.020) on grain yield at both genotypic and phenotypic. The indirect effects were positive *via* biological yield per plant (0.308, 0.215) and test weight (0.016, 0.001) at both genotypic and phenotypic levels. The indirect effects were negative *via* harvest

Table 4.4. Phenotypic(P) and Genotypic(G) path coefficient analysis of grain yield per plant with other characters in environment 1

Characters		Days to 50% flowering	Plant height (cm)	SPAD values	Flag leaf length (cm)	Flag leaf width (cm)	No. of tillers/plant	Spike length (cm)	No. of Spikelet/spike	No. of Grains/spike	Biological yield (g)	Test weight (g)	Harvest Index (%)	Correlation coefficient with Grain yield/ plant (g)
Days to 50% Flowering	G	0.011	0.022	-0.023	0.033	-0.018	-0.039	-0.003	-0.018	0.104	-0.182	-0.038	0.677	0.526*
	P	0.011	-0.011	0.022	0.022	0.030	-0.051	-0.001	0.028	-0.004	-0.097	-0.007	0.252	0.194
Plant height (cm)	G	0.004	0.058	-0.003	0.032	-0.009	-0.021	-0.005	-0.027	0.098	-0.039	-0.029	0.716	0.777**
	P	0.004	-0.031	0.021	0.026	0.030	-0.032	-0.004	0.018	-0.005	-0.0122	-0.007	0.377	0.383**
SPAD values	G	0.010	0.006	-0.024	0.031	-0.016	-0.021	0.003	-0.012	0.078	-0.162	-0.023	0.249	0.120
	P	0.004	-0.011	0.063	0.015	0.025	-0.046	0.001	0.007	-0.002	-0.131	-0.006	0.151	0.071
Flag leaf length (cm)	G	0.010	0.052	-0.021	0.036	-0.019	-0.018	-0.007	-0.025	0.128	-0.111	-0.044	0.867	0.849**
	P	0.004	-0.012	0.014	0.067	0.049	-0.035	-0.003	0.032	-0.009	-0.137	-0.011	0.503	0.463**
Flag leaf width (cm)	G	0.010	0.025	-0.019	0.033	-0.020	-0.014	-0.003	-0.020	0.100	-0.155	-0.016	0.776	0.699**
	P	0.003	-0.009	0.015	0.031	0.106	-0.005	-0.003	0.014	-0.007	-0.182	-0.004	0.475	0.391**
No. of tillers/plant	G	0.012	0.034	-0.014	0.018	-0.008	-0.035	-0.005	-0.015	0.047	0.118	-0.015	0.296	0.432
	P	0.005	-0.009	0.026	0.021	0.005	-0.113	-0.003	0.024	-0.006	0.132	-0.004	0.170	0.257
Spike length (cm)	G	0.004	0.037	0.009	0.027	-0.008	-0.019	-0.009	-0.018	0.067	0.055	-0.014	0.648	0.780**
	P	0.001	-0.009	-0.006	0.016	0.020	-0.028	-0.014	0.023	-0.007	0.179	-0.004	0.307	0.465**
No. of Spikelet/spike	G	0.009	0.072	-0.013	0.042	-0.018	-0.025	-0.007	-0.021	0.060	-0.061	-0.039	0.625	0.622**
	P	0.005	-0.009	0.007	0.036	0.026	-0.045	-0.005	0.060	-0.012	0.000	-0.006	0.330	0.389**
No. of Grains/spike	G	0.011	0.054	-0.018	0.044	-0.019	-0.016	-0.006	-0.012	0.104	-0.124	-0.040	0.877	0.854**
	P	0.002	-0.008	0.008	0.030	0.038	-0.036	-0.005	0.037	-0.020	0.003	-0.006	0.443	0.490**
Biological yield (g)	G	-0.005	-0.006	0.010	-0.010	0.008	-0.011	-0.001	0.003	-0.034	0.384	0.013	-0.192	0.159
	P	-0.002	0.001	-0.014	-0.016	-0.033	-0.026	-0.004	0.000	-0.001	0.618	0.004	-0.316	0.127
Test weight (g)	G	0.008	0.032	-0.011	0.030	-0.006	-0.011	-0.002	-0.016	0.081	-0.098	-0.051	0.435	0.390
	P	0.004	-0.011	0.019	0.038	0.024	-0.023	-0.003	0.023	-0.006	-0.109	-0.020	0.352	0.289*
Harvest index (%)	G	0.008	0.045	-0.007	0.034	-0.017	-0.012	-0.006	-0.015	0.100	-0.081	-0.025	0.911	0.936**
	P	0.003	-0.012	0.010	0.033	0.050	-0.019	-0.004	0.020	-0.009	-0.183	-0.007	1.006	0.888**

Genotypic Residual effect = -0.0109

Phenotypic Residual effect = -0.0615

*, ** significant at 5% and 1% level, respectively

Table 4.4.1 Phenotypic(P) and Genotypic(G) path coefficient analysis of grain yield/plant with other characters in environment 2

Characters		Days to 50% flowering	Plant height (cm)	SPAD values	Flag leaf length (cm)	Flag leaf width (cm)	No. of tillers/plant	Spike length (cm)	No. of Spikelet/spike	No. of Grains/spike	Biological yield (g)	Test weight (g)	Harvest Index (%)	Correlation coefficient with Grain yield/ plant (g)
Days to 50% Flowering	G	0.264	-0.133	-0.333	-0.609	0.795	0.062	-0.274	0.355	-0.485	0.323	0.278	-0.208	0.036
	P	-0.098	0.005	0.044	-0.091	0.106	-0.002	0.001	0.026	-0.052	0.158	0.049	-0.278	-0.131
Plant height (cm)	G	0.123	-0.286	0.084	-0.290	0.698	0.048	-0.088	-0.266	-0.485	0.323	0.278	-0.208	0.398
	P	-0.008	0.059	0.004	-0.063	0.101	-0.001	0.004	-0.029	-0.011	0.121	0.009	-0.029	0.115
SPAD values	G	0.318	0.087	-0.276	-0.431	0.474	0.074	-0.324	0.537	-0.352	0.229	0.089	-0.171	0.253
	P	-0.022	0.001	0.195	-0.115	0.087	-0.002	0.001	0.035	-0.024	0.085	0.049	-0.072	0.217
Flag leaf length (cm)	G	0.253	-0.131	-0.188	-0.634	0.080	0.076	-0.239	0.230	-0.025	0.356	0.380	-0.091	0.070
	P	0.028	0.0116	0.070	0.322	0.104	-0.002	0.001	0.011	-0.002	0.133	0.077	-0.064	-0.010
Flag leaf width (cm)	G	0.278	-0.265	-0.174	-0.068	0.753	0.060	-0.203	0.114	-0.052	0.384	0.092	-0.063	0.858**
	P	-0.024	0.014	0.039	-0.078	0.425	-0.003	0.001	0.043	-0.058	0.146	0.006	-0.064	0.473**
No. of tillers/plant	G	0.114	-0.097	-0.144	-0.339	0.320	0.142	-0.066	0.380	-0.244	0.333	0.034	0.069	0.503*
	P	-0.023	0.004	0.032	-0.084	0.120	-0.009	0.002	0.062	-0.043	0.123	-0.020	0.032	0.194
Spike length (cm)	G	0.316	-0.110	-0.392	-0.664	0.668	0.041	-0.228	0.765	-0.505	0.248	0.238	-0.070	0.307
	P	-0.030	0.006	0.061	-0.095	0.100	-0.001	0.004	-0.003	-0.002	0.088	0.067	-0.085	0.114
No. of Spikelet/spike	G	0.128	0.104	-0.203	-0.100	0.118	0.074	-0.240	0.729	-0.398	0.263	0.061	0.027	0.465
	P	-0.017	-0.012	0.046	-0.023	0.127	-0.004	-0.001	0.146	-0.086	0.132	-0.016	0.019	0.311*
No. of Grains/spike	G	0.191	-0.005	-0.145	-0.024	0.058	0.052	-0.172	0.434	-0.668	0.242	-0.021	-0.042	-0.101
	P	-0.024	0.003	0.023	-0.003	0.120	-0.002	0.001	0.060	-0.208	0.077	-0.045	-0.037	-0.037
Biological yield (g)	G	0.186	-0.239	-0.138	-0.493	0.633	0.104	-0.124	0.419	-0.354	0.457	0.045	-0.060	0.437
	P	-0.042	0.020	0.045	-0.115	0.171	-0.003	0.001	0.052	-0.044	0.371	0.014	-0.101	0.361**
Test weight (g)	G	0.189	-0.025	-0.063	-0.623	0.178	0.013	-0.140	0.115	0.037	0.053	0.387	-0.099	0.021
	P	-0.027	0.003	0.053	-0.138	0.013	0.001	0.002	-0.013	0.053	0.029	0.178	-0.129	0.025
Harvest index (%)	G	-0.217	0.032	0.187	0.226	-0.186	0.039	0.062	0.079	0.112	-0.108	-0.152	0.253	0.328
	P	0.057	-0.004	-0.029	0.043	-0.058	-0.001	-0.001	0.006	0.016	-0.078	-0.048	0.481	0.384 **

Genotypic Residual effect = -0.1262

Phenotypic Residual effect = 0.3619

*, ** significant at 5% and 1% level, respectively

Table 4.4.2 Phenotypic(P) and Genotypic(G) path coefficient analysis of grain yield/plant with other characters in environment 3

Characters		Days to 50% flowering	Plant height (cm)	SPAD values	Flag leaf length (cm)	Flag leaf width (cm)	No. of tillers/plant	Spike length (cm)	No. of Spikelet/s pike	No. of grains/spike	Biological yield (g)	Test weight (g)	Harvest Index (%)	Correlation coefficient with Grain yield/ plant (g)
Days to 50% Flowering	G	-0.441	0.066	0.128	-0.003	-0.037	-0.030	-0.001	-0.038	0.013	1.218	0.059	-0.638	0.297
	P	-0.063	0.006	0.001	-0.002	-0.001	-0.008	0.001	-0.010	0.001	0.414	-0.002	-0.269	0.069
Plant height (cm)	G	-0.209	0.138	0.113	0.024	-0.029	-0.040	0.001	-0.026	-0.016	0.308	0.016	-0.666	-0.3856
	P	-0.019	0.020	-0.001	-0.003	-0.001	0.001	-0.002	-0.008	-0.003	0.215	0.001	-0.297	-0.094
SPAD values	G	0.136	-0.038	-0.414	0.034	0.018	-0.038	-0.001	-0.004	-0.001	-0.462	0.168	0.004	-0.596*
	P	0.010	0.001	-0.007	-0.003	0.001	-0.001	-0.003	-0.007	-0.011	-0.144	-0.003	0.058	-0.110
Flag leaf length (cm)	G	0.017	0.038	-0.162	0.087	-0.028	-0.099	0.001	-0.036	0.003	0.098	0.118	-0.602	-0.569*
	P	-0.004	0.003	-0.001	-0.026	-0.001	-0.011	0.003	-0.013	-0.001	-0.092	-0.005	-0.222	-0.366**
Flag leaf width (cm)	G	-0.291	0.072	0.131	0.044	-0.056	-0.106	0.001	-0.027	0.005	0.300	0.052	-0.428	-0.304
	P	-0.026	0.004	0.001	-0.005	-0.001	-0.004	0.003	-0.013	0.007	0.334	-0.002	-0.257	0.024
No. of tillers/plant	G	-0.115	0.049	-0.138	0.076	-0.052	-0.113	0.001	-0.052	0.044	1.308	0.181	-0.701	0.487*
	P	-0.018	-0.001	-0.001	-0.010	-0.001	-0.028	0.003	-0.014	0.012	0.007	-0.009	-0.092	-0.148
Spike length (cm)	G	0.111	0.012	0.010	0.051	-0.016	-0.024	0.001	-0.006	0.021	-0.216	-0.035	0.206	0.115
	P	-0.001	-0.003	0.002	-0.006	-0.001	-0.007	0.012	-0.011	0.005	0.012	-0.001	-0.017	-0.012
No. of spikelet/spike	G	-0.307	0.066	-0.032	0.061	-0.027	-0.109	0.001	-0.054	0.017	1.268	0.141	-1.156	-0.131
	P	-0.012	0.003	-0.001	-0.006	-0.001	-0.007	0.002	-0.055	0.046	0.458	-0.005	-0.487	-0.063
No. of grains/spike	G	-0.153	-0.060	0.100	0.006	-0.008	-0.136	0.001	-0.026	0.036	1.811	0.076	-0.642	0.916**
	P	-0.001	-0.001	0.001	0.001	-0.001	-0.003	0.001	-0.024	0.104	0.468	-0.003	-0.231	0.310*
Biological yield (g)	G	-0.337	0.027	0.120	0.005	-0.011	-0.093	-0.001	-0.043	0.041	1.592	0.132	-1.145	0.288
	P	-0.021	0.004	0.001	0.002	-0.001	-0.001	0.001	-0.020	0.039	1.250	-0.003	-0.823	0.423**
Test weight (g)	G	-0.094	0.008	-0.250	0.037	-0.010	-0.073	-0.001	-0.027	0.100	0.753	0.279	-0.474	0.157
	P	-0.005	-0.001	-0.001	-0.007	-0.001	-0.012	0.001	-0.013	0.015	0.202	-0.020	-0.142	0.017
Harvest index (%)	G	0.190	-0.062	-0.001	-0.035	0.016	0.053	0.001	0.042	-0.016	-1.231	-0.089	1.480	0.347
	P	0.015	-0.005	-0.004	0.005	0.001	0.002	-0.002	0.023	-0.021	-0.891	0.003	1.155	0.284*

Genotypic Residual effect = -0.0315

Phenotypic Residual effect = 0.0926

*, ** significant at 5% and 1% level, respectively

Table 4.4.3 Phenotypic(P) and Genotypic(G) path coefficient analysis of grain yield/plant with other characters in environment 4

Characters		Days to 50% flowering	Plant height (cm)	SPAD values	Flag leaf length (cm)	Flag leaf width (cm)	No. of tillers/plant	Spike length (cm)	No. of spikelet/spike	No. of grains/spike	Biological yield (g)	Test weight (g)	Harvest Index (%)	Correlation coefficient with Grain yield/ plant (g)
Days to 50% Flowering	G	-0.090	-0.004	0.021	-0.014	0.033	0.016	-0.009	-0.014	-0.013	0.209	0.027	0.245	0.408
	P	-0.037	-0.001	0.002	-0.001	0.023	-0.004	0.002	0.003	-0.001	0.080	0.005	0.151	0.225
Plant height (cm)	G	0.012	0.026	-0.009	-0.016	0.021	-0.027	0.003	0.013	-0.008	0.498	-0.016	-0.819	-0.324
	P	0.001	0.024	-0.001	-0.003	0.003	0.007	-0.003	0.001	-0.001	0.174	-0.003	-0.318	-0.117
SPAD values	G	-0.819	-0.005	0.046	-0.090	0.035	0.060	-0.012	-0.036	-0.019	-0.174	0.083	0.506	0.353
	P	-0.005	-0.001	0.015	-0.008	0.011	-0.007	0.006	0.001	-0.002	-0.034	0.012	0.241	0.228
Flag leaf length (cm)	G	-0.016	0.005	0.051	-0.082	0.021	0.044	-0.013	-0.037	-0.031	0.237	0.048	-0.301	-0.075
	P	-0.001	0.002	0.004	-0.036	0.012	-0.004	0.004	0.002	-0.001	0.169	0.011	-0.096	0.068
Flag leaf width (cm)	G	-0.069	0.012	0.038	-0.040	0.043	0.058	-0.027	-0.049	-0.021	0.614	0.036	-0.217	0.380
	P	-0.012	0.001	0.002	-0.006	0.072	-0.010	0.003	0.003	-0.001	0.198	0.008	0.059	0.276*
No. of tillers/plant	G	-0.020	-0.010	0.040	-0.052	0.036	0.070	-0.019	-0.043	-0.003	0.071	0.045	0.200	0.313
	P	-0.007	-0.007	0.005	-0.006	0.030	-0.023	0.007	0.004	0.001	0.046	0.010	0.032	0.097
Spike length (cm)	G	-0.034	-0.003	0.023	-0.045	0.049	0.056	-0.024	-0.070	-0.006	0.312	0.051	0.320	0.628**
	P	-0.005	-0.005	0.005	-0.008	0.013	-0.010	0.017	0.003	-0.001	0.147	0.008	-0.087	0.083
No. of spikelet/spike	G	-0.022	-0.006	0.031	-0.056	0.039	0.056	-0.031	-0.054	-0.028	0.598	0.055	-0.302	0.278
	P	-0.009	0.002	0.001	-0.006	0.020	-0.007	0.004	0.012	-0.002	0.162	0.012	0.008	0.192
No. of grains/spike	G	-0.030	0.005	0.024	-0.067	0.025	0.006	-0.004	-0.040	-0.037	0.551	0.043	0.313	0.787**
	P	-0.001	0.001	0.004	-0.003	0.004	0.001	0.003	0.004	-0.007	0.150	0.005	0.079	0.236
Biological yield (g)	G	-0.018	0.013	-0.008	-0.019	0.026	0.005	-0.007	-0.032	-0.020	1.028	0.003	-0.969	0.049
	P	-0.004	0.005	-0.001	-0.008	0.018	-0.001	0.003	0.002	-0.001	0.786	0.001	-0.766	0.046
Test weight (g)	G	-0.030	-0.005	0.048	-0.050	0.020	0.039	-0.015	-0.038	-0.020	0.032	0.080	0.276	0.337
	P	-0.007	-0.003	0.007	-0.014	0.020	-0.009	0.005	0.005	-0.001	0.026	0.026	0.200	0.254
Harvest index (%)	G	-0.016	-0.015	0.017	0.018	-0.007	0.010	-0.005	0.012	-0.008	-0.707	0.016	1.409	0.722**
	P	-0.004	-0.006	0.003	0.003	0.003	-0.001	-0.001	0.001	-0.001	-0.484	0.004	1.241	0.753

Genotypic Residual effect = -0.0021

Phenotypic Residual effect = 0.0129

*, ** significant at 5% and 1% level, respectively

Table 4.4.4 Phenotypic(P) and Genotypic(G) path coefficient analysis of grain yield/plant with other characters in pooled environment

Characters		Days to 50% flowering	Plant height (cm)	SPAD values	Flag leaf length (cm)	Flag leaf width (cm)	No. of tillers/plant	Spike length (cm)	No. of spikelets/spike	No. of grains/spike	Biological yield (g)	Test weight (g)	Harvest Index (%)	Correlation coefficient with Grain yield/ plant (g)
Days to 50% Flowering	G	0.453	0.554	0.520	-0.321	-1.006	0.302	0.138	-0.004	-0.167	-0.342	0.299	0.001	0.425**
	P	0.080	0.050	0.007	-0.016	0.022	0.056	-0.001	-0.010	0.007	0.057	0.015	-0.016	0.250**
Plant height (cm)	G	0.141	1.781	0.003	0.038	-0.148	-0.134	-1.187	0.002	-0.074	-1.290	-0.322	-0.004	0.660**
	P	0.018	0.222	0.004	0.097	0.002	-0.030	0.018	0.005	0.007	0.262	-0.020	-0.067	0.520**
SPAD values	G	0.232	0.005	1.013	-1.764	-0.733	0.363	0.287	-0.007	-0.172	0.506	0.534	0.009	0.273**
	P	0.014	0.026	0.038	-0.055	0.007	0.045	0.001	-0.007	0.005	-0.068	0.025	0.145	0.177*
Flag leaf length (cm)	G	0.037	-0.848	0.450	-3.973	-0.974	0.306	2.058	-0.011	-0.114	1.932	0.828	0.020	-0.289**
	P	0.004	-0.071	0.007	-0.309	0.029	0.059	-0.025	-0.023	0.008	-0.419	0.056	0.437	-0.246**
Flag leaf width (cm)	G	0.282	0.163	0.459	-2.392	-1.618	0.251	1.621	-0.011	-0.166	1.057	0.516	0.017	0.179*
	P	0.023	0.007	0.004	-0.117	0.077	0.034	-0.015	-0.019	0.014	-0.168	0.026	0.284	0.149*
No. of tillers/plant	G	0.173	-0.304	0.467	-1.545	-0.516	0.787	0.405	-0.002	-0.026	0.383	0.414	0.007	0.243**
	P	0.024	-0.035	0.009	-0.096	0.014	0.191	-0.007	-0.007	0.001	-0.099	0.029	0.149	0.172*
Spike length (cm)	G	0.023	-0.753	0.104	-2.915	-0.935	0.114	2.806	-0.012	-0.129	0.889	0.445	0.006	-0.358**
	P	0.002	-0.065	-0.001	-0.126	0.018	0.022	-0.062	-0.016	0.007	-0.147	0.028	0.073	-0.267**
No. of spikelet/spike	G	0.119	-0.227	0.414	-2.829	-1.099	0.105	2.033	-0.016	-0.210	1.015	0.646	0.016	-0.034
	P	0.014	-0.018	0.005	-0.120	0.026	0.022	-0.017	-0.058	0.031	-0.166	0.031	0.246	-0.005
No. of grains/spike	G	0.211	0.366	0.487	-1.266	-0.749	0.057	1.007	-0.009	-0.359	0.238	0.404	0.014	0.400**
	P	0.009	0.023	0.003	-0.039	0.016	0.004	-0.006	-0.027	0.066	-0.038	0.012	0.183	0.205**
Biological yield (g)	G	0.060	0.882	-0.197	2.948	0.657	-0.116	-0.957	0.006	0.033	-2.604	-0.595	-0.031	0.084
	P	0.007	0.088	-0.004	0.196	-0.020	-0.029	0.014	0.015	-0.004	0.662	-0.047	-0.780	0.097
Test weight (g)	G	0.134	-0.566	0.534	-3.250	-0.825	0.321	1.231	-0.010	-0.143	1.531	1.013	0.018	-0.010
	P	0.014	-0.052	0.011	-0.201	0.023	0.065	-0.020	-0.021	0.009	-0.360	0.086	0.426	-0.019
Harvest index (%)	G	0.009	-0.161	0.227	-2.084	-0.730	0.139	0.463	-0.007	-0.131	2.132	0.486	1.891	0.382**
	P	-0.001	-0.015	0.006	-0.138	0.022	0.029	-0.005	-0.015	0.012	-0.527	0.038	0.979	0.385**

