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GENETICS AND PLANT BREEDING

Genetic Divergence and GGE Bi-plot Analysis of Multi-environment Trial Data of Barley (*Hordeum vulgare* L.) to Identify "Ideal" Genotype

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ABSTRACT

The present research revealed the study of genetic divergence and genotype (G) main effect and genotype by the environment (GE) interaction (G × GE) bi-plot analysis for multi-environmental trial data using yield data of three years. Since, genotypes were planted in 2017 in two dates like early and lates own condition hence, there was very slight differences in their yield so both the environments come together as compared to third environment (2018) which for from the two locations of year 2017. The objective of this study was to determine the effects of genotype, environment and their interaction on grain yield and to identify stable barley genotypes. The field experiment comprising of 69 barley genotypes laid out in a Randomized Block Design with three replications during *Rabi* 2016-2017. The extent of genetic variability, association between yield and yield components, frequency distribution of 25 top best genotypes in response to yield in three different environments, yield stability analysis and genetic diversity was studied. For stability analysis yield data of current year for one location and yield data of two locations/environments of previous year have been used. Field observations were recorded on six important characters days to 50% flowering, days to maturity, effective tillers per plant, plant height with awn, plant height without awn and 1000 grain weight (g). The result of bi-plot analysis using yield data of three years revealed that AXIS1 explained 57.6 per cent variation while AXIS2 was explained 31.07 per cent variation. Since, genotypes were planted in 2017 in two dates like early and late sown condition hence, there was very slight differences in their yield so both the environments come together (Figure1) as compared to third environment (2018) which for from the two locations of year 2017. Our result indicate that line G69 recommended as most stable genotype for yield potential and stability whereas lines G9, G55, G67 and G68 were consider as superior genotypes.

Highlights

- Effective tillers per plant show highest contribution 51.71% towards genetic divergence, 1000 grain weight (g) show high genetic advance (33.74) as percent of mean (5%) and days to 50% flowering, plant height with awn show high heritability.
- Line G69 as genotype K-603 recommended as most stable for yield potential and stability in three different environments.

Keywords: GGE bi-plot, Hordeum vulgare, multi environment trials, yield, D^2 Analysis, Yield performance

Barley (*Hordeum vulgare* L.) is an ancient and cereal grain crop of the world. It belongs to the family Poaceae (*syn. Gramineae*) and the tribe triticeae. In recent time, about two-thirds of the barley crop has been used for feed, one-third for malting and about 2 percent for food directly. Historically, barley consider as an important food source in the many

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parts of world, such as Middle East, North Africa and northern, eastern Europe and also in Asia. Barley is regarded as a convenient experimental organism because of different reasons: (1) It is an annual with short life cycle (2) It is diploid with only seven pairs of chromosomes (3) It is true breeding allowing multiple testing (4) It exhibit wide diversity in physiology, morphology, and genetics (5) A wide range of genetics stocks are available and (6) It has well-defined genetic maps.

Archaeological evidence suggests that in the past, barley known as Indra Jau and it was more popular in every religious ceremony as sacred grain. Barley was recognized early on as a hearting testing, high-energy food. The effectiveness of β-glucan in barley food products lowering the blood cholesterol and high β-content in barley make it appealing for functional food concepts and glycemic index has been reported in numerous publications and is widely accepted. Beside β-glucan and dietary fiber, barely contain also many other bioactive compounds. Barley is a rich source of tocols, including tocopherol and tocotrienols which are known to reduce serum lethal density level cholesterol through their antioxidant action. The barley grains composed of 4-9% β-glucan, lipid 2-3%, protein 10-17%, starch 65-68% and minerals 2-2.5% respectively.