Genotypic Residual effect = -0.32978

Phenotypic Residual effect = 0.26815

*, ** significant at 5% and 1% level, respectively

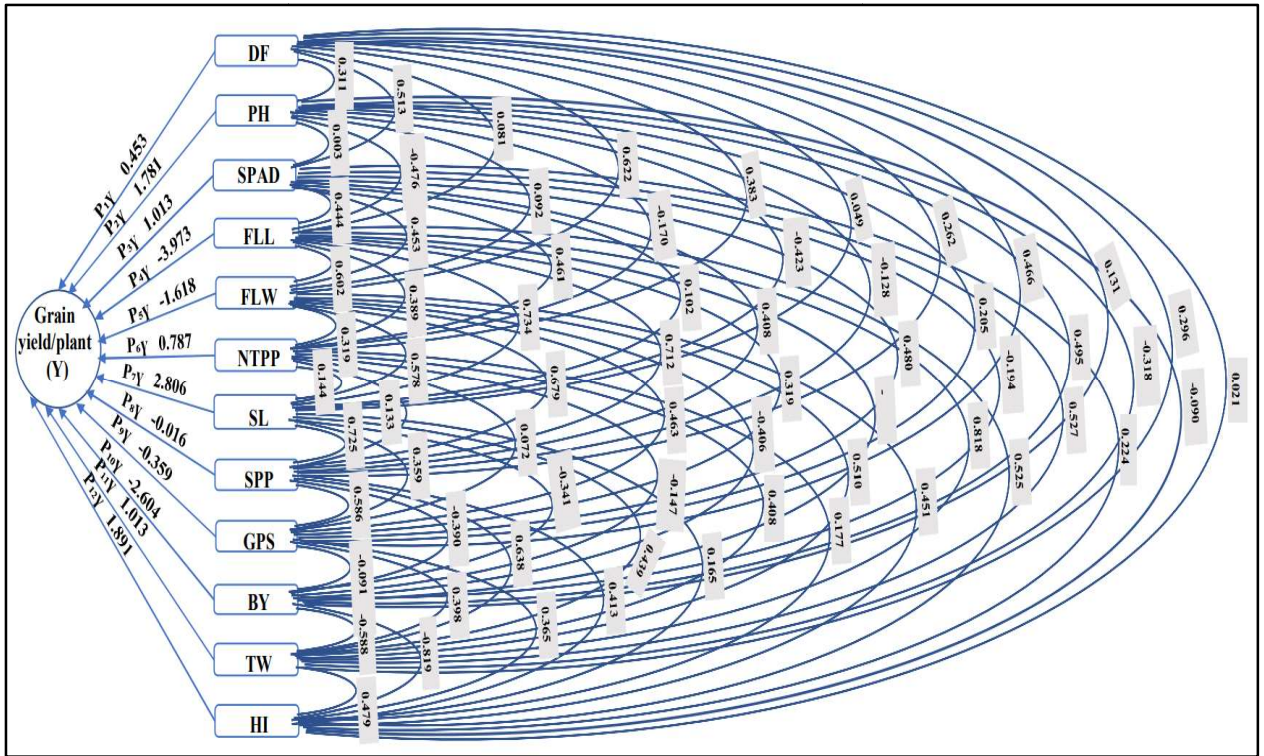


Figure 4.1 Genotypic path diagram for grain yield per plant

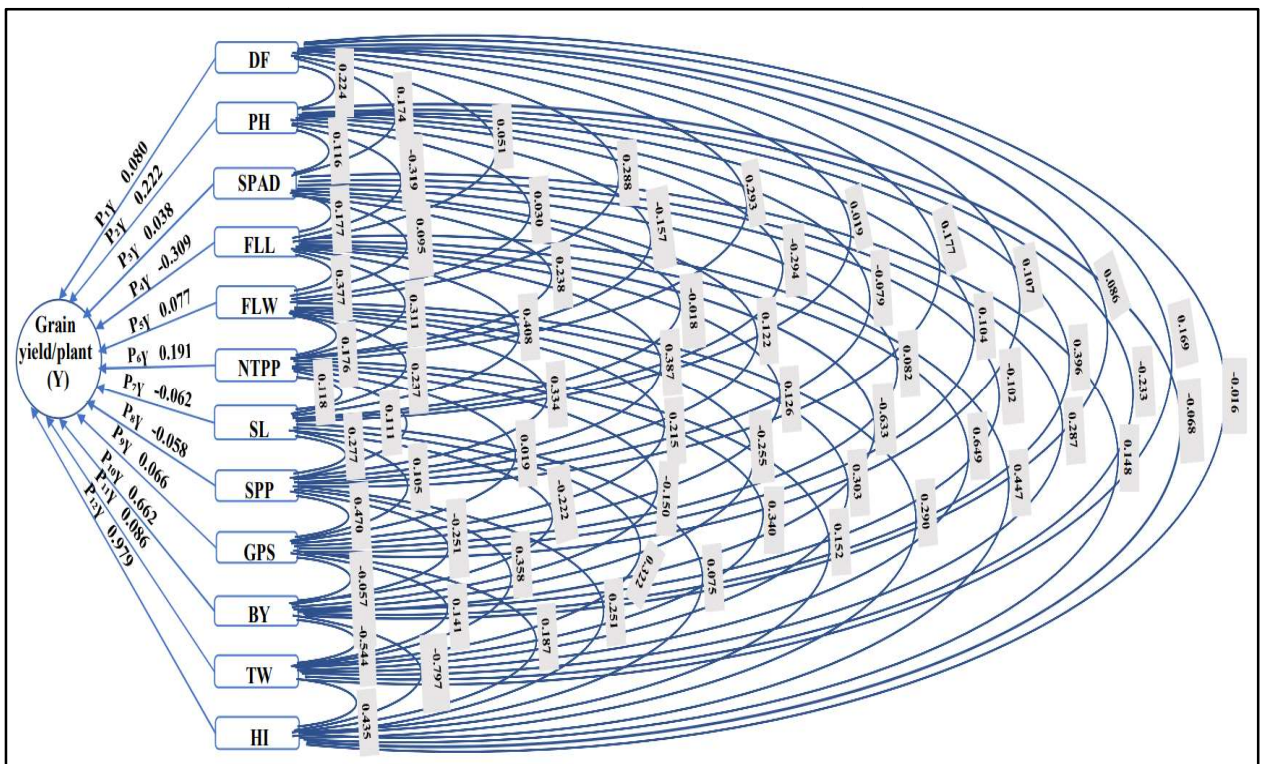


Figure 4.2 Phenotypic path diagram for grain yield per plant

index (-0.666, -0.297), flag leaf width (-0.029, -0.001), no. of spikelet per spike (-0.026, -0.008) and no. of grains per spike (-0.016, -0.003) at both genotypic and phenotypic levels.

In fourth environment E4, it showed positive and direct effect (0.026, 0.024) on grain yield at both genotypic and phenotypic levels. The indirect effects were positive *via* biological yield per plant (0.498, 0.175), flag leaf width (0.021, 0.003), no. of spikelet per spike (0.013, 0.001) and days to 50% flowering (0.012, 0.001) at both genotypic and phenotypic levels. The indirect effects were negative *via* harvest index (-0.819, -0.318), flag leaf length (-0.016, -0.003), no. of grains per spike (-0.008, -0.001), test weight (-0.016, -0.003) and SPAD values (-0.009, -0.001) at both genotypic and phenotypic levels.

In pooled environment this trait showed positive indirect effects on yield through days to 50% flowering (0.141, 0.018), flag leaf length (0.038, 0.097), SPAD values (0.003, 0.004) and no. of spikelet per spike (0.002, 0.005) at both genotypic and phenotypic level. The indirect effects were negative through test weight (-0.322, -0.020), number of tillers per plant (-0.134, -0.030) and harvest index (-0.004, -0.067) at both genotypic and phenotypic level.

SPAD values

In first environment E1, it had positive and direct effect (0.063) at phenotypic level and negative and direct effect (-0.024) at genotypic level on grain yield. The indirect effects were positive *via* harvest index (0.249, 0.151), flag leaf length (0.031, 0.015), days to 50% flowering (0.010, 0.004) and spike length (0.003, 0.001) at both genotypic and phenotypic levels. At genotypic and phenotypic levels it showed negative indirect effects on yield *via* biological yield/plant (-0.162, -0.131) and test weight (-0.023, -0.006) and no. of tillers /plant (-0.021, -0.046).

In second environment E2, it showed positive and direct effect (0.195) at phenotypic level and negative and direct effect (-0.276) at genotypic level on grain yield. The indirect effects were positive *via* no. of spikelet per spike (0.537, 0.035), flag leaf width (0.474, 0.087), biological yield per plant (0.229, 0.085), test weight (0.089, 0.049) and plant height (0.087, 0.001) at both genotypic and phenotypic levels and it showed negative indirect effect *via* flag leaf length (-0.431, -0.115), grains per spike (-0.352, -0.024), harvest index (-0.171, -0.072) at both genotypic and phenotypic levels.

In third environment E3, this trait showed negative and direct effects (-0.414, -0.007) on grain yield at both genotypic and phenotypic levels on yield. It had positive and indirect effect *via* days to 50% flowering (0.136, 0.010), flag leaf width (0.018, 0.001) and harvest index (0.004, 0.058) at both genotypic and phenotypic levels while it had negative indirect effect *via* biological yield (-0.462, -0.144), number of tillers per plant (-0.038, -0.001), spike length (-0.001, -0.003), no. of spikelet per spike (-0.004, -0.007) and no. of grains per spike (-0.001, -0.011) at both genotypic and phenotypic levels.

In fourth environment E4, it showed positive and direct effects (0.046, 0.015) on grain yield at both genotypic and phenotypic levels. It showed positive and indirect effect *via* test weight (0.083, 0.012), harvest index (0.506, 0.241) and flag leaf width (0.035, 0.011) at both genotypic and phenotypic levels while it had negative indirect effect *via* days to 50% flowering (-0.819, -0.005), biological yield (-0.174, -0.034), flag leaf length (-0.090, -0.008), no. of grains per spike (-0.019, -0.002), and plant height (-0.005, -0.001) at both genotypic and phenotypic levels.

In pooled environment this trait exhibited positive and direct effect (1.013, 0.038) on grain yield at both genotypic and phenotypic levels. It showed positive and indirect effect *via* test weight (0.534, 0.025), number of tillers per plant (0.363, 0.045), days to 50% flowering (0.232, 0.014), spike length (0.287, 0.001), harvest index (0.009, 0.145) and plant height (0.005, 0.026) at both genotypic and phenotypic levels while, it had negative and indirect effects *via* flag leaf length (-1.764, -0.055), no. of spikelet per spike (-0.007, -0.007) at both genotypic and phenotypic level.

Flag leaf length (cm)

In first environment E1, it showed positive and direct effect (0.036, 0.067) on grain yield at both genotypic and phenotypic levels. It showed positive and indirect effect *via* harvest index (0.867, 0.503) and days to 50% flowering (0.010, 0.004) at both genotypic and phenotypic levels while, it had negative and indirect effects *via* number of tillers per plant (-0.018, -0.035), biological yield (-0.111, -0.137), test weight (-0.044, -0.011), spike length (-0.007, -0.003) at both genotypic and phenotypic levels.

In second environment E2, it showed positive and direct effect (0.322) at phenotypic level and negative and direct effect (-0.634) at genotypic level on grain yield. It showed positive and indirect effect *via* test weight (0.380, 0.077), biological

yield per plant (0.356, 0.133), days to 50% flowering (0.253, 0.028), no. of spikelet per spike (0.230, 0.011) and flag leaf width (0.080, 0.104) at both genotypic and phenotypic levels while, it had negative and indirect effects *via* harvest index (-0.091, -0.064) and no. of grains per spike (-0.025, -0.002) at both genotypic and phenotypic levels.

In third environment E3, this trait showed negative and direct effect (-0.026) on grain yield at phenotypic level while it showed positive and direct effect (0.087) at genotypic level. The indirect effects were positive *via* plant height (0.038, 0.003) and spike length (0.001, 0.003) while, it showed negative indirect effect *via* harvest index (-0.602, -0.222), SPAD values (-0.162, -0.001), number of tillers per plant (-0.099, -0.011) and flag leaf width (-0.028, -0.001), at both genotypic and phenotypic levels.

In fourth environment E4, it showed negative and direct effects (-0.082, -0.036) on grain yield at both genotypic and phenotypic levels. The indirect effects were positive *via* biological yield (0.237, 0.169), test weight (0.048, 0.011), SPAD values (0.051, 0.004), flag leaf width (0.021, 0.012), plant height (0.005, 0.002) and spike length (0.001, 0.003) while, it showed negative indirect effect *via* harvest index (-0.301, -0.096), no. of grains per spike (-0.031, -0.001) and days to 50% flowering (-0.016, -0.001) at both genotypic and phenotypic levels.

In pooled environment, this trait revealed negative direct effects (-3.973, -0.309) on grain yield at both genotypic and phenotypic levels. Positive indirect effects were shown through test weight (0.828, 0.056), SPAD values (0.450, 0.007), number of tillers per plant (0.306, 0.059), days to 50% flowering (0.037, 0.004) and harvest index (0.020, 0.437) at both genotypic and phenotypic levels while, negative indirect effects were through no. of spikelet per spike (-0.011, -0.023) at both genotypic and phenotypic levels.

Flag leaf width (cm)

In first environment E1, it showed positive direct effect (0.106) at phenotypic level and negative direct effect (-0.020) at genotypic level on grain yield. It showed positive indirect effects through harvest index (0.776, 0.475), flag leaf length (0.033, 0.031) and days to 50% flowering (0.010, 0.003) at both genotypic and phenotypic levels while, negative direct effects were observed through biological yield/ plant (-0.155, -0.182), test weight (-0.016, -0.004), no. of tillers/plant (-0.014, -0.005) and spike length (-0.003, -0.003) at both genotypic and phenotypic levels.

In second environment E2, it showed positive direct effect (0.753, 0.425) on grain yield at both genotypic and phenotypic levels. It showed positive indirect effects through biological yield per plant (0.384, 0.146), no. of spikelet per spike (0.114, 0.043) and test weight (0.092, 0.006) at both genotypic and phenotypic levels while, negative direct effects were through flag leaf length (-0.068, -0.078), harvest index (-0.063, -0.064) and number of grains per spike (-0.052, -0.058) at both genotypic and phenotypic levels.

In third environment E3, this trait showed negative direct effect (-0.056, -0.001) on grain yield on yield at both genotypic and phenotypic levels through biological yield/plant (0.300, 0.334), SPAD values (0.131, 0.001), plant height (0.072, 0.004), no. of grains/ spike (0.005, 0.007) and spike length (0.001, 0.003). whileas, it showed negative indirect effects through harvest index (-0.428, -0.257), days to 50 percent flowering (-0.291, -0.026), no. of tillers/ plant (-0.106, -0.004) and no. of spikelet/ spike (-0.027, -0.013) at both genotypic and phenotypic levels.

In fourth environment E4, it showed positive direct effects (0.043, 0.072) on grain yield at both genotypic and phenotypic levels. It showed positive indirect effects through biological yield (0.614, 0.198), test weight (0.036, 0.008), SPAD values (0.038, 0.002) and plant height (0.012, 0.001) at both genotypic and phenotypic levels while, it showed negative indirect effects through days to 50% flowering (-0.069, -0.012), flag leaf length (-0.040, -0.006) and number of grains per spike (-0.021, -0.001) at both genotypic and phenotypic levels.

In pooled environment, this trait revealed negative direct effect (-1.618) at genotypic level and positive direct effect (0.077) at phenotypic level on grain yield. The positive indirect effects were shown through test weight (0.516, 0.026), SPAD values (0.459, 0.004), days to 50% flowering (0.282, 0.023), number of tillers per plant (0.251, 0.034), plant height (0.163, 0.007) and harvest index (0.017, 0.284) at both genotypic and phenotypic levels whereas, negative indirect effects were mainly shown through flag leaf length (-2.392, -0.117) and spikelet per spike (-0.011, -0.019) at both genotypic and phenotypic levels.

No. of tillers per plant

In first environment E1, it showed negative direct effect (-0.035, -0.113) on grain yield at both genotypic and phenotypic levels. It showed positive indirect effects

through harvest index (0.296, 0.170), biological yield per plant (0.118, 0.132), flag leaf length (0.018, 0.021) and days to 50% flowering (0.012, 0.005) at both genotypic and phenotypic levels while, negative direct effects were through test weight (-0.015, -0.004) and spike length (-0.005, -0.003) at both genotypic and phenotypic levels.

In second environment E2, it showed positive direct effect (0.142) at genotypic level and negative direct effect (-0.009) at phenotypic level on grain yield. Positive indirect effects were shown through spikelet per spike (0.380, 0.062) and biological yield (0.333, 0.123), flag leaf width (0.320, 0.120) and harvest index (0.069, 0.032) at both genotypic and phenotypic levels while negative indirect effects were shown through flag leaf length (-0.339, -0.084) and number of grains per spike (-0.244, -0.043) at both genotypic and phenotypic levels.

In third environment E3, this trait showed negative direct effect (-0.113, -0.028) on grain yield at both genotypic and phenotypic. Positive indirect effects were shown through biological yield (0.308, 0.007), grains per spike (0.044, 0.012) and spike length (0.001, 0.003) at both genotypic and phenotypic levels while negative indirect effects were shown through harvest index (-0.701, -0.092), SPAD values (-0.138, -0.001), days to 50% flowering (-0.115, -0.018), spikelet per spike (-0.052, -0.014) and flag leaf length (-0.052, -0.001) on grain yield at both genotypic and phenotypic levels.

In fourth environment E4, it showed positive direct effects (0.070) on grain yield at genotypic level and negative direct effect (-0.023) at phenotypic level. Positive indirect effects were shown through harvest index (0.200, 0.032), biological yield (0.071, 0.046), test weight (0.045, 0.010), SPAD values (0.040, 0.005) and flag leaf width (0.036, 0.030) on grain yield at both genotypic and phenotypic levels while negative indirect effects were shown through flag leaf length (-0.052, -0.006), days to 50% flowering (-0.020, -0.007) and plant height (-0.010, -0.007) on grain yield at both genotypic and phenotypic levels.

In pooled environment, this trait revealed positive direct effects (0.787, 0.191) on grain yield at both genotypic and phenotypic levels. The positive indirect effects were shown through SPAD values (0.467, 0.009), test weight (0.414, 0.029), days to 50% flowering (0.173, 0.024) and harvest index (0.007, 0.149) on grain yield at both genotypic and phenotypic levels. Negative indirect were shown through flag leaf length

(-1.545, -0.096), plant height (-0.304, -0.035) and spikelet per spike (-0.002, -0.007) on grain yield at both genotypic and phenotypic levels

Spike length (cm)

In first environment E1, it showed negative direct effect (-0.009, -0.014) on grain yield at both genotypic and phenotypic levels, whereas, it showed positive indirect effect through harvest index (0.648, 0.307), biological yield per plant (0.055, 0.179), flag leaf length (0.027, 0.016), days to 50% flowering (0.004, 0.001) on grain yield at both genotypic and phenotypic levels. It showed negative indirect effects on grain yield through no. of tillers/plant (-0.019, -0.028) and test weight (-0.014, -0.004) at both genotypic and phenotypic levels.

In second environment E2, it showed positive direct effect (0.004) on grain yield at phenotypic level and negative direct effect (-0.228) at genotypic level. Positive indirect effects were shown on grain yield *via* flag leaf width (0.668, 0.100), biological yield per plant (0.248, 0.088) and test weight (0.238, 0.067) and negative indirect effects were shown on grain yield *via* flag leaf length (-0.664, -0.095), grains per spike (-0.505, -0.002) and harvest index (-0.070, -0.085) at both genotypic and phenotypic levels.

In third environment E3, this trait showed positive direct effect (0.001, 0.012) on grain yield at both genotypic and phenotypic levels. Grains per spike (0.021, 0.005) and SPAD values (0.010, 0.002) showed positive indirect effect on grain yield at both genotypic and phenotypic level. Test weight (-0.035, -0.001), number of tillers per plant (-0.024, -0.007), flag leaf width (-0.016, -0.001) and spikelet per spike (-0.006, -0.011) showed negative indirect effect on grain yield at both genotypic and phenotypic level.

In fourth environment E4, it showed positive direct effect (0.017) on grain yield at phenotypic level and negative direct effect (-0.024) at genotypic level. Positive indirect effects were shown on grain yield *via* biological yield per plant (0.312, 0.147), test weight (0.051, 0.008), flag leaf width (0.049, 0.013), SPAD values (0.023, 0.005) at both genotypic and phenotypic levels while, negative indirect effects were shown on grain yield *via* number of flag leaf length (-0.045, -0.008), days to 50% flowering (-0.034, -0.005), grains per spike (-0.006, -0.001) and plant height (-0.003, -0.005) at both genotypic and phenotypic levels.

In pooled environment, this trait showed negative direct effect (-0.062) on grain yield at phenotypic level and positive direct effect (2.806) at genotypic level. Positive indirect effects were shown through test weight (0.445, 0.028), number of tillers per plant (0.114, 0.022), days to 50% flowering (0.023, 0.002) and harvest index (0.006, 0.073) on grain yield at both genotypic and phenotypic levels. Negative indirect effects were shown through flag leaf length (-2.915, -0.126), plant height (-0.753, -0.065) and spikelet per spike (-0.012, -0.016) on grain yield at both genotypic and phenotypic levels and grains per spike (-0.129) at genotypic level only.

Number of spikelets per spike

In first environment E1, it showed positive direct effect (0.060) on grain yield at phenotypic level and negative direct effect (-0.021) at genotypic level. This trait showed positive indirect effects on grain yield *via* harvest index (0.625, 0.330), flag leaf length (0.042, 0.036) and days to 50% flowering (0.009, 0.005) at both genotypic and phenotypic levels while, this trait showed negative indirect effects *via* test weight (-0.039, -0.006), number of tillers per plant (-0.025, -0.045) and spikelet per spike (-0.021, 0.060) on grain yield at both genotypic and phenotypic levels.

In second environment E2, it showed positive direct effect (0.729, 0.146) on grain yield at both genotypic and phenotypic levels. This trait showed positive indirect effects on grain yield *via* biological yield per plant (0.263, 0.132), spikelet per spike (0.118, 0.127) and harvest index (0.027, 0.019) at both genotypic and phenotypic levels while, this trait showed negative indirect effects on grain yield *via* grains per spike (-0.398, -0.086), spike length (-0.240, -0.001) and flag leaf length (-0.100, -0.023) at both genotypic and phenotypic levels.

In third environment E3, it showed negative direct effect (-0.054, -0.055) on grain yield at both genotypic and phenotypic levels. This trait showed positive indirect effects *via* biological yield per plant (1.268, 0.458), grains per spike (0.017, 0.046), plant height (0.066, 0.003) and spike length (0.001, 0.002) on grain yield at both genotypic and phenotypic levels while, this trait showed negative indirect effects *via* days to 50% flowering (-0.307, -0.01), harvest index (-1.156, -0.487), number of tillers per plant (-0.109, -0.007), SPAD values (-0.032, -0.001), flag leaf width (-0.027, -0.001) on grain yield at both genotypic and phenotypic levels.

In fourth environment E4, it showed positive direct effect (0.012) on grain yield at phenotypic level and negative direct effect (-0.054) at genotypic level. This trait showed positive indirect effects on grain yield *via* biological yield per plant (0.598, 0.162), test weight (0.055, 0.012), flag leaf width (0.039, 0.020), SPAD values (0.031, 0.001) at both genotypic and phenotypic levels while, this trait showed negative indirect effects on grain yield *via* flag leaf length (-0.056, -0.006), grains per spike (-0.028, -0.002) and days to 50% flowering (-0.022, -0.009) at both genotypic and phenotypic levels.

In pooled environment, this trait showed negative direct effect (-0.016, -0.058) on grain yield at both genotypic and phenotypic levels. This trait showed positive indirect effects *via* test weight (0.646, 0.031), SPAD values (0.414, 0.005), days to 50% flowering (0.119, 0.014), number of tillers per plant (0.105, 0.022) and harvest index (0.016, 0.246) at both genotypic and phenotypic levels while, this trait showed negative indirect effects *via* flag leaf length (-2.829, -0.120) and plant height (-0.227, -0.018) on grain yield at both genotypic and phenotypic levels.

Number of grains per spike

In first environment E1, it showed positive direct effect (0.104) on grain yield at genotypic level and negative direct effect (-0.020) at phenotypic level. Positive indirect effects were shown through harvest index (0.877, 0.443), flag leaf length (0.044, 0.030) and days to 50% flowering (0.011, 0.002) at both genotypic and phenotypic levels. The characters no. of tillers/plant (-0.016, -0.036), spike length (-0.006, -0.005) and test weight (-0.040, -0.006) had negative indirect effects on grain yield on grain yield at genotypic and phenotypic levels.

In second environment E2, it showed negative direct effect (-0.668, -0.208) on grain yield at both genotypic and phenotypic levels. Positive direct effects were shown through spikelet per spike (0.434, 0.060), biological yield per plant (0.242, 0.077), flag leaf width (0.058, 0.120) on grain yield at both genotypic and phenotypic levels while, negative indirect effects were shown through harvest index (-0.042, -0.037), flag leaf length (-0.024, -0.003) and test weight (-0.021, -0.045) on grain yield at both genotypic and phenotypic levels.

In third environment E3, it showed positive direct effect (0.036, 0.104) on grain yield at both genotypic and phenotypic levels. Positive indirect effects were shown

through biological yield per plant (1.811, 0.468), SPAD values (0.100, 0.001), flag leaf length (0.006, 0.001), spike length (0.001, 0.001) on grain yield at both genotypic and phenotypic levels. Negative indirect effects were shown through harvest index (-0.642, -0.231), days to 50% flowering (-0.153, -0.001), number of tillers per plant (-0.136, -0.003), plant height (-0.060, -0.001), spikelet per spike (-0.026, -0.024), flag leaf width (-0.008, -0.001) on grain yield at both genotypic and phenotypic levels.

In fourth environment E4, it showed negative direct effects (-0.037, -0.007) on grain yield at both genotypic and phenotypic levels. Positive indirect effects were shown through biological yield per plant (0.551, 0.150), harvest index (0.313, 0.079), test weight (0.043, 0.005), flag leaf width (0.025, 0.004), SPAD values (0.024, 0.004), number of tillers per plant (0.006, 0.001) and plant height (0.005, 0.001) on grain yield at both genotypic and phenotypic levels. Negative indirect effects were shown through flag leaf length (-0.067, -0.003) and days to 50% flowering (-0.030, -0.001) on grain yield at both genotypic and phenotypic levels.

In pooled environment, this trait showed positive direct effect (0.066) at phenotypic level and negative direct effect (-0.359) on grain yield at genotypic level. Positive indirect effects were shown through SPAD values (0.487, 0.003), test weight (0.404, 0.012), plant height (0.366, 0.023), days to 50% flowering (0.211, 0.009) and harvest index (0.014, 0.183) at both genotypic and phenotypic levels while, negative indirect effects were shown through flag leaf width (-1.266, -0.039) and spikelet per spike (-0.009, -0.027) on grain yield at both genotypic and phenotypic levels.

Biological yield per plant (g)

In first environment E1, it showed positive direct effect (0.384, 0.618) on grain yield at both genotypic and phenotypic levels. Positive indirect effects were shown by test weight (0.013, 0.004) and spikelet per spike (0.003, 0.001) while, negative indirect effects were shown through harvest index (-0.192, -0.316), grains per spike (-0.034, -0.001), number of tillers per plant (-0.011, -0.026), flag leaf length (-0.010, -0.016), days to 50% flowering (-0.005, -0.002) and spike length (-0.001, -0.004) on grain yield at both genotypic and phenotypic levels.

In second environment E2, it showed positive direct effect (0.457, 0.371) on grain yield at both genotypic and phenotypic levels. The positive indirect effects were primarily shown through flag leaf width (0.633, 0.171), spikelet per spike (0.419, 0.052)

and test weight (0.045, 0.014) on grain yield at both genotypic and phenotypic levels while, negative indirect effects were shown through flag leaf length (-0.493, -0.115), number of grains per spike (-0.354, -0.044) and harvest index (-0.060, -0.101) on grain yield at both genotypic and phenotypic levels.

In third environment E3, it showed positive direct effect (0.592, 0.250) on grain yield at both genotypic and phenotypic levels. Positive indirect effects were shown through SPAD values (0.120, 0.001), number of grains per spike (0.041, 0.039), plant height (0.027, 0.004) and flag leaf length (0.005, 0.002) while, negative indirect effects were shown through harvest index (-1.145, -0.823), days to 50% flowering (-0.337, -0.021), number of tillers per plant (-0.093, -0.001), spikelet per spike (-0.043, -0.020) and flag leaf width (-0.011, -0.001) on grain yield at both genotypic and phenotypic levels.

In fourth environment E4, it showed positive direct effect (0.328, 0.486) on grain yield at both genotypic and phenotypic levels. Flag leaf width (0.026, 0.018), plant height (0.013, 0.005) and test weight (0.003, 0.0010) showed positive indirect effects while, harvest index (-0.969, -0.766), number of grains per spike (-0.020, -0.001), flag leaf length (-0.019, -0.008), days to 50% flowering (-0.018, -0.004) and SPAD values (-0.008, -0.001) showed negative indirect effects on grain yield at both genotypic and phenotypic levels.

In pooled environment, this trait showed positive direct effect (0.662) on grain yield at phenotypic level and negative direct effect (-2.604) on grain yield at genotypic level. Flag leaf length (2.948, 0.196), plant height (0.882, 0.088), days to 50% flowering (0.060, 0.007) and spikelet per spike (0.006, 0.015) showed positive direct effects on grain yield at both genotypic and phenotypic levels. Test weight (-0.595, -0.047), SPAD values (-0.197, -0.004), number of tillers per plant (-0.116, -0.029) and harvest index (-0.031, -0.780) showed negative indirect effect on grain yield at both genotypic and phenotypic levels.

Test weight (g)

In first environment E1, it showed negative direct effects (-0.051, -0.020) on grain yield at both genotypic and phenotypic levels. Positive indirect effect was shown through harvest index (0.435, 0.352), flag leaf length (0.030, 0.038) and days to 50% flowering (0.008, 0.004) on grain yield at both genotypic and phenotypic levels.

Whereas, negative indirect effect was observed via biological yield (-0.098, -0.109), number of tillers/plant (-0.011, -0.023) and spike length (-0.002, -0.003) on grain yield at genotypic and phenotypic levels.

In second environment E2, it showed positive direct effect (0.387, 0.178) on grain yield at both genotypic and phenotypic levels. Harvest index (-0.099, -0.129) showed negative indirect effect on grain yield at both genotypic and phenotypic levels. Positive indirect effect was shown through flag leaf width (0.178, 0.013), biological yield/ plant (0.053, 0.029), no. of grains/ spike (0.037, 0.053) and no. of tillers/ plant (0.013, 0.001) on grain yield at both genotypic and phenotypic levels. Negative indirect effect was shown through flag leaf length (0.178, 0.013) and harvest index (-0.099, -0.129) on grain yield at both genotypic and phenotypic levels.

In third environment E3, this trait showed positive direct effect (0.279) on grain yield at genotypic level while negative direct effect (-0.020) on grain yield at phenotypic level. Positive indirect effect was shown through biological yield/ plant (0.753, 0.202) and no. of grains/ spike (0.100, 0.015) on grain yield at both genotypic and phenotypic levels while, negative indirect effect was shown through harvest index (-0.474, -0.142), days to 50% flowering (-0.094, -0.005), number of tillers per plant (-0.073, -0.012), spikelet per spike (-0.027, -0.013) SPAD values (-0.250, -0.001) and flag leaf width (-0.010, -0.001) on grain yield at both genotypic and phenotypic levels.

In fourth environment E4, it showed positive direct effect (0.080, 0.026) on grain yield at both genotypic and phenotypic levels. Positive indirect effect was shown through harvest index (0.276, 0.200), SPAD values (0.048, 0.007), biological yield per plant (0.032, 0.026) and flag leaf width (0.020, 0.020) on grain yield at both genotypic and phenotypic levels while, negative indirect effect was shown through flag leaf length (-0.050, -0.014), days to 50% flowering (-0.030, -0.007), number of grains per spike (-0.020, -0.001) and plant height (-0.005, -0.003) on grain yield at both genotypic and phenotypic levels.

In pooled environment, this trait showed positive direct effect (1.013, 0.086) on grain yield at both genotypic and phenotypic levels. SPAD values (0.534, 0.011), number of tillers per plant (0.321, 0.065), days to 50% flowering (0.134, 0.014) and harvest index showed positive indirect effect on grain yield at both genotypic and phenotypic levels while, negative indirect effect on grain yield was shown through flag

leaf length (-3.250, -0.201), plant height (-0.566, -0.052) and spikelet per spike (-0.010, -0.021) at both genotypic and phenotypic levels.

Harvest index (%)

In first environment E1, this trait showed positive direct effect (0.911, 0.806) on grain yield at both genotypic and phenotypic levels. This trait showed positive indirect effects on grain yield *via* flag leaf length (0.034, 0.033) and days to 50% flowering (0.008, 0.003) at both genotypic and phenotypic levels. This trait showed negative indirect effects on grain yield *via* biological yield/ plant (-0.081, -0.183), test weight (-0.025, -0.007), no. of tillers/ plant (-0.012, -0.019) and spike length (-0.006, -0.004) at genotypic and phenotypic levels.

In second environment E2, it showed positive direct effect (0.253, 0.481) on grain yield at both genotypic and phenotypic levels. This trait showed positive indirect effects on grain yield *via* flag leaf length (0.226, 0.043), number of grains per spike (0.112, 0.016) and spikelet per spike (0.079, 0.006) at both genotypic and phenotypic levels. This trait showed negative indirect effects on grain yield *via* flag leaf width (-0.186, -0.058), test weight (-0.152, -0.048) and biological yield per plant (-0.108, -0.078) at both genotypic and phenotypic levels.

In third environment E3, this trait showed positive direct effect (0.480, 0.155) on grain yield at both genotypic and phenotypic levels. This trait showed positive indirect effects on grain yield *via* days to 50% flowering (0.190, 0.015), number of tillers per plant (0.053, 0.002), spikelet per spike (0.042, 0.023) and flag leaf width (0.016, 0.001). This trait showed negative indirect effects on grain yield *via* biological yield/ plant (-1.231, -0.891), plant height (-0.062, -0.005), no. of grains/ spike (-0.016, -0.021) and SPAD values (-0.001, -0.004) at both genotypic and phenotypic levels.

In fourth environment E4, this trait showed positive direct effect (0.409, 0.241) on grain yield at both genotypic and phenotypic levels. This trait showed positive indirect effects on grain yield *via* flag leaf length (0.018, 0.003), SPAD values (0.017, 0.003), test weight (0.016, 0.004) and spikelets per spike (0.012, 0.001) at both genotypic and phenotypic levels while, this trait showed negative indirect effects on grain yield *via* biological yield per plant (-0.707, -0.484), days to 50% flowering (-0.016, -0.004), plant height (-0.015, -0.006) and number of grains per spike (-0.008, -0.001) at both genotypic and phenotypic levels.

In pooled environment, this trait showed positive direct effect (1.891, 0.979) on grain yield at both genotypic and phenotypic levels. This trait showed positive indirect effects on grain yield *via* test weight (0.486, 0.038), flag leaf length (0.227, 0.006) and number of tillers per plant (0.139, 0.029) at both genotypic and phenotypic levels while, this trait showed negative indirect effects on grain yield *via* flag leaf length (-2.084, -0.138), plant height (-0.161, -0.015) and spikelet per spike (-0.007, -0.015) at both genotypic and phenotypic levels.

4.5 Stability analysis studies

The performance with changing environmental factors within a given location is referred to as stability. It consists of two steps: analysis of variance over environments and pooled analysis of variance. Knowledge of G x E interaction is important for successful crop improvement. If the G x E interaction is found to be significant for the given characters, then further stability analysis can be performed. Stability analysis was carried out as per model given by Eberhart and Russell (1966). According to this model, a stable variety is the one which has regression coefficient (*b*) equal to unity ($b=1$) and deviation from regression is minimum ($S^2 di = 0$). A genotype with significant *b* value ($b>1$) is said to be a highly responsive-suitable for favourable environments and with *b* value ($b<1$) is said to be low responsive-suitable for unfavourable environments.

4.5.1 Joint regression analysis of variance (Eberhart and Russell's (1966) stability model)

The analysis of variance of Eberhart and Russell's model for stability is presented in Table 4.5. In the joint regression analysis, mean squares due to genotypes was found for all the characters except flag leaf length, no. of grains per spike and harvest index indicating sufficient variability among genotypes. The environments showed significant differences among all the characters. The genotype x environment interaction component showed significant differences among all the characters except flag leaf width, number of tillers per plant. Environment (linear) showed significant differences among all the characters except no. of spikelets per spike. Genotype x environment (linear) interaction showed significant differences among all the characters except days to 50% flowering, SPAD values, flag leaf length, biological yield per plant and harvest index. Pooled deviation of mean sum of squares was tested

against pooled error and was highly significant for almost all the characters except spikelet per spike and no. of grains per spike indicating the importance of non-linear component in the genotype x environment interaction.

4.5.2 Stability parameters

The results related to stability parameters is presented in Table. 4.5.1.

Days to 50% flowering

The mean values for this trait ranged from 74 (BH-959) days to 83 (RD-2592) days with a general mean value of 79.27. The regression coefficient values ranged from -0.18 (BH-959) to 2.58 (RD-2907). The S^2d_i values of genotypes RD-2052(8.63), RD-2592(7.97), RD-2715(4.78), RD-2794(18.46), RD-2907(18.37), BH-902(17.93), BH-946(4.82), BHS-400(11.04), VLB-118(9.94) were significantly deviated from zero. The regression coefficient was found non-significant for all the genotypes. Genotype LOCAL had shown low mean value along with non-significant regression coefficient nearing unity was found to be stable and desirable. Genotypes BHS-380 and BH-959 showed low mean values with regression coefficient less than unity and were found to be stable under low performing environmental conditions. Genotype RD-2849 had higher mean than general mean and regression coefficient greater than unity is stable for high performing environment.

Plant height(cm)

The mean values for this trait ranged from 78.01cm (BH-959) to 91.05cm (BHS-400) with a general mean value of 86.91. The regression coefficient ranged from 0.09 (BH-946) to 1.37 (BHS-400). The S^2d_i values of genotypes RD-2035(28.22), RD-2052(31.31), RD-2552(18.30), BH-902(18.41), were significantly deviated from zero. The regression coefficient values were found non-significant for genotypes RD-2035(0.92), RD-2052(0.27), RD-2552(1.1) and BH-902(1.77). Genotypes BHS-352, VLB-118, BHS-380 had shown high mean value along with non-significant regression coefficient nearing unity and were found to be stable and desirable. Genotypes RD-2907, LOCAL, BHS-400, exhibited higher mean values along with regression coefficient values greater than unity were found stable for favourable environment. Genotypes RD-2794 and BH-946 exhibited higher mean values along with regression coefficient values lower than unity were found stable for unfavourable environment.