The major share of production of barley in India comes from the traditionally barley growing states like Rajasthan, Uttar Pradesh, Madhya Pradesh and Haryana. However, Punjab, Himachal Pradesh, Jammu and Kashmir also contribute but in the limited extent. Uttar Pradesh and Rajasthan have great significance in both area and production of barley. The cultivated area under barley in Uttar Pradesh was estimated about 1.46 lakh hectare with the production of 358 lakh tones with an average productivity of 24.5 q/ha. (ICAR-IIWBR, Kernel Progress Report 2015-2016). United States Department of Agriculture (USDA) estimated that the barley production in India during the crop year 2016-17 are lower by 1.90 lakh tones i.e., about 15.10 lakh tones. Barley grain contains 11.5% Protein, 69.6% Carbohydrate, 1.3 % fat, 1.2% Fibre and 3.9% Mineral (Singh, 1998).Use of stable cultivar over the several environments for high seed yield and quality characteristics is the important for many crops. When cultivars are tested in the term of seed yield at the multi-environmental trials, great difference are commonly observed in the yield performance over environments. Raffi *et al*. (2004) reported that G × E interaction is of much value in the selection of better genotypes. G × E interaction investigated that the breeder can decide to restructure a programme to minimize interaction effect, or to produce varieties with the specific adaptation of particular environments (Eisenmann *et al.* 1990). This interaction indicates that the genotypes react in different ways to the variable environmental conditions.

Bi-plot analysis is one of the best ways to visualize interaction patterns between the genotypes and environments (Yan and Kang 2003). This approach is being used to estimate genotype by year (G×Y) interaction using AMMI model, to identify barley genotypes with stable and high yield performance and to observe association of different meteorological variables with tested growing seasons. The GGE bi-plot technique is a powerful tool to estimate and visualize genotype by the environment interaction, which is widely used by the breeders and agronomists all over the world (Agyeman *et al.* 2015). The genotypes were identified by the Breeder was stable with relatively performance across a range of environments (Mohammedi *et al.* 2014). Rao *et al.* (2011) revealed that AMMI bi-plot and genotype of main effect and genotype × environment interaction (GGE) bi-plot have been used to visualize genotype and environment interaction.

The main two methods one is AMMI analysis, referred to as double-centered principal component analysis (PCA), and second GGE bi-plot analysis is based on environment-centered PCA. The AMMI model incorporates the analysis of variance (ANOVA) and PCA in a single statistical model (Gauch and Zobel 1996). The AMMI bi-plot analysis that, the first interaction principal component (IPCA1) had explained 13.6% of the genotype by environment interaction and the AMMI 1 had a model 92.4% fitness by treatment sum of square of genotype by the environment interaction of barley genotypes and was explained 7.6% noise. For the selection of genotype by environment interaction of barley genotypes, AMMI 1 model gives the best model fit.

Yan, Kang *et al.* (2003) state that, the analysis

of variance showed that the effects of genotype (G), environment (E) and their interaction (G × E) on grain yield were statistically significant is and regarded as irrelevant for the genotype evaluation. This is the reason that E is removed from the phenotypic data observed, which helps to concentrate on G and GE effects, which are relevant for the genotype evaluation. The environment (E) effect was a predominant source of the variation and accounted for 71.93% of the total sum of squares (TSS), while G and GE interaction sources of variation accounted for 5.97% and 22.10% of the total variation, respectively. The GE effect was about four times greater than the G effect, which suggesting the possible existence of different mega environments with the different top-yielding genotypes. Recently GGE bi-plot analysis considered to be one best method (Yan *et al*. 2000) being used for many purposes like stability analysis, multi environment testing, genotype by environment interaction study, genotype by pathogen interaction study, genotype by trait interaction study and selection of best parent and parental combination study etc. which are directly or indirectly immensely helps to the researchers during research/experiment beneficial for human being.

MATERIALS AND METHODS

Experimental site

This experiment was conducted during *Rabi* (winter) season of 2017-18 at the Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University and Varanasi. For the yield stability performance of 69 genotypes, yield data of same genotypes of two environments planted in previous year is used. All genotypes were planted in randomized complete plot design with three replications and each genotype was sown in line having 2.75 m length with row to row where distance plant to plant is 25 cm and 10 cm, respectively to raise the good crops.

Climate and weather

Geographically, Varanasi is situated at 25.280N latitude and 82.950E longitude in North Gangetic plain in eastern part of Uttar Pradesh (India). The dry summer starts in April and lasts until June followed by the monsoon season from July to September. The ranges of temperature are between 22 and 46 °C in the summers. In Varanasi winter experience a very large variations with downright cold nights and warm days. The average annual rainfall is 1100 mm (44 inch).