Table 4.5. Joint regression analysis for yield and contributing traits under different environments (Eberhart and Russell Model, 1966)

Source of variation	d.f.	Days to 50% flowering	Plant height (cm)	SPAD values	Flag leaf length (cm)	Flag leaf width (cm)	Tillers/plant	Spike length (cm)	No. spikelets/spike (cm)	No. of grains/spike	Biological yield/plant (g)	Grain yield/plant (cm)	Test weight (cm)	Harvest index(%)
Genotypes	16	32.15**	49.2**	29.43**	8.67	0.09*	4.97*	1.42*	8.07**	21.20	0.63**	0.109*	58.85**	22.88
Environments	3	124.98**	2933.4**	52.65*	504.7**	0.08*	312.25*	9.50**	57.82**	110.78	85.49**	2.470*	1284.30*	65552.63**
G x E	48	17.12**	26.24**	15.23**	7.33**	0.02	2.67	0.75**	3.16*	47.52**	0.28*	0.028*	53.97**	89.98**
E+ G x E	51	10.95	73.55**	7.35	12.20	0.03*	6.75**	0.46	2.64	17.39	1.75**	0.086*	41.66**	153.9**
E(linear)	1	132.82**	2919.48*	49.55*	500.88*	0.20**	313.4**	8.66**	56.21	127.60*	84.67**	2.416*	1292.69*	6481.9**
G x E(linear)	16	5.77	30.14*	4.81	3.14	0.03*	2.82*	1.50*	3.73*	22.27*	0.08	0.098*	33.10**	14.70
Pooled deviation	34	9.95**	15.28*	7.35**	4.97**	0.01*	1.44**	0.61**	1.61	11.29	0.09*	0.050*	9.82**	35.43**
Pooled error	136	3.59	9.51	3.10	1.17	0.01	1.31	0.11	1.14	8.18	0.05	0.020	2.47	1.88

*, ** significant at 5% and 1% level, respectively

Table 4.5.1 Stability parameters of different traits (Eberhart and Russell,1966)

S. No.	Genotypes	Days to 50% flowering			Plant height (cm)			SPAD values			Flag leaf length(cm)		
		\bar{X}	(bi)	S ² di	\bar{X}	(bi)	S ² di	\bar{X}	(bi)	S ² di	\bar{X}	(bi)	S ² di
1	RD-2035	83.08	1.15	-3.57	87.3	0.92	28.22*	51.06	0.98*	-2.65	21.32	0.86*	0.07
2	RD-2052	79.50	1.13	8.63*	83.01	0.27	31.31*	40.15	0.92	11.52**	18.62	1.02*	0.16
3	RD-2552	81.25	0.94	0.66	86.22	1.1	18.30*	38.10	0.81	-2.4	18.41	1.52*	-0.99
4	RD-2592	83.15	0.55	7.97*	89.24	0.69*	-9.01	39.91	-1.29	14.17**	17.63	1.21	2.66*
5	RD-2715	80.92	1.59	4.78*	84.83	0.87*	9.65	39.49	0.723	6.95*	17.3	1.26*	1.16
6	RD-2794	79.08	2.48	18.46**	87.92	0.90*	11.62	38.53	-0.05	6.41*	17.86	1.22*	-0.59
7	RD-2849	80.42	1.13	1.33	85.94	0.97*	-9.82	40.24	2.85**	1.15	18.65	1.39*	-0.73
8	RD-2899	80.00	0.04	2.99	83.69	0.45*	-8.61	37.78	0.62	-2.72	20.33	0.87	4.15*
9	RD-2907	76.50	2.58	18.37**	90.23	1.25*	-6.66	36.28	0.65	-0.21	18.83	1.07	1.65*
10	LOCAL	78.25	0.81*	0.11	87.52	1.21*	4.1	39.58	3.28	-2.01	17.54	0.601	0.55
11	BH-902	79.25	1.49	17.93**	83.51	1.77	18.41*	39.01	2.02	1.12	16.97	0.65**	0.2
12	BH-946	77.67	1.71	4.82*	87.65	0.09*	0.03	37.87	2.62	1.14	17.64	1.11*	-1.05
13	BHS-352	83.00	0.13	3.54	90.59	1.07*	5.84	50.27	1.62	1.41	21.2	1.12*	0.37
14	BHS-400	80.25	1.00	11.04*	91.05	1.37*	-5.09	39.53	1.35	-0.08	19.53	1.22	3.64*
15	VLB-118	77.75	0.68	9.94*	90.48	1.04*	-3.41	37.89	-1.53	2.4	19.56	0.85	3.09*
16	BHS-380	75.42	-0.25	0.87	90.23	1.03*	-0.75	37.38	0.38	22.67**	16.55	0.16	-0.93
17	BH-959	74.25	-0.18	-2.01	78.01	0.971*	3.21	38.73	1.05	9.61*	16.32	0.78*	0.48
	Total	1349.74			1477.42			681.8			314.26		
	General mean	79.40			86.91			40.11			18.46		
	SE±m	1.18			1.73			1.03			0.66		

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S. No.	Genotypes	Flag leaf width(cm)			No. of tillers/plant			Spike length(cm)		
		\bar{X}	(bi)	S ² di	\bar{X}	(bi)	S ² di	\bar{X}	(bi)	S ² di
1	RD-2035	1.17	1.43	0.03	10.75	0.77	0.54*	7.91	-0.56	-0.08
2	RD-2052	1.01	0.8	-0.02	9.92	0.98*	0.26	6.89	1.92*	-0.07
3	RD-2552	1.03	0.45	-0.02	8.33	0.57**	0.23	6.9	1.37	-0.03
4	RD-2592	1.11	1.06	0.08*	9.92	0.80*	0.12	6.58	1.14	0.03
5	RD-2715	1.04	0.53	0.05	8.5	1.32*	-0.38	7.06	0.38	-0.1
6	RD-2794	1.07	1.46*	-0.04	9.17	0.99*	-0.01	6.82	0.64	0.14
7	RD-2849	1	2.34	0.03	9	1.04	0.43	6.89	2.78**	0.14
8	RD-2899	0.99	1.87	0.01	8.75	0.97	1.37*	7.01	1.14	0.98**
9	RD-2907	1.05	1.96*	-0.04	8.08	1.12	0.08	7.03	0.66	0.24*
10	LOCAL	1.08	1.2	-0.03	8.17	1.18*	-0.22	7.01	0.86	-0.01
11	BH-902	1.08	1.57	-0.04	9.08	1.03	0.12	6.69	1.32	0.05
12	BH-946	1.11	1.88	0.04	8.5	0.84*	0.03	7.1	0.82	-0.04
13	BHS-352	1.16	-0.78	-0.02	11	1.13	0.42	7.5	2.23 **	0.12
14	BHS-400	1.1	-0.73*	-0.04	9.84	1.02	-0.02	7.12	2.29*	-0.07
15	VLB-118	1.03	0.58	0.01	9.67	1.2	-0.12	7.07	0.09	0.03
16	BHS-380	0.93	1.10**	-0.04	8.33	1.23	0.29	6.59	0.98	0.04
17	BH-959	0.81	0.24	0.02	8.09	0.85	-0.28	6.78	-1.04	0.1
	Total	17.77			151.1			118.95		
	General mean	1.05			9.25			7		
	SE±m	0.04			0.44			0.21		

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S. No.	Genotypes	No. of Spikelet/spike			No. of Grains/spike			Biological yield/plant(g)		
		\bar{X}	(bi)	S ² di	\bar{X}	(bi)	S ² di	\bar{X}	(bi)	S ² di
1	RD-2035	20.42	1.08	0.10	56.92	2.69	3.84	89.91	1.06	0.03*
2	RD-2052	17.75	1.33	-0.45	52.25	0.89	-7.08	78.50	0.77	0.05**
3	RD-2552	18.92	2.08	2.56*	50.67	1.10	12.68*	68.82	1.03	0.02*
4	RD-2592	17.67	1.55	0.50	52.75	4.03	0.66	68.91	0.98	0.05**
5	RD-2715	17.67	1.36*	-1.15	51.25	0.63	-3.68	67.69	0.84	0.18**
6	RD-2794	17.58	-0.39	2.01*	51.92	1.58*	-8.24	68.69	0.94	0.07**
7	RD-2849	17.25	1.73**	-0.57	51.67	2.19	22.02*	64.57	0.76	0.25**
8	RD-2899	17.58	0.59	-0.98	54.58	-0.13	-5.95	70.17	1.14	0.10**
9	RD-2907	16.75	1.28**	-0.77	49.17	1.78	32.01**	68.42	1.09*	0.01
10	LOCAL	16.33	0.31	-1.11	49.84	-1.48	6.19	70.37	1.07	0.38**
11	BH-902	17.50	0.75	7.48**	51.42	-1.53	-0.28	70.10	1.22*	0.01
12	BH-946	16.10	1.18*	-0.54	52.08	2.93*	-6.70	72.17	0.94*	0.01
13	BHS-352	20.50	0.78	0.05	54.17	0.81	-4.64	63.66	1.11	0.09**
14	BHS-400	19.09	1.59**	-0.47	52.42	-1.69	15.92*	66.77	1.03	0.08**
15	VLB-118	17.00	1.67	0.28	52.25	0.62	0.42	66.60	1.00	0.02*
16	BHS-380	16.33	-0.03	-0.89	48.59	-0.18	27.20*	53.89	1.03	0.05**
17	BH-959	15.42	0.14	0.01	47.08	1.58	1.49	51.10	0.89	0.11**
	Total	300.75			878.10			1160.31		
	General mean	17.697			51.710			68.25		
	SE±m	0.59			1.59			3.93		

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S. No.	Genotypes	Grain yield/plant (g)			Test weight (g)			Harvest index (%)		
		\bar{X}	(bi)	S ² di	\bar{X}	(bi)	S ² di	\bar{X}	(bi)	S ² di
1	RD-2035	30.32	0.95	0.00	52.40	0.57	18.50**	33.39	1.06	71.89**
2	RD-2052	26.35	1.04	0.01**	51.29	0.60	14.73**	29.09	0.70	45.17**
3	RD-2552	20.18	1.08	0.02**	47.52	1.43	4.35*	32.28	0.77	71.69**
4	RD-2592	22.07	1.60*	0.00	42.57	1.11	6.07*	26.61	1.19	4.15*
5	RD-2715	18.33	1.14	0.01**	46.11	1.79	8.90**	32.08	0.55	10.97**
6	RD-2794	22.22	1.19*	-0.00	49.02	0.85**	3.00	30.96	0.88*	-1.69
7	RD-2849	22.23	1.03*	-0.00	48.33	0.66	5.74*	35.36	0.92	15.87**
8	RD-2899	23.89	0.78*	0.00	49.34	1.84*	-0.20	28.22	1.26*	-0.96
9	RD-2907	18.09	1.16	0.03**	46.44	1.64	4.05*	25.93	1.25	16.41**
10	LOCAL	17.58	0.88	0.10**	41.56	0.31	4.82*	31.55	1.12	40.50**
11	BH-902	22.19	0.98	0.00	43.34	1.17	21.98**	29.30	1.01	22.55**
12	BH-946	22.86	1.19*	0.00	43.98	1.22	4.28*	38.99	1.01	9.67**
13	BHS-352	24.99	0.60	0.02**	51.80	1.46	7.52*	30.98	1.15	69.70**
14	BHS-400	20.01	0.50	0.01**	43.22	0.35	7.52*	33.18	0.92	13.35**
15	VLB-118	20.77	1.19	0.00*	47.87	1.06*	-1.95	32.54	1.10	5.58*
16	BHS-380	16.58	0.95	-0.00	40.78	-0.67	4.53*	30.19	1.14	59.27**
17	BH-959	15.60	0.74	0.01**	40.79	1.61*	0.59	534.55	0.97	69.09**
	Total	364.23			786.36			31.44		
	General mean	21.43			46.26			33.39		
	SE±m	1.53			1.36			2.17		

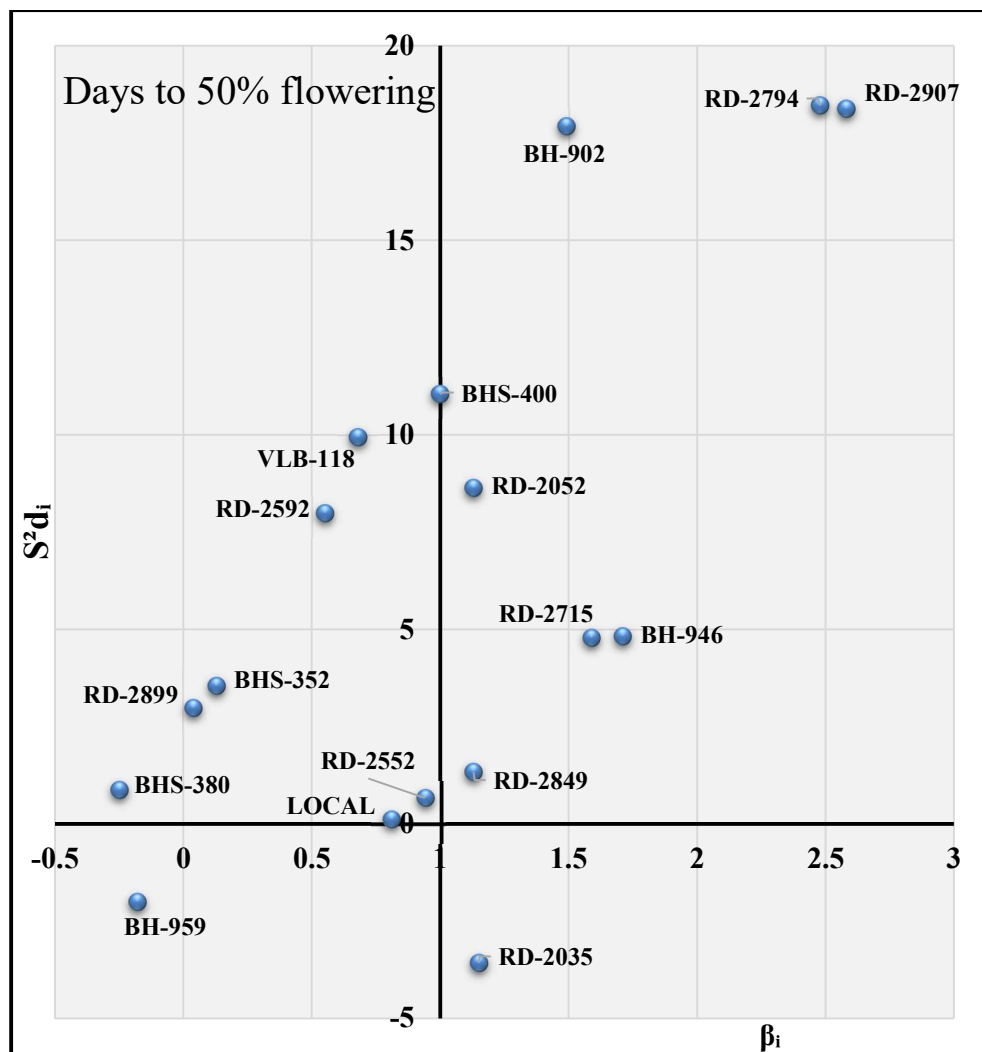


Figure 4.3 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for days to 50% flowering

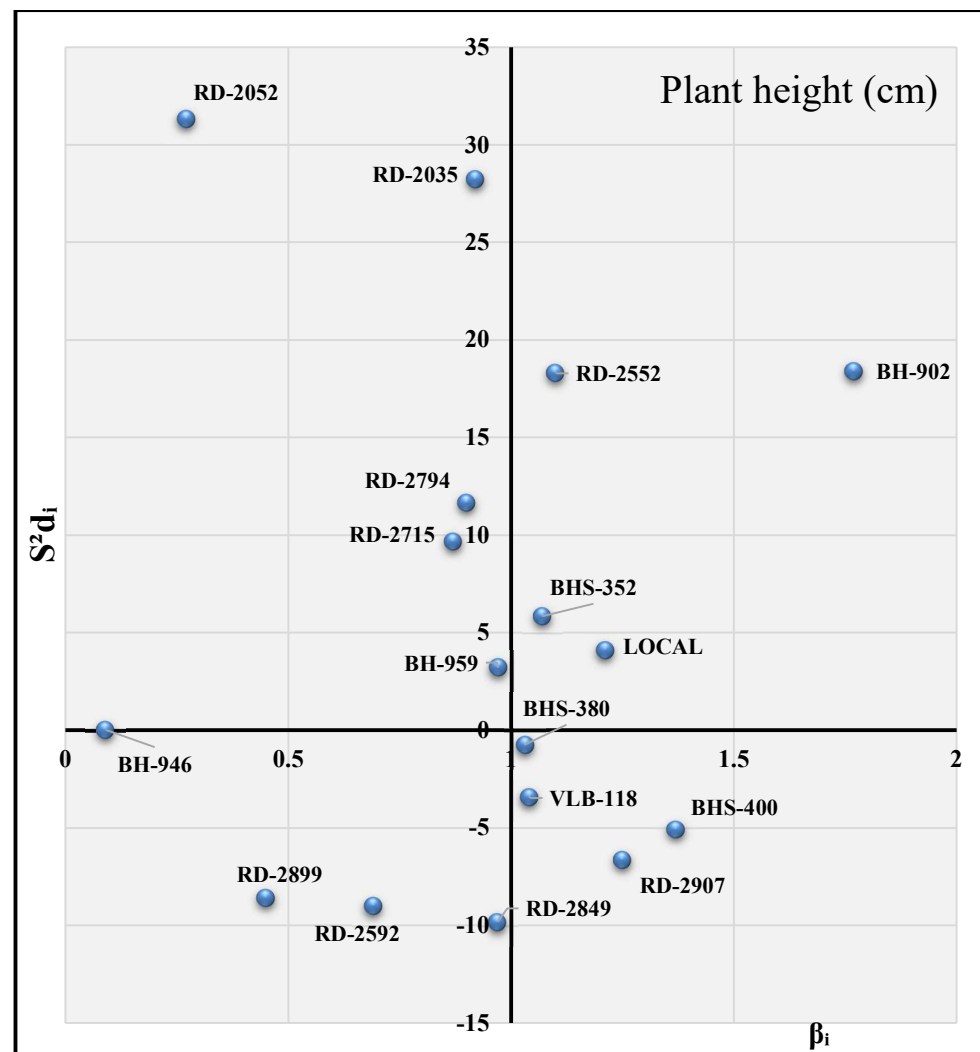


Figure 4.4 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for plant height (cm)

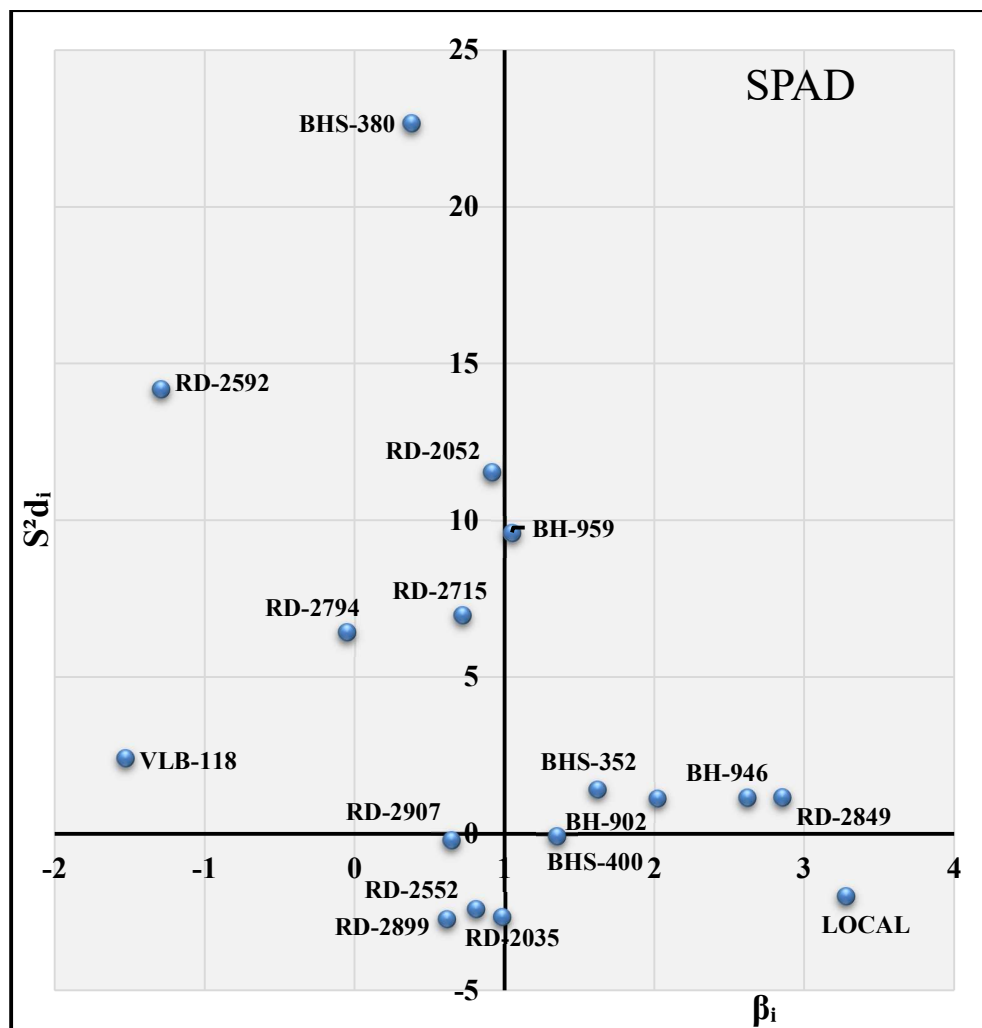


Figure 4.5 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for SPAD values

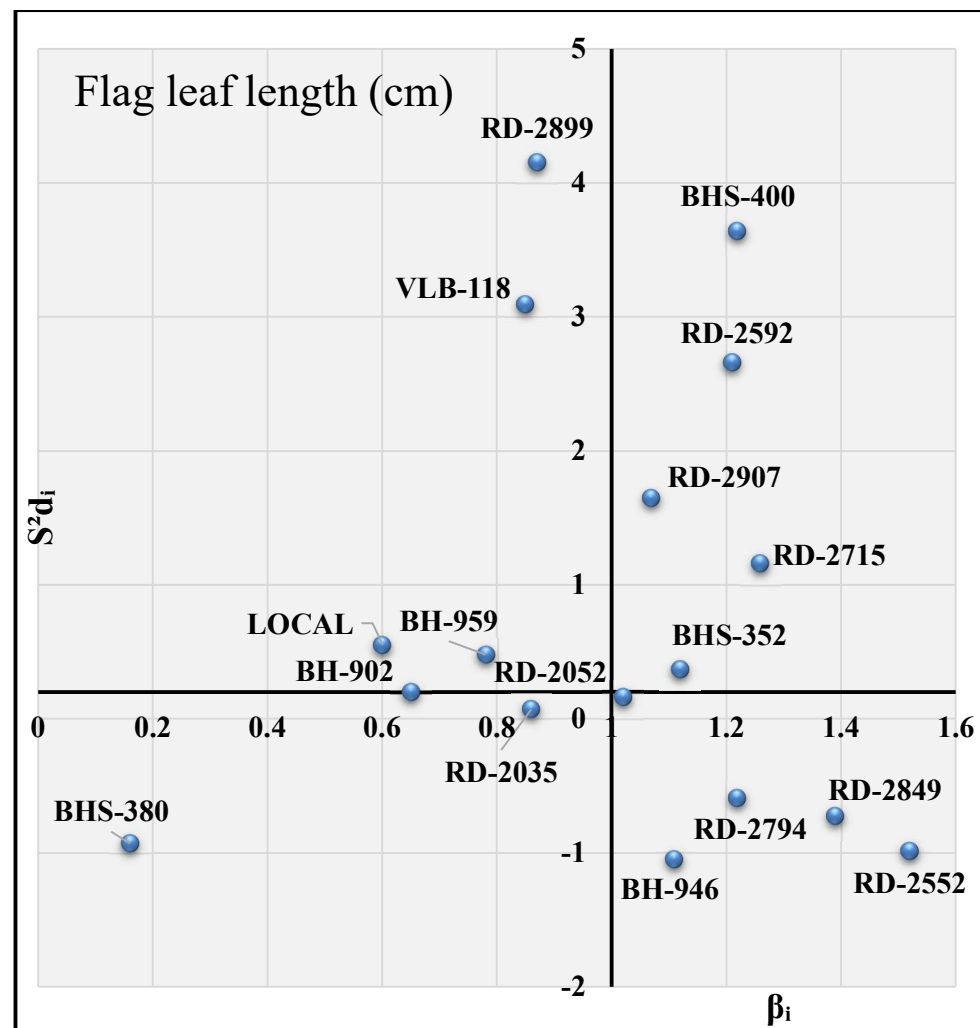


Figure 4.6 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for flag leaf length (cm)

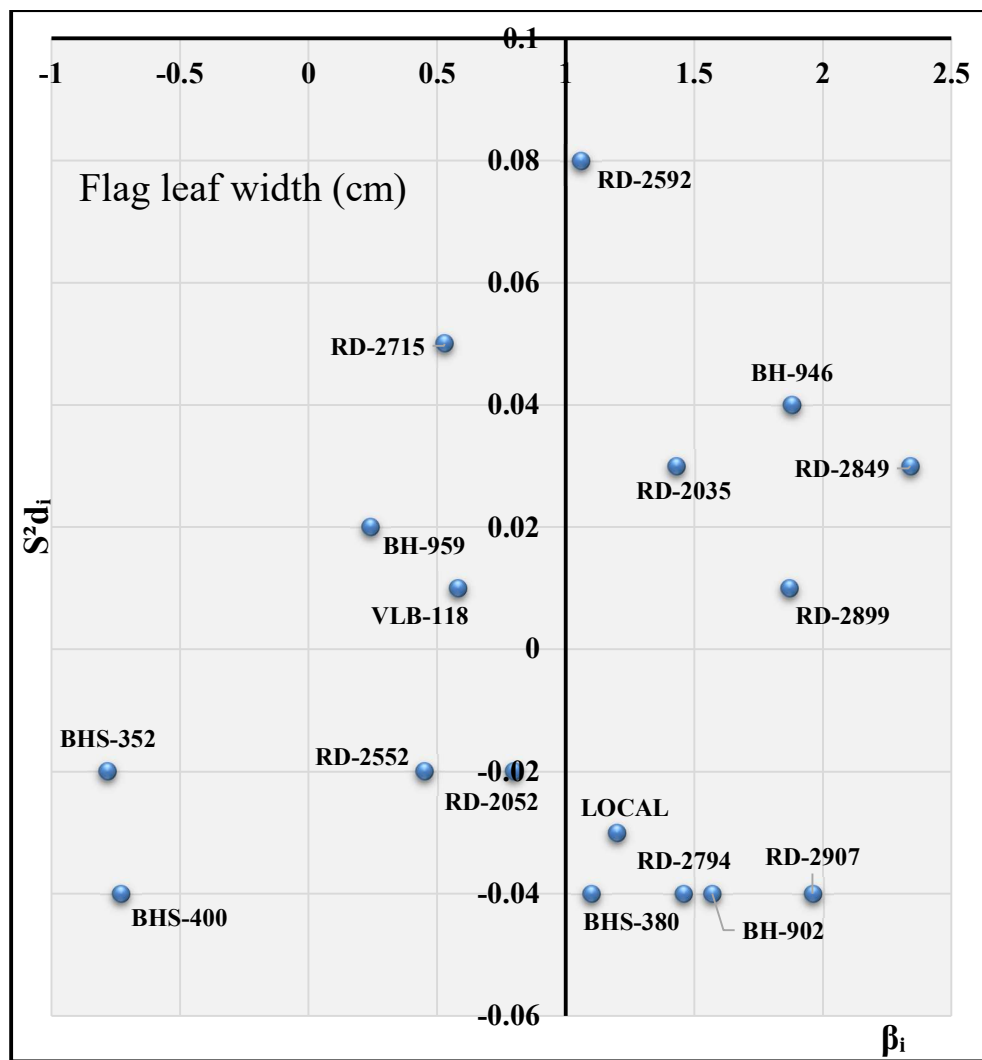


Figure 4.7 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for flag leaf width (cm)

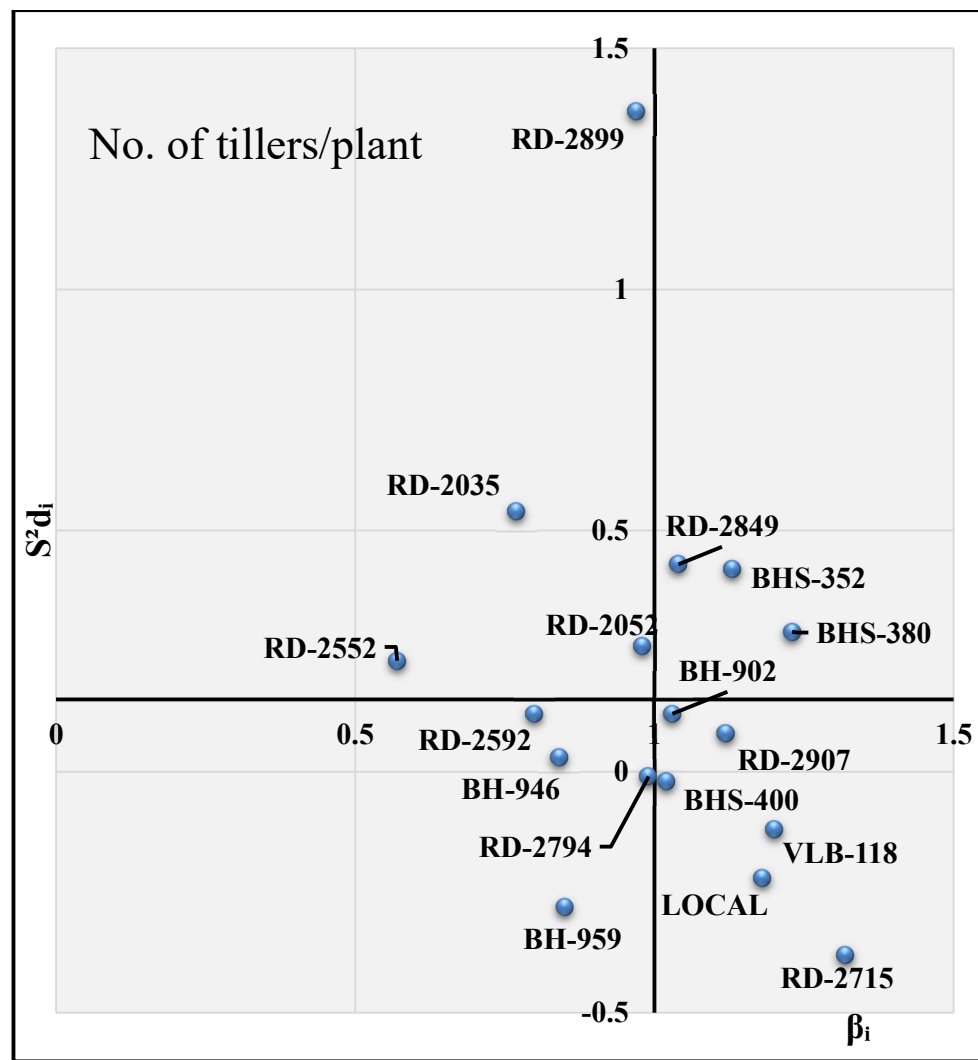


Figure 4.8 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for number of tillers/plant

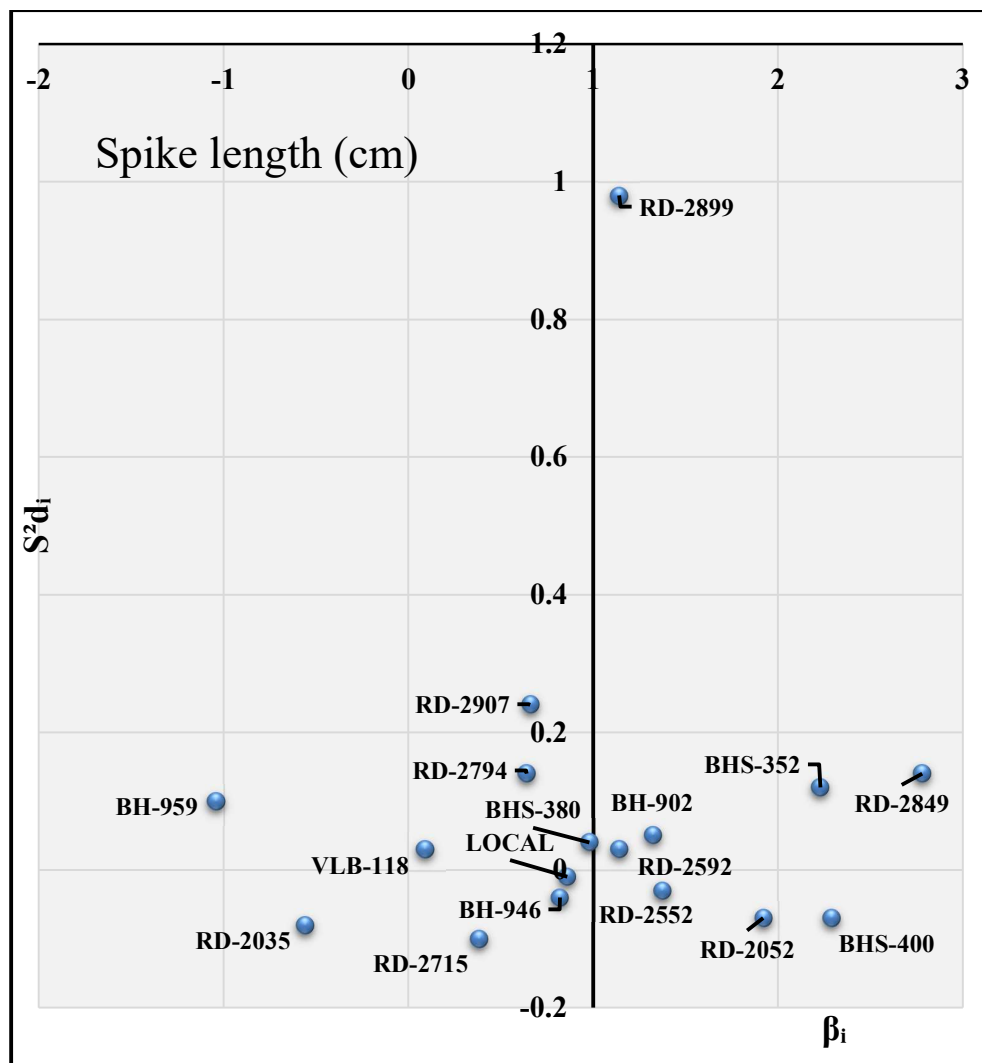


Figure 4.9 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for spike length (cm)

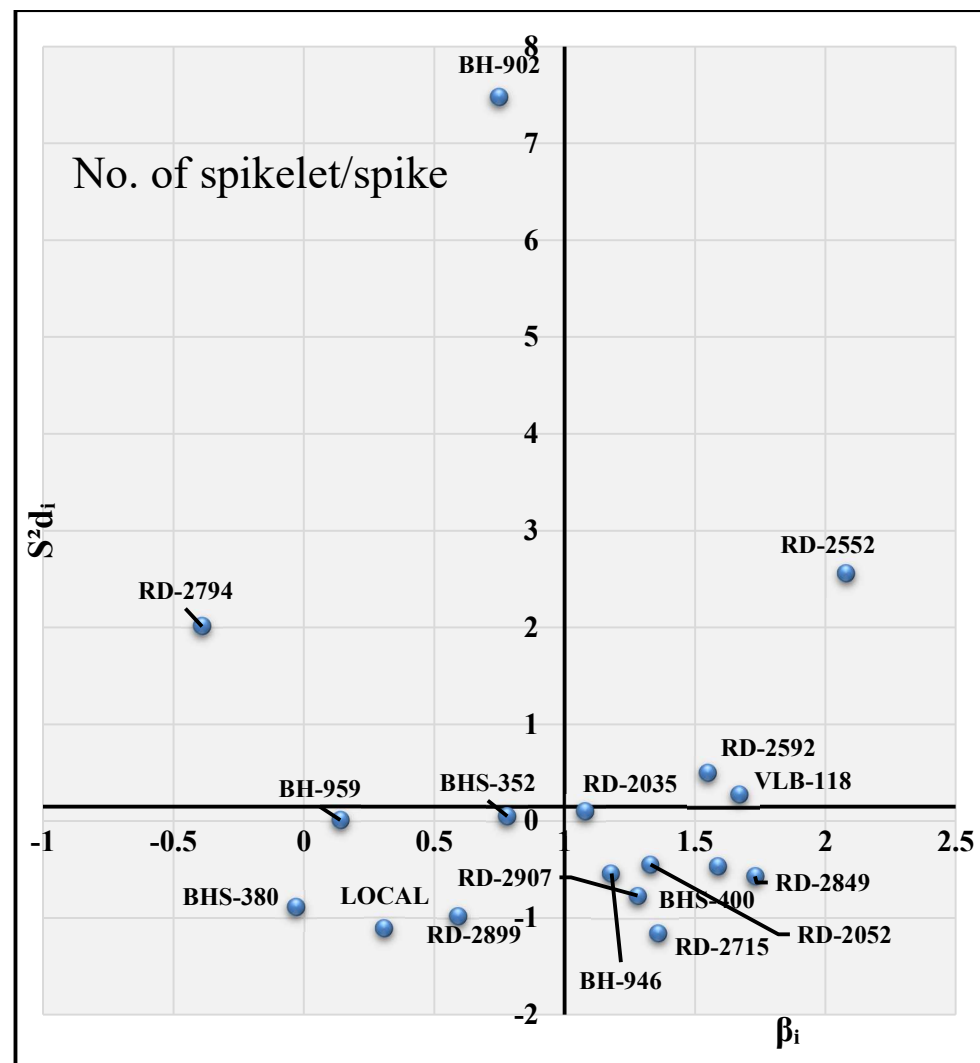


Figure 4.10 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for number of spikelet/spike

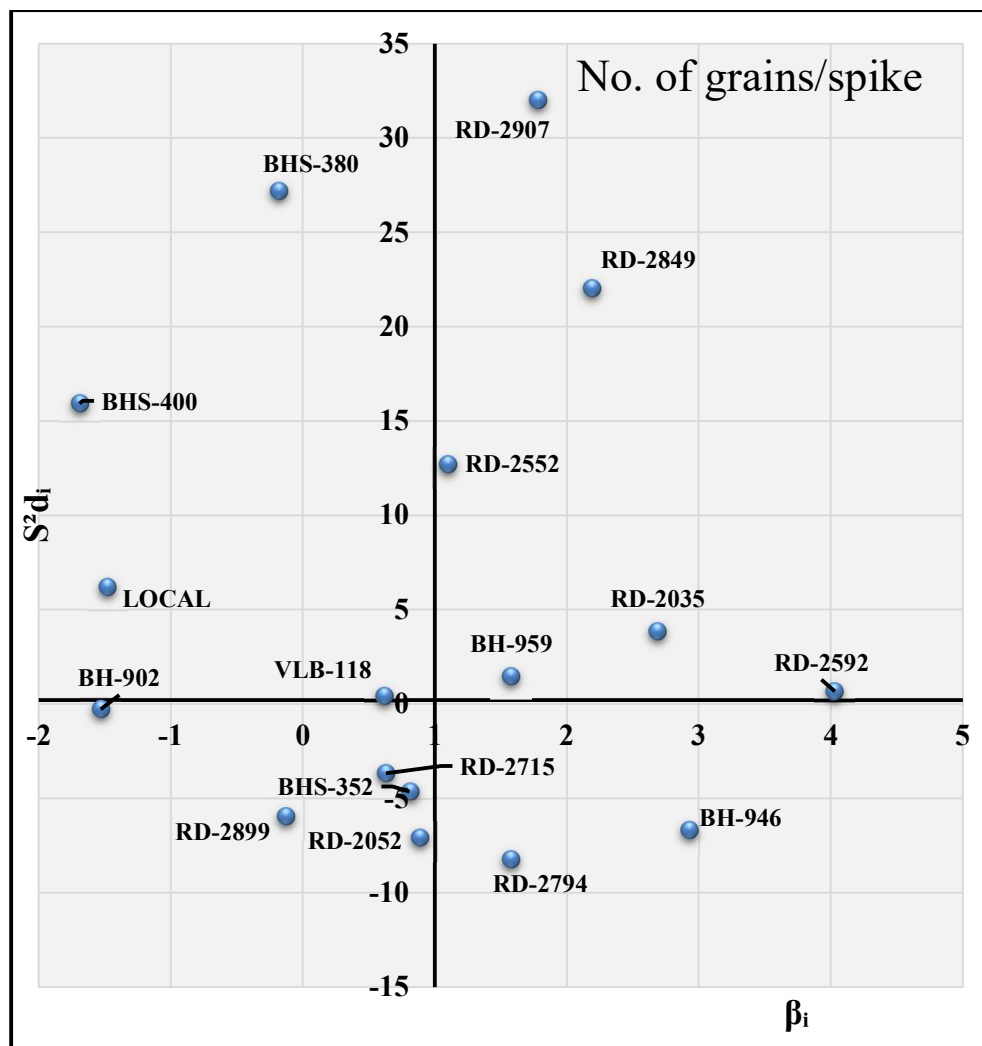


Figure 4.11 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for number of grains/spike