GGE bi-plot analysis for yield stability performance

GGE bi-plot analysis is one of the most paramount approach to know the yield stability of genotypes across the location or environment, to know the best mega environment to explore the genotypes of a particular crop and yield performance of a genotypes in different environment with its actual potential. First time bi-plot analysis was introduced by Gabriel (1971) while still it is very new technique to many scientists. More recently the term GGE bi-plot analysis was proposed and uses by Yan *et al.* (2000) for genotype and environment interaction study. Under present investigation GGE bi-plot was performed through online R software using data of three locations of 69 barley genotypes for yield stability analysis. Besides this there are several important uses of the bi-plot analysis like multi environment testing, genotype by trait interaction study, locations discriminating value and stability and genotype by pathogen interaction study etc.

STATISTICAL ANALYSIS

The data obtained were analysed using genotype and genotype by environment interaction (GGE) bi-plot. The model for the GGE bi-plot based on singular value decomposition (SVD) of first two principal components is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

where, Y_{ij} is the mean yield of genotype i in environment *j*, μ – the grand mean, β_j – the mean yield of all the genotypes in environment j, λ_1 and λ_2 – the singular values (SVs) of the 1st and 2nd principal components (AXIS1 and AXIS2), ξ_{i1} and ξ_{i2} – the eigenvectors of genotype *i* for AXIS1 and AXIS, respectively, η_{j1} and η_{j2} – the eigenvectors of environment *j* for AXIS1 and AXIS2, respectively, ε_{ij} – the residual associated with genotype *i* in environment *j*.

To generate a bi-plot can be used for visual analysis

of multi-environmental trial data, and singular values have to be partitioned into the genotype and environment so that the above model can be as,

$$Y_{ij} - \mu - \beta_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij}$$

where $g_{i1}e_{1j}$ and $g_{i2}e_{2j}$ are AXIS1 and AXIS2 scores for genotype *i* and environment *j*, respectively. In a bi-plot, genotype *i* is displayed as a point defined by all g_i values, and environment *j* is displayed as a point defined by all e_j values. All bi-plots presented in this paper were generated using the *R* software.

Genetic Divergence by D² statistic

Genetic divergence amongst different genotypes (recombinant Inbred Lines derived from two diverse parents *viz.*, highly resistance and highly susceptible) is assessed based on *inter se* genetic distances amongst 69 lines/genotypes. D² statistic of Mahalanobis (1936) is one of the most effective tools being used to measure the genetic distance between the genotypes. Genetic distance is defined as the extent of gene differences between genotypes as measured by allelic frequencies at a sample of loci. Genetic similarity, on the other hand is defined as the converse of the genetic divergence i.e., the extent of genetic similarity among the genotypes.

The D² values between the genotypes were obtained as the sum of squares of differences of the values of the corresponding transformed variables. For each pair of combinations, the mean deviation, i.e., $di = Yi^1 - Yi^2$, where *Yi* denotes the transformed variables (I = 1, 2, 3, 4, 5……...p) were calculated and the D² was then calculated as sum of the squares of those deviations, i.e.,

$$D^2 = \sum (Yi^1 - Yi^2)^2$$

Where,

P = number of characters.

The significance of the D^2 values were tested by treating them as chi-square at *p* degrees of freedom where *p* is the number of characters considered:

Grouping of genotypes by Tocher's method

After arranging the D^2 values of all combinations of one genotype with the others in ascending order of magnitudes the barley genotypes/lines were grouped into a number of clusters by Tocher's method as described by Rao (1952). The analysis of data for D² was performed through Windostate software. The criterion used in the method was that any two varieties/ genotypes belonging to the same cluster, at least on an average show a smaller D² value than those belonging to two different clusters. Then inter and intra cluster distance were calculated and their relationships were dramatically represented.