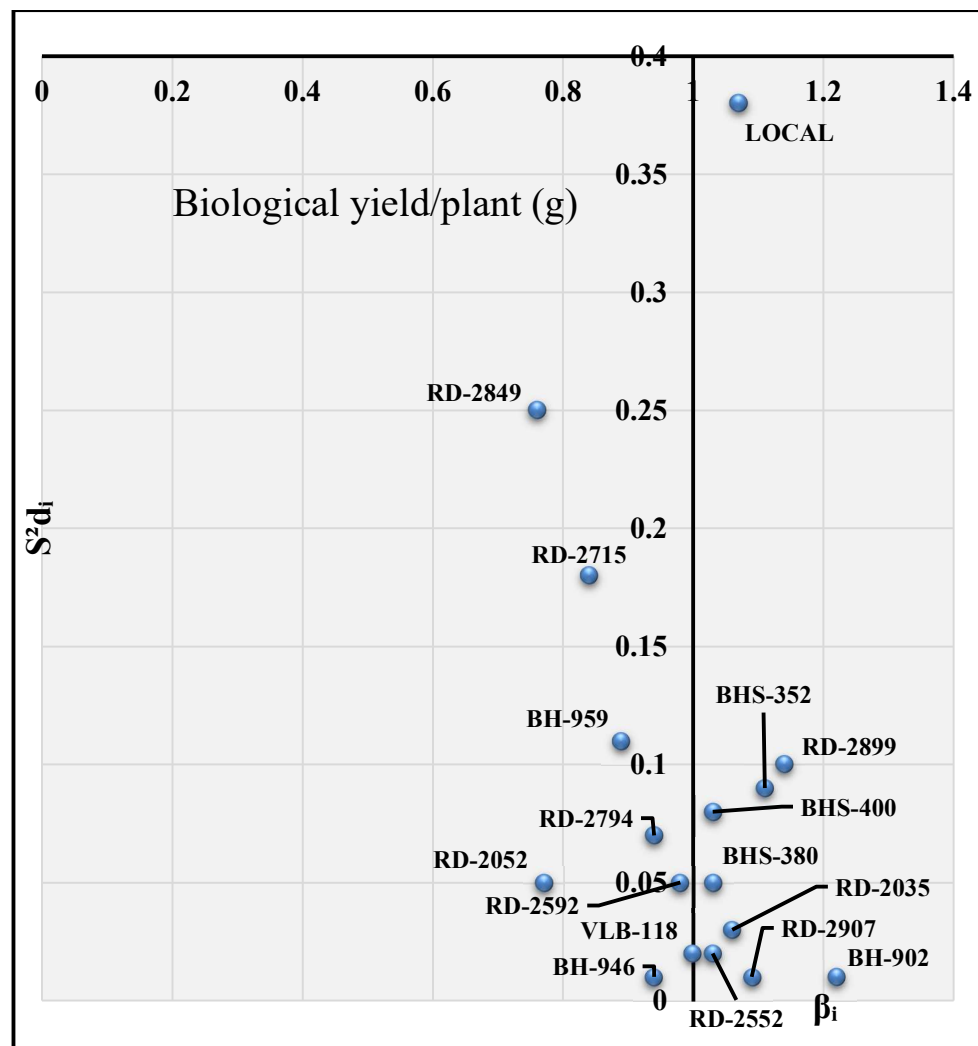


Figure 4.12 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for biological yield/plant (g)

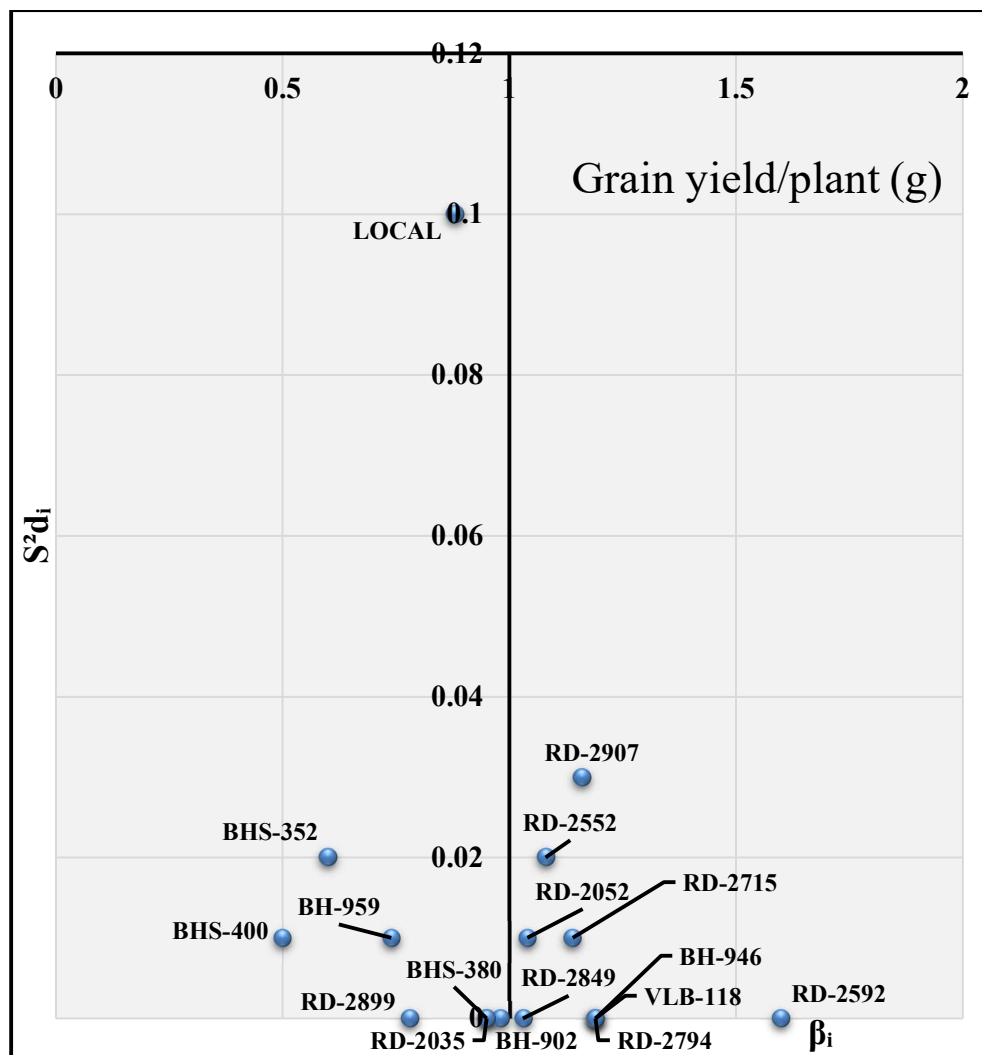


Figure 4.13 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for grain yield/plant (g)

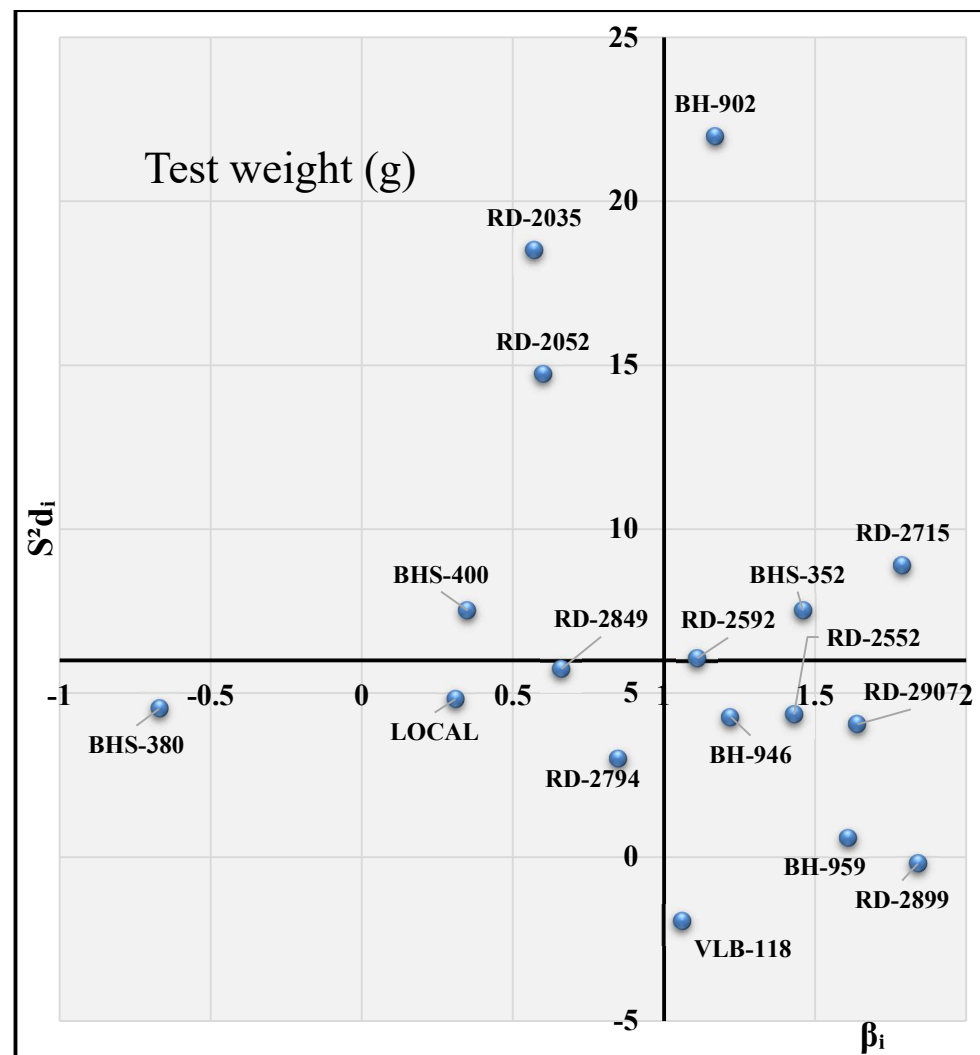


Figure 4.14 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for test weight (g)

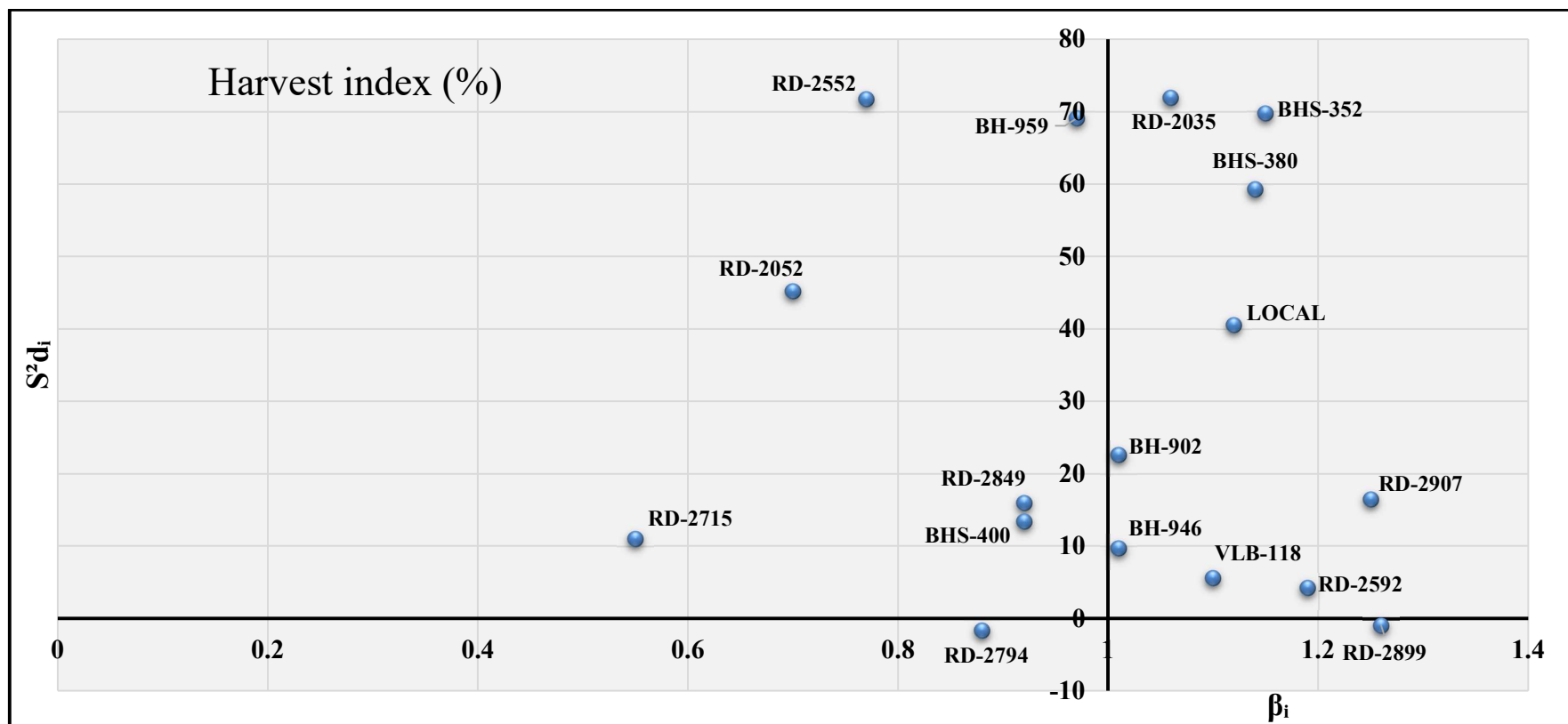


Figure 4.15 Stability and performance of seventeen Barley (*Hordeum vulgare* L.) genotypes for harvest index (%)

SPAD values

The mean values for this trait ranged from 37.38 (BHS-380) to 51.06 (RD-2035) with a general mean value of 41.49. The regression coefficient ranged from -1.29 (RD-2592) to 3.28 (LOCAL). The S^2d_i values of genotypes RD-2052(11.52), RD-2592(14.17), RD-2715(6.95), RD-2794(6.41), BH-380(22.67) and BH-959(9.61) were significantly deviated from zero. The regression coefficient values were non-significant for all the genotypes except RD-2849(2.85). Genotype RD-2035 had high mean value along with non-significant regression coefficient nearing unity was found to be stable and desirable. Genotype RD-2849 and BHS-352 showed high mean value as compared to general mean with regression coefficient more than unity is stable under high performance environment.

Flag leaf length(cm)

The mean values for this trait ranged from 16.32 (BH-959) to 21.32 (RD-2035) with a general mean value of 18.46. The regression coefficient values ranged from 0.16 (BHS-380) to 1.52 (RD-2552). The S^2d_i values of genotypes RD-2592(2.66), RD-2899(4.15), RD-2907(1.65), BHS-400(3.64), VLB-118(3.09) were significantly deviated from zero. The genotypes RD-2592(1.21), RD-2899(0.87), RD-2907(1.07), LOCAL(0.60), BHS-400(1.22), VLB-118(0.85), BHS-380(0.16) showed non-significant regression coefficient. Genotype RD-2052 had shown high mean value along with regression coefficient nearing unity were found to be stable and desirable. Genotype RD-2035 showed high mean value than general mean with regression coefficient less than unity was found to be stable under low performance environment. Genotype RD-2849 and BHS-352 showed high mean value than general mean with regression coefficient more than unity were found to be stable under high performance environment.

Flag leaf width(cm)

The mean values for this trait ranged from 0.81 (BH-959) to 1.17 (RD-2035) with a general mean value of 1.05. The regression coefficient values ranged from -0.73 (BHS-400) to 2.34 (RD-2849). The S^2d_i values of genotypes RD-2592(0.08) significantly deviated from zero. The regression coefficient was found non-significant for all the genotypes except RD-2794(1.46), RD-2907(1.96), BHS-400(-0.73), BHS-380(1.10).

Genotype RD-2052, BHS-352, BHS-400 showed high mean value than general mean with regression coefficient less than unity were found to be stable under low performance environment. Genotype RD-2035, RD-2794, RD-2849, RD-2899, RD-2907, LOCAL, BH-902, BH-946, showed high mean value than general mean with regression coefficient more than unity were found to be stable under high performance environment.

Number of tillers per plant

The mean values for this trait ranged from 8.08 (RD-2907) to 11 (BHS-352) with a general mean value of 9.25. The regression coefficient values ranged from 0.57 (RD-2552) to 1.32 (RD-2715). The S^2d_i values of genotypes RD-2035(0.54) and RD-2899(1.37) significantly deviated from zero. The regression coefficient was found non-significant for all the genotypes except RD-2052(0.98), RD-2552(0.57), RD-2592(0.80), RD-2715(1.32), RD-2794(0.99), LOCAL(1.18), BHS-946(0.84). Genotype RD-2035 showed high mean value than general mean with regression coefficient less than unity was found to be stable under low performance environment. Genotypes BHS-352, BHS-400, VLB-118 showed high mean value than general mean with regression coefficient more than unity were found to be stable under high performance environment.

Spike length(cm)

The mean values for this trait ranged from 6.58 (RD-2592) to 7.91 (RD-2035) with a general mean value of 7. The regression coefficient values ranged from -0.56 (RD-2035) to 2.78 (RD-2849). The S^2d_i values of genotypes RD-2899(0.98), RD-2907(0.24) significantly deviated from zero. The genotypes RD-2052(1.92), RD-2849(2.78), BHS-352(2.23), BHS-400(2.29) showed significant regression coefficient. Genotype RD-2035, RD-2715, LOCAL, BH-946, VLB-118 showed high mean value than general mean with regression coefficient less than unity were found to be stable under low performance environment. Genotype BHS-352 and BHS-400 showed high mean value than general mean with regression coefficient more than unity were found to be stable under high performance environment.

Number of spikelets per spike

The mean values for this trait ranged from 15.42 (BHS-959) to 20.50 (BHS-352) with a general mean value of 17.69. The regression coefficient values ranged from -0.03 (BHS-380) to 2.08 (RD-2552). The S^2d_i values of genotypes RD-2552(2.56), RD-2794(2.01), BHS-902(7.48) significantly deviated from zero. The genotypes that showed significant regression coefficient were RD-2715(1.36), RD-2849(1.73), RD-2907(1.28), BHS-946(1.18), BHS-400(1.59). Genotype, RD-2035 had high mean value along with regression coefficient nearing unity was found to be stable and desirable. Genotype BHS-352 showed high mean value than general mean with regression coefficient less than unity was found to be stable under low performance environment. Genotype RD-2052, RD-2715 and BHS-400 showed high mean value than general mean with regression coefficient more than unity were found to be stable under high performance environment.

Number of grains per spike

The mean values for this trait ranged from 47.08 (BHS-959) to 56.92 (RD-2035) with a general mean value of 51.71. The regression coefficient values ranged from -0.13 (RD-2899) to 4.03 (RD-2592). The S^2d_i values of genotypes RD-2552(12.68), RD-2849(22.02), RD-2907(32.01), BHS-400(15.92), BHS-380(27.20) significantly deviated from zero. The genotypes that showed significant regression coefficient were RD-2794(1.58), BHS-946(2.93). Genotype, RD-2052 had high mean value along with regression coefficient nearing unity was found to be stable and desirable. Genotypes, BH-902, BHS-352 showed high mean value than general mean with regression coefficient less than unity were found to be stable under low performance environment. Genotype RD-2035, RD-2592, RD-2794 and BHS-946 showed high mean value than general mean with regression coefficient more than unity were found to be stable under high performance environment.

Biological yield per plant(g)

The mean values for this trait ranged from 51.10 (BHS-959) to 89.91 (RD-2035) with a general mean value of 68.25. The regression coefficient values ranged from 0.76 (RD-2849) to 1.22 (BH-902). The S^2d_i values of all the genotypes were significantly deviated from zero except for RD-2907(0.01), BH-902(0.01) and BH-946(0.01). The genotypes that showed significant regression coefficient were RD-2907(1.09), BH-902(1.22), BH-

946(0.94). Genotype BH-946 had high mean value along with regression coefficient nearing unity was found to be stable and desirable. Genotypes BHS-902 and RD-2907 showed high mean value than general mean with regression coefficient more than unity were found to be stable under high performance environment.

Grain yield per plant(g)

The mean values for this trait ranged from 15.60 (BHS-959) to 30.32 (RD-2035) with a general mean value of 21.43. The regression coefficient values ranged from 0.60 (BHS-352) to 1.60 (RD-2592). The S^2d_i values of genotypes RD-2052(0.01), RD-2552(0.02), RD-2715(0.01), RD-2907(0.03), LOCAL(0.10), BHS-352(0.02), BHS-400(0.01), VLB-118(0.00), BH-959(0.01) significantly deviated from zero. The genotypes that showed significant regression coefficient were RD-2592(1.60), RD-2794(1.19), RD-2849(1.03), RD-2899(0.78), BH-946(1.19). Genotypes RD-2035, RD-2849, BH-902 had high mean value along with regression coefficient nearing unity was found to be stable and desirable. Genotypes RD-2592, BH-946 showed high mean value than general mean with regression coefficient more than unity is found to be stable under high performance environment. RD-2899 showed high mean value than general mean with regression coefficient less than unity found to be stable under low performance environment

Test weight(g)

The mean values for this trait ranged from 40.78 (BHS-380) to 52.40 (RD-2035) with a general mean value of 46.26. The regression coefficient values ranged from -0.67 (BHS-380) to 1.79 (RD-2715). The S^2d_i values of all the genotypes were significantly deviated from zero except for RD-2794(3.00)), RD-2899(-0.20)), VLB-118(-1.95), BH-959(0.59). The genotypes that showed significant regression coefficient were RD-2794(0.85), RD-2899(1.84), VLB-118(1.06) and BH-959(1.61). Genotype VLB-118 had high mean value along with regression coefficient nearing unity was found to be stable and desirable. Genotypes, RD-2899, BH-959 showed high mean value than general mean with regression coefficient more than unity were found to be stable under high performance environment. Genotype RD-2794 showed high mean value than general mean with regression coefficient less than unity was found to be stable under low performance environment.

Harvest index (%)

The mean values for this trait ranged from 25.93 (LOCAL) to 38.99 (BHS-352) with a general mean value of 33.78. The regression coefficient values ranged from 0.55 (RD-2715) to 1.26 (RD-2899). The S^2d_i values of all the genotypes were significantly deviated from zero except RD-2794(-1.69), RD-2899(-0.96). The genotypes that showed significant regression coefficient were RD-2794(0.88), RD-2899(1.26). Genotype RD-2899 showed high mean value than general mean with regression coefficient more than unity was found to be stable under high performance environment and genotype RD-2794 showed high mean value than general mean with regression coefficient less than unity was found to be stable under low performance environment.

Chapter-V

Discussion

DISCUSSION

The present investigation “**Stability analysis in Barley (*Hordeum vulgare* L.) for yield and contributing traits under varied conditions**” comprising of 17 genotypes was conducted with objectives to study the G×E interaction for stability of grain yield and component traits in barley genotypes and to study character association for yield and component traits and also to identify the stable genotypes of barley for different component traits.

The results obtained from the analysis of variance of 17 genotypes in all the environments *i.e.*, E1, E2, E3, E4 was found to be significant for all the characters, this indicated the presence of genetic variability among the genotypes. The results thus obtained are discussed under following captions.

5.1 Correlation coefficient and path analysis.

The association between yield contributing traits and their direct and indirect effects on grain yield per plant was determined. Correlation studies among yield contributing characters plays a crucial role in developing more effective genotypes with increased yield. Yield is a complicated character, and improving it directly is tough thus, the correlation studies provide a better understanding of relationship between grain yield with other characters.

The value of genotypic correlation is higher than the value of phenotypic correlation. In the present investigation, in environment E1 grain yield per plant showed positive and significant association with plant height, flag leaf length, flag leaf width, no. of tillers/ plant, spike length, no. of spikelets/ spike, no. of grains/ spike, biological yield/ plant and harvest index similar findings were also reported by Lodhi *et al.*, (2015), Singh *et al.*, (2015), Srivastava *et al.*, (2012), Sunil *et al.*, (2017). In environment EII grain yield per plant showed positive and significant association with flag leaf width and negative association with number of grains per spike similar results were also found by Singh *et al.*, (2015), Srivastava *et al.*, (2012). In environment E3 grain yield / plant showed positive and significant correlation with no. of grains per spike (Sunil *et al.*, 2017). Negative association was observed with plant height, SPAD values, spikelet per spike, Shrivastava *et al.*, (2012), Vinesh *et al.*, (2018), Haile *et al.*, (2015).

In pooled environment positive and significant correlation coefficient was observed for grain yield with days to 50 % flowering, plant height, flag leaf length, flag leaf width, no. of tillers/plant, number of grains/spike and harvest index both at phenotypic and genotypic levels. Similarly, positive and significant association of grain yield per plant was found with days to 50% flowering our results are in consonance with Shahinnia, *et al.*, (2005). Likewise, positive and significant correlation of grain yield was observed with plant height, SPAD values, no of tillers/ plant, no of grains/spike, harvest index similar findings were also reported by Al- Tabbal *et al.*, (2012) and Blum *et al.*, (1989), Sharief *et al.*, (2011), Singh *et al.*, (2014), Srivastava *et al.*, (2012), Bhutta *et al.*, (2005), Ahmad *et al.*, (2005), Rajbir & Kaul (1989). Positive and significant association of grain yield per plant was found with SPAD values, similar results were reported by Mehmet *et al.*, (2011). Positive and significant association of grain yield per plant with flag leaf width was similar with findings of Dere and Yildirim (2006). Whereas, grain yield showed negative and significant association with spike length and negative non-significant association with number of spikelets per spike while negative non-significant association with test weight similar results were reported by Haile *et al.*, (2015), Kumar *et al.*, (2018).

Days to 50% flowering exhibited significant and positive association with plant height, SPAD values, flag leaf width, no. of tillers/ plant, no. of spikelets/ spike, grains/ spike, test weight and showed negative association with harvest index. Positive association with plant height, SPAD values, no. of tillers/ plant, no. of spikelets/ spike, test weight, similar findings were obtained by Shahinnia, *et al.*, (2005), Vinesh *et al.*, (2018). Negative association of days to 50% flowering with harvest index was found similar with findings of Yadav *et al.*, (2014).

Plant height had positive and significant association with biological yield per plant similar results were reported by Ayer *et al.*, (2017). The negative and significant association of plant height was recorded with number of tillers per plant, spike length and test weight, whereas, negative and non-significant association was recorded for plant height with harvest index, similar findings were also obtained by Pilania and Dhaka (2014).

SPAD values had positive and significant association with flag leaf length, no. of tillers per plant, test weight and harvest index. It showed positive and significant correlation with test weight, harvest index, similar results were also shown by Ayer *et al.*, (2017).

Likewise, it showed negative association with biological yield per plant, similar findings were also obtained by Perween *et al.*, (2020).

The characters flag leaf length and flag leaf width showed positive association with number of tillers per plant, grains per spike and test weight similar results were also reported by Singh *et al.*, (2015).

Number of tillers per plant had positive and significant association with spike length, test weight and harvest index similar findings were also reported by Najeeb and Wani (2004), Drikvand *et al.* (2011), Shahinnia *et al.* (2005), Pal *et al.* (2010) and Yadav *et al.* (2014).

Spike length had positive and significant association with spikelet per spike, grains per spike, test weight and harvest index, similar findings were also obtained by Srivastava *et al.*, (2012), Lodhi R. *et al.*, (2015), Najeeb and Wani (2004).

Number of spikelets per spike showed positive and significant association with number of grains per spike, test weight and harvest index, similar findings were obtained by Tas and Celik (2011), Dyulgerova (2012), Gocheva (2014) and Doneva *et al.*, (2015).

Number of grains per spike showed positive and significant association with test weight and harvest index. Negative association was shown by Number of grains per spike with biological yield per plant and similar findings were obtained by Doneva *et al.*, (2015), Tabassum *et al.*, (2018).

Biological yield per plant showed negative significant association with test weight and harvest index and similar findings were also shown by Tabassum *et al.*, (2018), Pilania and Dhaka (2014), Srivastava *et al.*, (2012).

Test weight showed positive and significant association with harvest index, similar results were also reported by Ayer *et al.*, (2017), Dubey, *et al.*, (2018).

Path-coefficient analysis is an important statistical measure to partition the observed correlation coefficients into direct and indirect effects of component traits on grain yield. Path-coefficient analysis differs from correlations because it points out the causes and their effects, while latter deals with the mutual association. Partitioning of genotypic correlations between grain yield per plant and its component characters indicated that the direct effects were showed higher magnitude than that of indirect effects for most of the characters.

In the present investigation, path coefficient analysis of pooled environment was carried out taking grain yield per plant as a dependent variable and other twelve

characters as independent variables. Out of twelve characters days to fifty percent flowering, plant height, number of tillers/plant, test weight and harvest index directly affected the grain yield per plant in a positive direction, Kara (2008), Najeeb and Wani (2004), Mittal *et al.* (2009), Eshghi *et al.* (2011) and Zaefizadeh *et al.* (2011) also reported similar findings. Likewise, SPAD values also showed positive direct effect with grain yield per plant similar findings were also reported by Blackmer and Schepers, (1995), Ramesh *et al.*, (2002) and Boggs *et al.*, (2003).

Flag leaf width had negative direct effect on grain yield per plant though it showed a positive and significant correlation with grain yield. However, no. of grains/spike showed negative direct effect on grain yield per plant. Similar results were also reported by Singh *et al.*, (2015) and Pilania and Dhaka, (2014)

Biological yield per plant revealed highest direct and positive effects in E3 followed by harvest index and grains/ spike. Harvest index showed highest positive direct effect on grain yield in E1, E2, E4 and pooled environment followed by flag leaf width, number of spikelets per spike and biological yield per plant in E2 and test weight in E4 and plant height, test weight, number of tillers per plant and days to 50% flowering in pooled environment similar findings were also reported by Kumar *et al.* (1986), Leilah and Al-Khateeb, (2005), Ali and Shakor, (2012), Reza *et al.*, (2014), Srivastava *et al.*, (2012), Najeeb and Wani (2004), Ozturk *et al.* (2007) and Singh *et al.* (2008). Days to 50% flowering, plant height, flag leaf length, spike length showed negative direct effect at phenotypic level similarly, no. of spikelets per spike along with number of grains per spike showed negative direct effects with grain yield per plant genotypic level similar results were also reported by Doneva *et al.*, (2015), Pilania and Dhaka (2014), Sharma *et al.*, (2018), Ayer *et al.*, 2017, Vinesh *et al.*, (2018) and Singh *et al.*, (2015)..

Therefore, from this study the components *viz* biological yield per plant, harvest index, no. of grains/spike, flag leaf width, no. of spikelets/spike, plant height, test weight, no. of tillers /plant were found to be important components which effects grain yield per plant.

Residual effect factor *i.e.*, G (-0.0109), P (-0.0615) in (E1), G (-0.1262), P (0.3619) in (E2), G (-0.0315), P (0.0926) in (E3), G (-0.0021), P (0.0129) in (E4), G (-0.32978), P (0.26815) in pooled environment indicated that the yield traits components were responsible for considerable variability in the grain yield per plant.

5.2 Genotype x Environment interactions

The main objective of plant breeding is to develop high yielding varieties with stable performance. Stability analysis has become an important factor in breeding to check the performance of genotypes because, different genotypes perform differently in changing environment. G x E interaction study helps breeders to identify stable genotypes with superior performance across the environments. Both linear (bi) and non-linear (S^2di) components of G x E interactions are required for evaluating stability. A regression coefficient (bi) almost equals to 1 with an S^2di of 0 indicates average stability (Eberhart and Russell, 1966).

Joint regression with respect to mean performance of a genotype on environmental index (bi) is the popular approach in which deviation from regression (S^2di) is used as measure of stability. Environmental variance revealed significant difference among E1, E2, E3, E4 and of pooled environments. Genotypes when tested against pooled deviation were found to be significant for all the characters except for flag leaf length and number of grains per spike. Genotype x environment interaction were found to be significant for days to 50% flowering, plant height, SPAD values, flag leaf length, spike length, no. of spikelets/ spike, no. of grains/ spike, biological yield/plant, grain yield/ plant, test weight and harvest index, similar results were also reported by Costa and Bollero (2006), Lodhi *et al.* (2015) and Verma *et al.* (2016). G x E (linear) mean squares when tested against pooled deviation were found significant for all the characters except for days to 50% flowering, SPAD values, flag leaf length, and biological yield per plant. Environment (linear) has also shown significant values for all the characters except spikelet per spike. E+ (G x E) was found to be significant for plant height, flag leaf width, no of tillers/ plant, biological yield/ plant, grain yield/ plant, test weight and harvest index. Mean sum of squares due to pooled deviation was non-significant for no. of spikelets/ spike and no. of grains/ spike. Thus, it showed the significant role of non-linear component of genotype \times environment interaction in determining the stability of performance for all the characters. The present results are in agreement with those of Yadav and Choudhary (2004), El-Badawy (2012), Ranjana and Kumar (2013) and Pansuriya *et al.* (2014).

5.3 Stability analysis

Stability performance is the most important property of a genotype for its wide adaptability. The stability parameters viz., (X_i) over the environments, (bi) and (S^2di) were calculated as per Eberhart and Russell (1966) for 13 characters to evaluate the

relative stability of genotypes over environments. As per Eberhart and Russell (1966) stability model, the genotypes which shows high mean, regression coefficient ($b_i=1$) and minimum deviation from regression line ($S^2d_i=0$), shows better performance among different environments and considered as stable genotypes.

Stability parameters of different traits showed that LOCAL as most stable for days to 50% flowering, BHS-352, VLB-118, BHS-380 for plant height and RD-2035 for SPAD values. Similarly, RD-2052 for flag leaf length, BH-946 for Spike length, RD-2035 for number of spikelets per spike while, RD-2052 and BHS-352 for number of grains per spike, BH-946 and RD-2907 showed high stability for biological yield per plant. RD-2035, RD-2849 and BH-902 was found most stable genotypes for grain yield per plant and VLB-118 was found stable for test weight. These genotypes had higher mean than general mean and regression coefficient close to unity. Similar results were obtained by findings of Mosa *et al.* (2009), Abd EL-Moula (2011) and Abdallah *et al* (2011).

The genotypes showing S^2d_i values significantly deviating from zero were described as unstable (unpredictable) with respect to mean performance and responsiveness. It has also been recognized that the term stability should be used to refer the absence or a low magnitude of the unpredictable (non-linear) change in response to an environment, the predictable (linear) component which represent definite response to a genotype to environment changes could be termed as more appropriate measure of responsiveness to the genotype.

Table 5.1 Barley genotypes exhibiting best performance, responsiveness, and stability of different characters.

Character	Responsiveness		High mean, unit regression coefficient, non-significant deviation from regression.
	Most responsive	Least responsive	
Days to 50% flowering	RD-2849	BHS-380	LOCAL
Plant height (cm)	BHS-400, RD-2907	BHS-946, RD-2715	BHS-352, BHS-380
SPAD values	RD-2849, BHS-352	RD-2552	RD-2035
Flag leaf length (cm)	RD-2849, BHS-352	RD-2035	RD-2052
Spike length (cm)	BHS-352, BHS-400	RD-2035, RD-2715	BH-946
No. of spikelets per spike	RD-2052	BHS-352	RD-2035
No. of grains per spike	RD-2035	BH-902	RD-2052, BHS-352
Biological yield/plant (g)	BHS-902	BH-946	RD-2907
Grain yield/plant (g)	RD-2592, BH-946	RD-2899	RD-2035, RD-2849, BH-902
Test weight (g)	RD-2899	RD-2794	VLB-118

Chapter-VI

Summary and Conclusions

SUMMARY AND CONCLUSIONS

The present investigation “**Stability analysis in Barley (*Hordeum vulgare* L.) for yield and contributing traits under varied conditions**” comprised of 17 genotypes was conducted with objectives to study the G×E interaction for stability of grain yield and correlation and path analysis for yield and yield contributing traits in barley genotypes.

Observations were recorded on randomly selected plants for 13 morphological characters viz., days to 50 % flowering, plant height, chlorophyll content of leaf (SPAD values), flag leaf length (cm), flag leaf width, no. of tillers/ plant, spike length, no. of spikelets/spike, no. of grains/ spike, biological yield/plant, grain yield/plant, test weight, harvest index.

The analysis of variance revealed significant differences among the genotypes for most of the characters in all the environments indicating the presence of sufficient genetic variability present in the studied genotypes.

From the mean performance of the genotypes for different quantitative traits in four environments and pooled environment, it was found that genotypes RD-2035, RD-2052 were promising for grain yield per plant. Genotypes RD-2907, BHS-380, BH-959 were found early in days to 50% flowering. Genotypes RD-2035, RD-2899 were promising for number of grains per spike.

The study of environment-wise path coefficient analysis indicated that the characters harvest index had positive direct effects while it showed positive and significant correlation with grain yield per plant in all the four environments as well as pooled environment while biological yield showed positive direct effects along with positive and significant correlation with grain yield per plant in environment E2 and environment E3. Therefore, simultaneous improvement of grain yield per plant is possible through selection of these characters.

Pooled analysis of variance for stability showed that genotypes had significant differences for all the characters except flag leaf length and number of grains per spike. Environmental component, was significant for all the characters but environment (linear) was significant for all the characters except spikelet per spike which showed that environments were divergent. The genotype x environment (linear) interactions were significant for plant height, flag leaf width, no. of tillers/ plant, spike length, no. of spikelets/ spike, no. of grains/ spike, grain yield/ plant and test weight. Pooled deviation component was highly significant for all the characters except number of spikelet/ spike & no. of grains spike indicating the importance of non-linear component in the genotype x environment interaction.

Perusal of stability analysis as per Eberhart and Russell model showed that, the genotypes LOCAL for days to 50% flowering, RD-2035 for SPAD values and no. of spikelet per spike. Similarly, BHS-352, VLB-118, BHS-380 for plant height. RD-2052 for flag leaf length, BH-946 for Spike length, RD-2052 and BHS-352 for no. of grains per spike, BH-946 and RD-2907 for biological yield per plant showed high stability. RD-2035, RD-2849, BH-902 for grain yield per plant, VLB-118 for test weight, RD-2899 for harvest index were found to have high stability for favourable environmental conditions.

The genotype BHS-380 was found to be stable for low performing environments for days to 50% flowering. Likewise, RD-2794 for plant height, RD-2552 for SPAD values, RD-2035 for flag leaf length and spike length, BHS-352 for no. of spikelet per spike, BH-902 for no. of grains per spike, RD-2794 for test weight and harvest index.

The genotype RD-2907 have shown stable performance for plant height for high performing environments. Likewise, RD-2849 for SPAD values and flag leaf length, BHS-352 for spike length, RD-2052 for no. of spikelet per spike, RD-2035 for no. of grains per spike, BHS-902 for biological yield per plant, RD-2592 for grain yield per plant, RD-2899 for test weight.

In the present investigation, the genotypes, RD-2035, RD-2849, BH-902, VLB-118 and RD-2899 were found to be most promising on the basis of stability parameters for grain yield per plant and main yield attributing traits over all environments and can be used for future breeding programmes as well as for cultivation under varied environments for higher yield.