Experimental Research materials

Sl. N.	Genotypes	Rowed	SN	Genotypes	Rowed
1	INBON-05-79	Six	36	24th IBON-1	Six
2	INBON-05-72	Six	37	25th IBON-45-1	Six
3	WfBCB-88	Six	38	25th IBYT-10-3	Six
4	IBGP-03-49	Six	39	25th IBON-54-1	Six
5	IBGP-03-65	Six	40	25th IBON-11	Two
6	IBSCGP-05-16	Six	41	25th IBON-03-11	Six
7	ISBCB-02-13	Six	42	25th IBON-03-6	Six
8	ISBCB-02-9	Six	43	26th IBYT-16	Six
9	ISBCB-02-10	Six	44	26th IBYT-11-1	Six
10	NBPGR-07-08	Six	45	26th IBYT-49	Six
11	BCB-73	Two	46	29th IBON-6	Six
12	BCB-W-03-92	Six	47	AMBER	Six
13	11th HBSN-127	Six	48	SONU	Six
14	11th HBSN-175	Six	49	RATNA	Six
15	11th HBSN-91	Six	50	ATHOULPA	Six
16	11th EMBSN-22	Six	51	HORMAL	Two
17	11th EMBSN-23	Two	52	MARRIA	Six
18	11th EMBSN-26	Six	53	PL-825	Six
19	11th EMBSN-20	Six	54	HIMANI	Six
20	11th EMBSN-21	Six	55	YARDU	Six
21	11th EMBSN-37-1	Two	56	PL-751	Six
22	11th EMBSN-40	Six	57	V-MORALES	Six
23	11th EMBSN-47-03	Six	58	HANLEY	Two
24	12th EMBSN-2	Six	59	RD-2715	Six
25	14th HBSN-05-6	Six	60	CANUT	Six
26	14th HBSN-05-8	Six	61	JAGRATI	Six
27	22nd IBYT-7	Six	62	AZAD	Six
28	22nd IBYT-5-1	Six	63	K-551	Six
29	22nd IBYT-04-86	Six	64	MOROC-9-75	Six
30	22nd IBYT-9-2	Six	65	KARAN-16	Six
31	22nd IBYT-01-2-2-4	Six	66	JYOTI	Six
32	22nd IBYT-7-2	Six	67	RD2552	Six

33	22nd IBYT-99-11	Six	68	LAKHAN	Six
34	22nd IBYT-04-85	Six	69	K-603	Six
35	24th IBON-40-1	Six			

RESULTS AND DISCUSSION

The experimental results obtained from the present study conducted during *Rabi* 2017 on 69 genotypes of barley are discussed with the following heads:

Analysis of variance:

1. GGE bi-plot analysis for yield stability performance.
2. Genetic Divergence using Tocher's method.
3. Yield performance of 25 best genotypes in three environments.

Analysis of Variance

The analysis of variance for 6 quantitative traits including grain yield in 69 barley genotypes were performed using Windostate software and excel approach, ANOVA revealed that the treatments (genotypes) showed significant differences for all the traits except effective tiller numbers under study (Table 1). The *per se* performance of genotypes for all the 6 quantitative traits were showed with range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance as percent of mean genetic advance etc. given in the table 2.

GGE bi-plot analysis for yield stability performance 69 barley genotypes

The result of bi-plot analysis using yield data of three years revealed that AXIS1 explained 57.6 per cent variation while AXIS2 was explained 31.07 per cent variation. Since, genotypes were planted in 2017 in two dates like early and late sown condition hence, there was very slight differences in their yield so both the environments come together (Fig. 1) as compared to third environment (2018) which for from the two locations of year 2017. Genotypes like G4, G9, G47G52, G53, G55, G67, G69, etc. belonging to very close to environment (2018) to be considered good to select for crop improvement program. Fig. 2 (which won where/what) indicates that genotypes are located close to centre of figure are very stale in response to yield can be select and recommend to the farmers for cultivation across the locations. In other hand genotypes namely G9, G55, G67 and G68 were high yielding in 2018 but not so

Table: 1. Analysis of variance for six traits in 69 barley genotypes

Source	D.f.	DF	DM	ET	PH Awn+	PH Awn-	1000GW
Replication	2	58.60*	16.00	2.88	21.13*	50.04**	13.08**
Treatment	68	64.63***	82.41	4.44	15.83***	24.40***	99.40***
Error	136	8.59	79.56	3.47	5.24	4.99	1.74

**, **, ***Significant at 5%, 1% and 0.1% level respectively.*

Table 2: Estimation of range, mean, components of variance and genetic parameters for 6 traits in 69 barley genotypes