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Appendix

APPENDIX- 1

Mean performance of Barley genotypes for yield and yield contributing traits under different environments

Genotypes	Days to 50% flowering					Plant height(cm)					SPAD values				
	E I	E II	E III	E IV	Pooled	E I	E II	E III	E IV	Pooled	E I	E II	E III	E IV	Pooled
RD-2035	83.00	85.33	83.67	80.33	83.08	86.37	82.50	99.67	80.67	87.30	52.20	50.53	51.80	49.70	51.06
RD-2052	79.67	83.67	79.33	75.33	79.50	82.30	86.53	87.87	75.33	83.01	35.43	40.60	42.80	41.77	40.15
RD-2552	78.33	83.67	80.67	82.33	81.25	79.13	86.60	99.33	79.83	86.22	38.17	39.63	37.47	37.13	38.10
RD-2592	79.67	82.00	84.67	86.33	83.15	85.53	85.67	96.83	88.93	89.24	45.27	38.87	37.17	38.33	39.91
RD-2715	75.67	82.33	82.67	83.00	80.92	80.37	77.00	93.53	88.40	84.83	39.37	42.87	36.23	39.47	39.49
RD-2794	78.00	83.00	83.67	71.67	79.08	77.23	88.33	95.93	90.17	87.92	41.63	39.53	36.03	36.93	38.53
RD-2849	76.67	82.33	80.67	82.00	80.42	79.83	81.87	96.30	85.77	85.94	37.50	41.97	44.03	37.47	40.24
RD-2899	78.33	81.00	78.33	82.67	80.00	81.60	80.67	88.87	83.60	83.69	38.30	38.33	37.97	36.50	37.78
RD-2907	72.33	76.00	84.67	73.00	76.50	81.40	87.63	103.87	88.03	90.23	34.73	38.23	35.33	36.83	36.28
LOCAL	76.33	80.33	79.33	77.00	78.25	76.43	83.53	98.83	91.27	87.52	36.87	42.60	42.37	36.47	39.58
BH-902	80.00	82.00	82.33	72.67	79.25	70.53	73.53	100.73	89.23	83.51	38.60	39.53	42.13	35.77	39.01
BH-946	76.67	81.33	79.67	73.00	77.67	77.10	85.93	98.07	89.50	87.65	37.53	42.20	36.87	34.87	37.87
BHS-352	80.67	82.33	83.00	86.00	83.00	86.87	85.47	103.67	86.33	90.59	52.90	50.37	49.53	48.27	50.27
BHS-400	77.00	79.00	84.67	83.33	80.25	82.70	83.70	105.43	92.37	91.05	37.23	42.07	39.30	39.50	39.53
VLB-118	77.67	82.33	75.33	75.67	77.75	81.20	87.50	100.50	92.70	90.48	36.43	37.43	36.20	41.50	37.89
BHS-380	74.33	75.33	74.00	78.00	75.42	80.60	89.90	100.67	89.73	90.23	32.33	35.83	41.87	39.47	37.38
BH-959	74.33	72.67	75.33	74.67	74.25	73.57	70.33	88.33	79.80	78.01	40.57	37.33	41.93	35.07	38.73
Mean	77.57	80.88	80.71	78.65	79.40	80.16	83.34	97.55	86.57	86.91	39.71	41.05	40.53	39.14	40.11
Min	72.33	72.67	74.00	71.67	74.25	70.53	70.33	87.87	75.33	78.01	32.33	35.83	35.33	34.87	36.28
Max	83.00	85.33	84.67	86.33	83.15	86.87	89.90	105.43	92.70	91.05	52.20	50.53	51.80	49.70	51.06
C.D.	5.28	6.18	5.40	5.63	3.28	8.16	10.13	9.09	9.14	4.82	5.92	4.74	5.93	4.09	2.86
C.V.	4.09	4.59	4.02	4.30	4.80	6.12	7.31	5.60	6.35	4.79	9.24	7.09	9.00	6.48	6.67

Contd...

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Genotypes	Flag leaf length(cm)					Flag leaf width (cm)					No. of tillers per plant				
	E II	E II	E II	E II	Pooled	E I	E II	E III	E IV	Pooled	E I	E II	E III	E IV	Pooled
RD-2035	24.73	23.00	19.87	17.67	21.32	1.30	1.13	1.23	1.03	1.17	8.33	13.33	10.33	11.00	10.75
RD-2052	20.97	21.90	15.07	16.53	18.62	1.00	1.10	1.00	0.93	1.01	8.00	13.33	8.00	10.33	9.92
RD-2552	22.93	22.10	13.93	14.67	18.41	1.10	1.00	1.00	1.00	1.03	7.00	10.33	7.00	9.00	8.33
RD-2592	22.10	19.60	12.67	16.13	17.63	1.20	1.20	0.97	1.07	1.11	8.33	12.67	8.33	10.33	9.92
RD-2715	20.87	20.63	12.43	15.27	17.30	1.10	0.97	1.13	0.97	1.04	6.33	13.33	6.67	7.67	8.50
RD-2794	22.07	20.20	14	15.17	17.86	1.13	1.13	1.10	0.93	1.07	7.33	12.67	7.33	9.33	9.17
RD-2849	22.90	21.93	14.27	15.50	18.65	1.17	1.17	0.77	0.87	1.00	7.67	13.00	8.00	7.33	9.00
RD-2899	22.93	22.37	20.40	15.63	20.33	1.10	1.00	1.07	0.80	0.99	6.33	12.33	9.00	7.33	8.75
RD-2907	22.37	20.97	17.73	14.23	18.83	1.13	1.13	1.07	0.87	1.05	5.33	12.00	7.00	8.00	8.08
LOCAL	19.80	18.50	14.70	17.17	17.54	1.10	1.17	1.07	0.97	1.08	5.67	12.33	6.67	8.00	8.17
BH-902	19.93	17.40	14.67	15.87	16.97	1.13	1.17	1.10	0.93	1.08	8.00	13.00	7.33	8.00	9.08
BH-946	20.70	20.63	14.50	14.73	17.64	1.13	1.20	1.20	0.90	1.11	7.00	11.67	8.00	7.33	8.50
BHS-352	24.60	23.83	19.53	16.83	21.20	1.10	1.10	1.23	1.20	1.16	9.67	15.33	9.67	9.33	11.00
BHS-400	21.87	23	19.53	13.73	19.53	1.07	1.07	1.07	1.17	1.10	8.67	13.67	8.00	9.00	9.84
VLB-118	21.77	22.07	15.23	19.17	19.56	1.03	1.13	0.97	1.00	1.03	7.00	14.00	8.67	9.00	9.67
BHS-380	17.00	16.93	16.70	15.57	16.55	0.97	1.00	0.90	0.83	0.93	7.00	13.00	6.33	7.00	8.33
BH-959	18.80	18.00	15.60	12.87	16.32	0.90	0.73	0.80	0.80	0.81	6.67	11.00	6.67	8.00	8.09
Mean	21.55	20.77	15.83	15.69	18.46	1.10	1.08	1.04	0.96	1.05	7.33	12.77	7.82	8.59	9.25
Min	17.00	16.93	12.43	12.87	16.32	0.90	0.73	0.77	0.80	0.81	5.33	10.33	6.33	7.00	8.08
Max	24.73	23.83	20.40	19.17	21.32	1.30	1.20	1.23	1.20	1.17	9.67	15.33	10.33	11	11.00
C.D.	1.42	1.38	1.15	1.12	1.83	0.05	0.08	0.08	0.07	0.11	0.40	0.74	0.80	0.54	1.23
C.V.	3.99	3.97	3.35	3.22	8.84	0.16	0.20	0.23	0.21	8.27	1.16	2.14	2.30	1.56	8.74

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Genotypes	Spike length(cm)					Spikelet/spike					No. of grains/spike				
	E II	E II	E II	E IV	Pooled	E I	E II	E III	E IV	Pooled	E I	E II	E III	E IV	Pooled
RD-2035	7.77	7.77	8.33	7.77	7.91	22.00	19.33	21.33	19.00	20.42	57.33	53.00	64.00	53.33	56.92
RD-2052	7.70	7.10	5.77	7.00	6.89	20.00	16.67	17.67	16.67	17.75	54.00	52.33	52.67	50.00	52.25
RD-2552	7.37	7.20	6.00	7.03	6.90	22.00	17.00	20.33	16.33	18.92	47.00	51.33	57.33	47.00	50.67
RD-2592	6.87	6.93	5.73	6.80	6.58	19.67	19.00	16.00	16.00	17.67	55.67	55.00	57.67	42.67	52.75
RD-2715	7.37	6.90	6.97	7.00	7.06	19.67	17.67	17.00	16.33	17.67	49.33	51.33	54.00	50.33	51.25
RD-2794	6.77	7.20	6.13	7.17	6.82	18.00	15.67	17.33	19.33	17.58	53.33	51.33	54.33	48.67	51.92
RD-2849	8.33	7.43	5.67	6.13	6.89	19.33	17.33	17.67	14.67	17.25	54.67	44.33	57.33	50.33	51.67
RD-2899	7.50	7.20	6.73	6.60	7.01	18.67	17.33	17.00	17.33	17.58	56.00	55.00	53.00	54.33	54.58
RD-2907	7.80	6.53	7.10	6.70	7.03	18.67	16.00	17.00	15.33	16.75	55.67	41.67	51.33	48.00	49.17
LOCAL	7.37	6.87	6.43	7.37	7.01	17.00	16.00	16.00	16.33	16.33	48.67	54.67	46.00	50.00	49.84
BH-902	7.57	6.77	6.30	6.13	6.69	17.67	21.00	15.33	16.00	17.50	51.67	54.33	46.67	53.00	51.42
BH-946	7.23	8.43	6.33	6.40	7.10	18.33	18.00	16.33	15.33	16.10	54.00	52.67	56.33	45.33	52.08
BHS-352	8.30	7.80	6.03	7.87	7.50	21.67	21.33	19.00	20.00	20.50	57.00	53.33	54.00	52.33	54.17
BHS-400	8.40	7.00	6.07	7.00	7.12	21.00	19.00	19.67	16.67	19.09	55.67	55.00	45.00	54.00	52.42
VLB-118	7.33	6.60	7.17	7.17	7.07	20.00	15.67	16.33	16.00	17.00	56.00	50.00	51.67	51.33	52.25
BHS-380	7.27	6.17	6.20	6.73	6.59	16.00	17.00	16.33	16.00	16.33	41.67	52.00	52.00	48.67	48.59
BH-959	6.47	6.13	7.40	7.10	6.78	15.00	16.33	16.00	14.33	15.42	45.00	46.33	52.33	44.67	47.08
Mean	7.49	7.06	6.49	6.94	7.00	19.10	17.69	17.43	16.57	17.69	52.51	51.39	53.29	49.65	51.71
Min	6.47	6.13	5.67	6.13	6.58	15.00	15.67	15.33	14.33	15.42	41.67	41.67	45.33	42.67	47.08
Max	8.40	8.43	8.33	7.87	7.91	22.00	21.33	21.33	20.00	20.50	57.33	55.00	64.00	54.33	56.92
C.D.	0.30	0.38	0.42	0.30	0.59	1.20	1.09	1.16	0.95	1.66	3.04	2.71	3.28	2.40	4.45
C.V.	0.86	1.09	1.20	0.87	8.1	3.46	3.15	3.34	2.73	7.25	8.76	7.79	9.45	6.90	7.72

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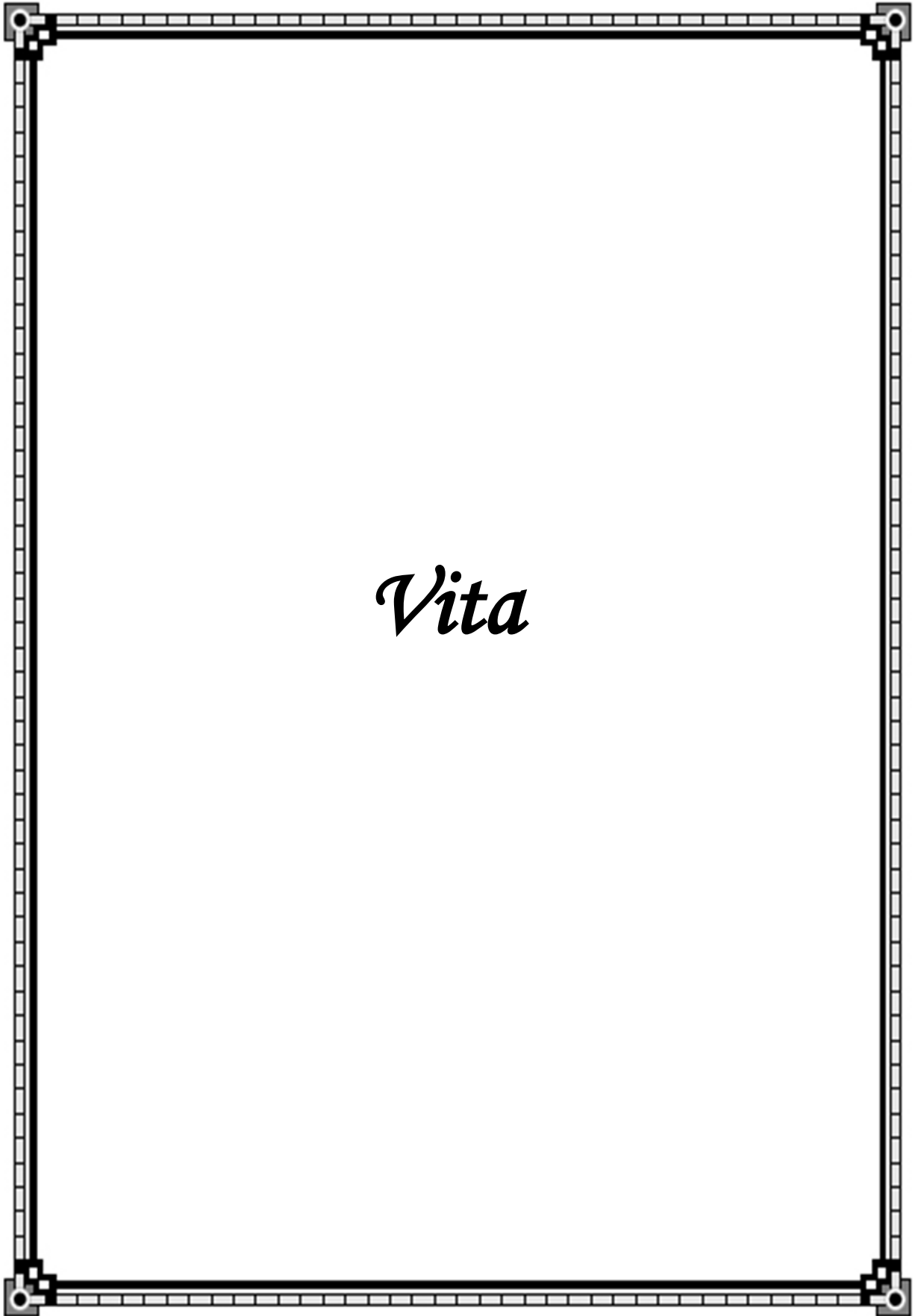
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Genotypes	Biological yield/plant (g)					Grain yield/plant (g)					Test weight (g)				
	E I	E II	E III	E IV	Pooled	E I	E II	E III	E IV	Pooled	E I	E II	E III	E IV	Pooled
RD-2035	88.91	97.11	82.33	91.30	89.91	30.32	29.26	32.28	29.40	30.32	59.30	51.33	48.83	50.13	52.40
RD-2052	74.69	90.09	65.77	83.45	78.50	24.85	35.11	21.33	24.11	26.35	57.53	50.33	50.63	46.67	51.29
RD-2552	55.83	92.21	57.59	69.65	68.82	16.88	29.82	16.43	17.58	20.18	51.33	56.23	40.93	41.57	47.52
RD-2592	52.99	89.03	58.19	75.43	68.91	21.09	32.61	17.49	17.07	22.07	45.47	49.67	36.40	38.73	42.57
RD-2715	61.23	84.58	56.17	68.76	67.69	17.01	27.97	13.37	14.98	18.33	54.47	54.03	37.13	38.80	46.11
RD-2794	64.34	76.40	68.68	65.33	68.69	19.56	30.46	19.23	19.62	22.22	50.03	54.53	48.30	43.20	49.02
RD-2849	54.74	88.93	55.79	58.82	64.57	21.02	29.55	22.73	15.61	22.23	50.13	51.27	49.57	42.33	48.33
RD-2899	57.84	96.26	51.23	75.33	70.17	20.32	38.63	21.27	15.32	23.89	57.33	56.97	44.60	38.47	49.34
RD-2907	69.27	74.35	65.45	64.59	68.42	14.93	27.88	15.69	13.84	18.09	50.30	55.77	43.67	36.03	46.44
LOCAL	55.47	93.43	50.22	82.34	70.37	11.01	30.74	12.36	16.19	17.58	39.90	45.60	40.27	40.47	41.56
BH-902	62.13	84.42	53.44	54.65	63.66	19.18	34.42	15.52	13.94	20.77	46.40	48.73	45.37	32.87	43.34
BH-946	53.79	87.47	66.37	59.45	66.77	17.32	32.19	17.90	12.63	20.01	45.83	52.37	39.73	38.00	43.98
BHS-352	74.56	76.30	68.77	60.75	70.10	23.26	30.85	24.54	21.32	24.99	60.53	56.00	47.00	43.67	51.80
BHS-400	60.94	92.62	58.34	76.77	72.17	20.11	35.91	14.66	20.75	22.86	41.67	47.77	40.73	42.70	43.22
VLB-118	64.02	81.53	62.97	57.89	66.60	20.57	28.78	20.11	19.30	22.19	52.47	52.33	44.90	41.77	47.87
BHS-380	55.67	60.13	51.66	48.09	53.89	10.91	26.32	13.23	15.87	16.58	37.40	38.93	40.20	46.57	40.78
BH-959	52.88	54.27	49.96	47.29	51.10	14.49	23.95	12.80	11.16	15.60	48.27	47.00	36.67	31.23	40.79
Mean	62.31	83.48	60.17	67.05	68.25	18.99	30.85	18.29	17.57	21.43	49.90	51.11	43.23	40.78	46.26
Min	52.88	54.27	49.96	47.29	51.10	10.91	23.95	12.36	11.16	15.60	37.40	38.93	36.40	31.23	40.78
Max	88.91	97.11	82.33	91.30	89.91	30.32	38.63	32.28	29.40	30.32	60.53	59.96	50.63	50.13	52.40
C.D.	8.78	8.97	8.27	9.28	11.21	2.03	2.56	2.31	2.22	4.35	1.51	1.80	1.56	1.47	3.81
C.V.	15.68	14.42	14.35	18.63	11.51	16.01	11.93	17.60	17.53	14.24	4.35	5.19	4.50	4.23	9.00

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Genotypes	Harvest index (%)				
	E II	E II	E II	E IV	Pooled
RD-2035	34.10	30.13	39.21	32.20	33.91
RD-2052	33.27	38.97	32.43	28.89	33.39
RD-2552	30.23	32.34	28.53	25.24	29.09
RD-2592	39.80	36.63	30.06	22.63	32.28
RD-2715	27.78	33.07	23.80	21.79	26.61
RD-2794	30.40	39.87	28.00	30.03	32.08
RD-2849	38.40	33.23	25.67	26.54	30.96
RD-2899	35.13	40.13	41.52	24.66	35.36
RD-2907	21.55	37.50	23.97	29.87	28.22
LOCAL	26.55	32.90	24.61	19.66	25.93
BH-902	30.87	40.77	29.04	25.51	31.55
BH-946	32.20	36.80	26.97	21.24	29.30
BHS-352	44.74	40.43	35.68	35.09	38.99
BHS-400	33.00	38.77	25.13	27.03	30.98
VLB-118	32.13	35.30	31.94	33.34	33.18
BHS-380	25.77	43.77	27.61	33.00	32.54
BH-959	27.40	44.13	25.62	23.60	30.19
Mean	31.96	37.34	29.40	27.08	31.44
Min	21.55	30.13	23.80	19.66	25.93
Max	39.80	44.13	41.52	35.09	33.91
C.D.	5.45	4.24	5.06	4.86	6.18
C.V.	17.57	10.89	17.85	17.16	13.78



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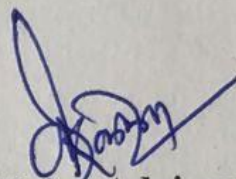
Name of the Student	:	Ms. Neha Manhas
Father's Name	:	Mr. Ramesh Kumar
Mother's Name	:	Mrs. Kamlesh Rani
Nationality	:	Indian
Date of Birth	:	13.03.1995
Permanent Home Address	:	Vill: Chak Koura, Teh: Khour Dist: Jammu, J&K
E-mail ID	:	nehamanhasjk@gmail.com
Contact No.	:	6005814825

EDUCATIONAL QUALIFICATIONS

Bachelor Degree	:	B. Sc. Agriculture
University/Institution	:	Ropar Institute of Management and Technology, Shekhupur, Ropar
Year of Award	:	2019
OGPA/ % marks	:	7.95/10 (79.50%)
Master's Degree OGPA	:	8.09/10 M. Sc. (Ag.) Plant Breeding & Genetics

CERTIFICATE-IV

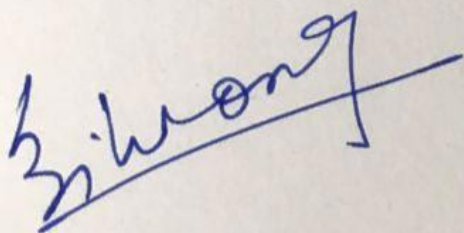
Certified that all the necessary corrections as suggested by the external examiner and advisory committee have been duly incorporated in the thesis entitled “Stability analysis in Barley (*Hordeum Vulgare* L.) for yield and contributing traits under varied conditions”, submitted by Miss Neha Manhas, Registration No. J-19-M-664.



Major Advisor
Dr. Subhash Chander
Asstt. professor, PBG
SKUAST, Jammu

Place: Jammu

Date: 27/12/21



Head of the Division