	DF	DM	ET	PH Awn+	PH Awn-	1000GW
Min.	2.00	3.00	3.665	5.40	76.75	26.80
Max.	2.00	05.00	11.16	97.25	93.00	60.25
Mean	68.63	98.65	6.14	1.61	84.11	41.92
GCV	7.71	1.21	11.34	2.51	3.70	16.66
PCV	8.81	9.12	32.37	3.54	4.55	16.96
Vg	28.01	1.42	0.48	5.29	9.70	48.82
Vp	36.61	80.99	3.95	10.54	14.70	50.57
Heritability (%)	96	87	62	94	89	87
Gen. Adv. at 5 %	13.89	0.331	8.18	3.66	6.19	33.74
CV (%)	4.27	9.04	30.32	2.49	2.65	3.15
Env. Var.	8.59	9.56	3.47	5.24	4.99	1.746

DF = Days to 50% flowering, DM = Days to maturity, ET = effective tillers/plant, PH Awn+ = plant height with awn, PH Awn= plant height without awn, 1000GW= 1000 grain weight/plant.

stable followed by genotypes like G17, G21, G51 and G44 of environment 2017 early and late sown. So, environment/location wise genotypes G69 of environment 2018 was high yielding but for from the centre considered that it is not stable followed by G17, G21, G 44 and G51 of both environments of year 2017. Through Fig. 3 it could be concluded that which one genotype out of G69 is better for higher yield or higher yield with its stable performance across the environment and which environment/ location is good for exploring the particular genotype completely through the help of centre of vector and straight red line symbol as well as cross over of the vector.

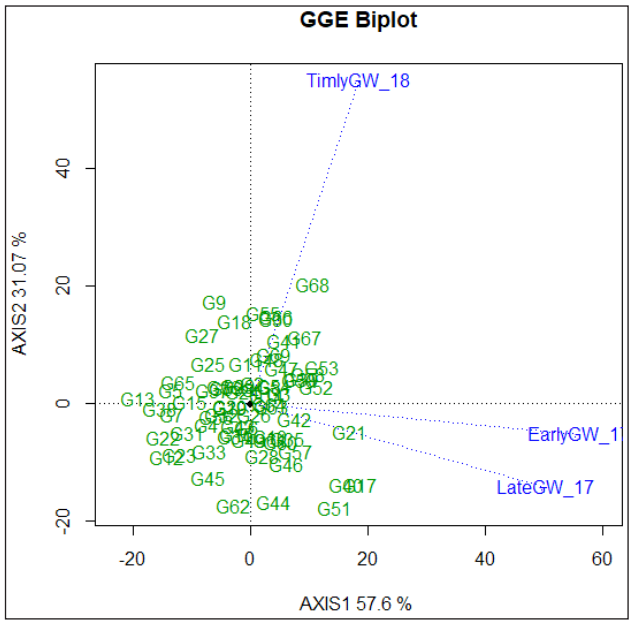

Fig. 1: GGE Bi-plot analysis among 69 barley genotypes using yield data of three locations

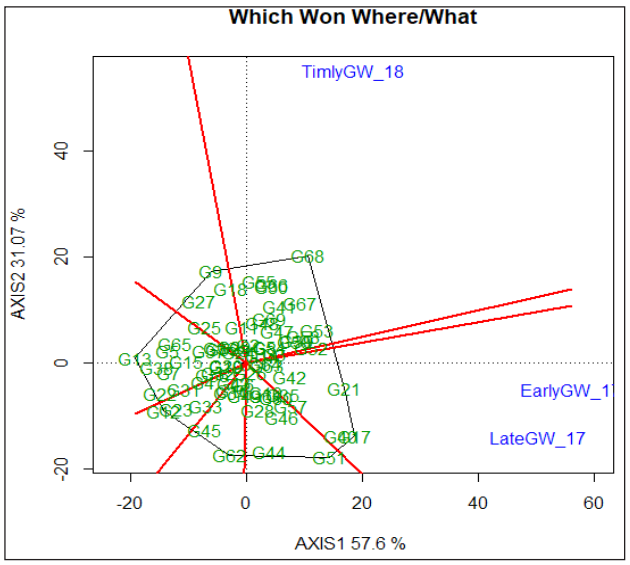

Fig. 2: GGE Bi-plot analysis among 69 barley genotypes to know which won where/with at

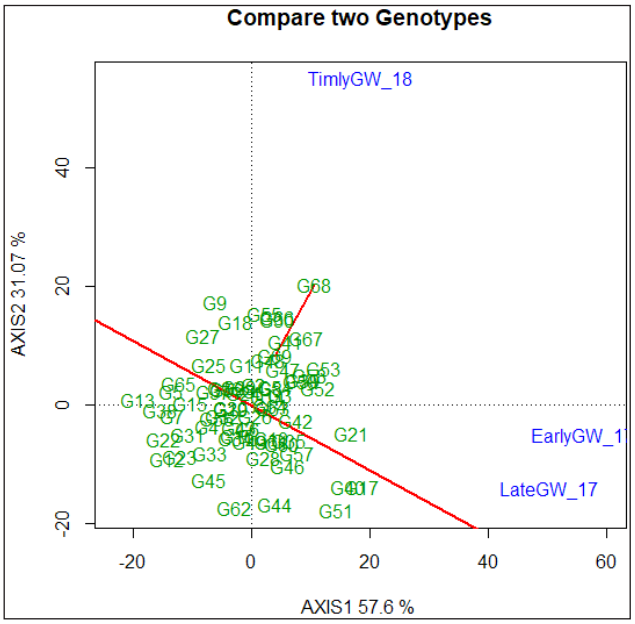

Fig. 3: GGE Bi-plot analysis among 69 genotypes to compare the genotypes of three locations

Genetic Divergence

Genetic divergence was studied based on D^2 statistics, the compositions of different clusters obtained from the analysis have been presented in table 3 and 4 respectively.

Table 3: Intra & inter-cluster D^2 values of four clusters of 69 genotypes by Tocher's Method

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	2811.19	12239.10	7302.33	26007.87
Cluster 2	12239.10	275.27	32705.81	68008.57
Cluster 3	7302.87	32705.81	0.00	6436.33
Cluster 4	26007.87	68008.57	6436.33	0.00

Note: *Bold figures indicates intra cluster D^2 values.*

Table 4: Cluster mean values for six traits of 69 genotypes estimated using Tocher's method

Cluster	DF	DM	ET	PH Awn+	PH Awn-	1000 GW
Cluster 1	68.24	98.48	6.15	91.50	83.89	41.69
Cluster 2	76.33	100.83	4.50	94.10	88.71	44.38
Cluster 3	63.50	94.00	7.83	85.90	77.75	45.30
Cluster 4	52.00	101.50	7.00	89.15	76.75	37.75

Note: *Bold figures indicates highest and lowest values for traits in the cluster.*

Sixty-nine barley genotypes are grouped into four different clusters based on the *inter-se* genetic distance. This indicates presence of considerable genetic diversity among barley genotypes used for present investigation. In this table cluster I comprises with 62 genotypes followed by cluster II consisted of five genotypes, cluster III and cluster IV having single genotype each. Inter and intra cluster distance (D values) have been presented in the table 6 dramatically shown in Fig. 4.

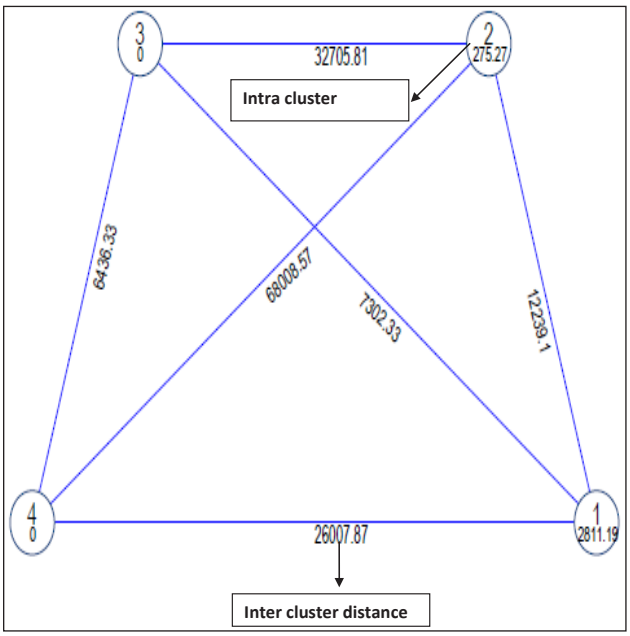

Fig. 4: Inter and Intra Cluster distance among four cluster using Tocher's Method

The cluster I which is largest one among the four and it has also maximum intra cluster distance value (2811.19) followed by cluster II (275.27). The highest inter cluster distance was found between cluster II and cluster IV i.e., 68008.57 followed by cluster I and cluster IV (26007.87) and also by cluster II and cluster III (32705.81) respectively presented in table 3 and fig. 4. The smallest inter cluster distance found between cluster III and IV (6436.35) presented in table 3. The cluster mean values for different six traits of different clusters have been presented in table 4. The highest cluster mean value of cluster II (76.33) was found for days to 50% flowering while it lowest (52.00) in the cluster IV. Similarly, highest cluster mean value (101.50) for days to maturity in the cluster IV and lowest in the cluster III (94.00). For 1000 grain weight highest mean value (45.30) in the cluster III, lowest (37.75) in cluster IV, for effective tillers per plant it was highest (7.83), lowest mean value (4.50) in the cluster II, for plant height with awn highest mean value (94.10) in the cluster II and lowest mean value (85.90) in the cluster III while for plant height without awn it was higher (88.71) in the cluster II and lowest (76.75) for cluster IV respectively.

Based on intra and inter cluster distance, cluster mean values and presence of adequate genotypes having different desirable traits showed greater scope to select the genotypes to be used in breeding programme for crop improvement. The trait (s) contributed highest towards divergence, maximum and minimum values suggesting the enough scope to improve the population in any direction yield or yield contributing traits as Ali *et al.* (2007) reported the same for the trait like days to 50% flowering under late sown condition.

Contribution of the individual characters towards divergence

The perusal of the comparison on contribution of different character towards genetic diversity was based on ranking method (Table 5) and it was observed that number of effective tillers per plant contributed 51.71 per cent followed by plant height with awn (42.63%) and another trait.

Table 5: The percent contribution of the individual trait towards divergence and their rank in barley

Sl. No.	Sources/Traits	Time Ranked 1st	Contribution (%)
1	Days to 50% flowering	5	0.21%
2	Days to maturity	4	0.17%
3	Effective Tillers per plant	1213	51.71%
4	Plant height with Awn	1000	42.63%
5	Plant height without Awn	0	0.0%
6	1000GW	124	5.29%

Top 25 best outstanding genotypes in response to yield in three different environments

Out of 69 barley genotypes top 25 genotypes in response to their yield in three different environments are presented in table 7. The yield range of top 25 genotypes sown early in the year 2017 was 40.70 gm to 57.30 gm while this range was for late sown condition in the same year 37.50 to 49.00 gm respectively. The yield range of

Table 6: Intra Cluster distance values of four clusters and number of genotypes belonging in each cluster developed through Tocher's method

	Intra Cluster D value	Total Genotypes/lines
Cluster 1	2811.19	**62** (NBON-05-72, WfBCB-88, BGP-03-65, IBSCGP-05-16, ISBCB-02-13, ISBCB-02-9, NBPGR-07-08, BCB-73, BCB-W-03-92, 11th HBSN-127, 11th HBSN-175, 11th HBSN-91, 11th EMBSN-22, 11th EMBSN-23, 11th EMBSN-26, 11th EMBSN-20, 11th, EMBSN-21, 11th EMBSN-37-1, 11th EMBSN-40, 11th EMBSN-47-03, 12th EMBSN-2, 14th HBSN-05-6, 14th HBSN-05-8, 22nd IBYT-7, 22nd IBYT-5-1, 22nd IBYT-04-86, 22nd IBYT-01-2-2-4, 22nd IBYT-99-11, 22nd IBYT-04-85, 24th IBON-40-1, 24th IBON-1, 25th IBYT-10-3, 25th IBON-54-1, 25th IBON-11, 25th IBON-03-11, 25th IBON-03-6, 26th IBYT-16, 26th IBYT-49, 29th IBON-6, AMBER, SONU, RATNA, ATHOULPA, HORMAL, MARRIA, PL-825, YARDU, PL-751, V-MORALES, HANLEY, RD-2715, CANUT, JAGRATI, AZAD, K-551, MOROC-9-75, KARAN-16, JYOTI, RD2552, LAKHAN, K-603).
Cluster 2	275.27	**05** (ISBCB-02-10, 22nd IBYT-9-2, 22nd IBYT-7-2, 25th IBON-45-1, 26th IBYT-11-1, HIMANI).
Cluster 3	0.00	**01** (INBON-05-79).
Cluster 4	0.00	**01** (IBGP-03-49).

Table 7: Top 25 best genotypes in response to yield in three different environments

Sl. No.	Genotypes Year-2018 (timely sown)	1000 GW	Genotypes Year-2017 (early sown)	1000 GW	Genotypes Year-2017 (late sown)	1000 GW
1	29th IBON-6	60.2	IBRWAGP-04-66	57.3	IBRWAGP-04-66	49.0
2	24th IBON-40-1	55.1	12th HBSN-7	55.9	12th HBSN-7	47.0
3	24th IBON-1	54.5	ISBCB-02-10	55.5	22nd IBYT-7-2	46.1
4	11th EMBSN-23	54.3	22nd IBYT-7-2	54.7	ISBCB-02-10	45.5
5	CIHO-7603	54.1	13th EMBSN-71	51.0	22nd IBYT-99-11	45.5
6	IBSCGP-05-16	52.8	29th IBON-6	50.3	14th HBSN-05-6	45.1
7	26th IBYT-49	52.8	26th IBYT-49	49.5	22nd IBYT-04-85	44.7
8	12th EMBSN-2	51.9	25th IBON-45-1	48.5	25th IBYT-10-3	44.6
9	22nd IBYT-04-85	50.6	25th IBON-39-1	47.9	22nd IBYT-7	43.7
10	25th IBYT-10-3	49.2	11th EMBSN-34	47.1	INBON-05-79	43.5
11	AMBER	49.2	22nd IBYT-04-85	46.2	11th EMBSN-54	42.9
12	11th HBSN-127	49.1	22nd IBYT-99-11	45.0	22nd IBYT-01-2-2-4	41.5
13	22nd IBYT-5-1	49.1	22nd IBYT-5-1	45.0	INBON-07-08-8	41.5
14	11th EMBSN-54	48.1	AMBER	44.6	CIHO-8355	40.2
15	22nd IBYT-99-11	47.8	CIHO-5923	44.3	11th HBSN-91	40.2
16	22nd IBYT-5-1	47.7	12th EMBSN-2	44.1	11th HBSN-127	39.6
17	22nd IBYT-01-2-2-4	47.7	26th IBYT-11-1	44.1	INBON-07-08-71	39.3
18	WfBCB-88	47.2	22nd IBYT-01-2-2-4	44.0	25th IBON-45-1	39.2
19	11th EMBSN-21	45.8	11th EMBSN-23	43.6	CIHO-6260	38.7
20	INBON-05-79	45.7	11th EMBSN-54	43.1	25th IBON-03-6	38.6
21	INBON-07-08-71	45.6	25th IBYT-10-3	43.0	25th IBON-11	38.5
22	INBON-07-08-8	45.3	22nd IBYT-7	42.5	22nd IBYT-99-14-1	38.3
23	BCB-W-03-92	44.8	7th HMBSN-1-2-1-1	42.3	11th EMBSN-34	37.8
24	CIHO-5923	44.6	25th IBON-11	42.2	25th IBON-46	37.8
25	BCB-73	43.7	25th IBON-03-6	40.7	24th IBON-1	37.5

25 best genotypes for the year 2018 under timely sown was 43.70 to 60.25 gm. Declining the yield performance in late sown condition was because of unfavourable condition but still yield performance these genotypes were satisfactory hence, this genotypes could be easily taken for breeding programe for crop improvement.

CONCLUSION

The study revealed that timely sowing barley yield was highly influenced by variable cultivation

environments followed by the differences among genotypic effects, and genotype by environment interaction (G × E) contributing the least. This study also clearly demonstrated that the GGE bi-plot model was effective for the determination of the magnitude and pattern of G × E effect and visualizing the yield potential and stability of barley genotypes as well as discriminating ability and representativeness of the test environments.

The study results identified timely sowing barley variety in 2018, G69 as the closest to the "ideal" genotype in terms of yield potential and stability. Varieties G9,G55,G67 and G68 were also selected as superior genotypes.

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