Identifying superior feed barley genotypes using GGE biplot for diverse environments in India

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Abstract

Barley (*Hordeum vulgare* L.) is an important feed purpose cereal grown under diverse production conditions and harsh environments. The present investigation was carried out to study performance of advanced breeding lines and identify superior genotypes of feed barley using multi-environment trial data from All India Coordinated Wheat and Barley Improvement Programme (AICW&BIP). Ninety three experimental genotypes and five released cultivars were tested across eleven locations during four years. Grain yield and other agronomic traits were analyzed. Stability and genotype superiority for grain yield and other traits were determined using genotype and genotype × environment (GGE) biplot analysis. The result showed that environment and genotype contributed 32.9 to 67.4% and 4.7 to 20.4% of the total variation, respectively. The genotype × environment interaction contributed 27 to 44% of total variation. The experimental genotypes showed arrays of variation for grain yield in each year, with mean values ranging from 2.12 to 5.36 t/ha. Twelve experimental genotypes were identified, which were either superior or equal performance to the best check based on their high yield and stability across environments. The locations Varanasi, Kanpur, Vijapur and Durgapura discriminated the genotypes more than other sites for grain yield and agronomic traits. The findings provided valuable information on wide adaptation of feed barley genotypes, which could be useful for barley improvement programmes.

Key words: Barley, GGE biplot, multi-location trials, grain yield, mega-environment

Introduction

Barley (*Hordeum vulgare* L.), the fourth most important cereal crop widely grown over 100 countries (FAOSTAT, © FAO Statistics Division 2012, http://faostat.fao.org) is considered suitable under diverse production conditions for its tolerance to biotic and abiotic stresses. It is mainly grown as feed crop in many parts of the world including Indian sub-continent. High fodder and grain yield is one of the most important objectives of most of the barley improvement programmes. However, both these traits are highly influenced by environment and genotype × environment (GE) interactions. The Barley Network under All India Coordinated Wheat and Barley Improvement Programme (AICW&BIP) aims at developing new cultivars to sustain barley cultivation in the country through multi-location yield trials. For a new cultivar to be accepted by the barley growers, it must show higher and stable yield than the existing commercially successful cultivars. Several statistical models have been used to understand complex GE interactions [1] for identifying superior genotypes of different crops. Usually analysis of variance (ANOVA), principal component analysis (PCA) and linear regression (LR) analysis are used to study multi-location data. ANOVA can only describe the genotypic main effects being an additive model [2], while, PCA being a multiplicative model, does not describe the additive main effects [3]. The linear regression models although combine both additive and multiplicative components but the interaction gets confounded with the main effects compromising the power of general significance test [4]. The additive main effects and multiplicative interaction (AMMI) model, explains GE interaction much effectively. The use of biplot methodology [5] explains the complex GE interaction in a much

simplistic graphical manner. To understand GE, two types of biplots, the AMMI biplot [6] and the GGE biplot [7] are most commonly used. The performance of a cultivar in a test environment is a cumulative measurement of genotype main effect (G), environment main effect (E) and the GE interaction [1, 8]. The GGE biplot removes the E and integrates the G with GE interaction effect and thus detects GE interaction in the data besides it identifies 'which-won-where' pattern and mega-environments [9]. Different statistical analysis like AMMI biplot [6]; GGE biplot [7]; shifted multiplicative model (SHMM) [10] or pattern analysis [11] have widely been used to understand the G and GE interaction in many crop species including rice [12], wheat [13, 14] and barley [15].

In multi-environment trials (MET) the genotype by environment interaction can be subdivided into genotype by location (GL) interaction, genotype by year (GY) interaction and in genotype by year by location interaction (GYL). The presence of such type of interactions make it difficult to predict the performance of genotype in different locations (GL) in different years (GY) and location over years (GYL). The repeatability or non-repeatability of GL interaction is determined by multi-locations trials repeated over years. GY interaction is the variable response of genotypes across years which cannot be exploited since it is not possible to predict future climate [16]. The large variation due to environment (E) is irrelevant in cultivar evaluation while it is G and GE that are more relevant [17]. The significant GE interaction in an experiment is due to changes in the relative rankings or magnitude of the differences among genotypes in different environments [18]. The barley testing locations under AICW&BIP are distributed across latitude, longitude representing diverse barley growing situations in India. For developing improved and stable cultivars, nature and magnitude of the effects of genotype, test environments and interaction between the two must be understood. This study was conducted to determine the performance of elite genotypes, identify superior genotypes, examine association among the testing locations and identify locations that discriminated among the genotypes more than others using GGE biplot techniques.

Materials and methods

Data used in the present study was obtained from feed barley initial varietal trials under irrigated condition (IVT-FB-IR) of four years [2007-08 (2008) to 2010-11 (2011) crop seasons] under AICW&BIP. A total of 93

advanced breeding lines from different centres and five checks were used in the study (Table 1). Eleven diverse locations spread across eight states were included in the study resulting 39 environments. The experiment was conducted using randomized complete block design (RBD) with four replications. Individual plots of 6.9 m^2 consisted of six rows of 5 m length sown at 23 cm row spacing. The standard crop management practices in terms of fertilization, sowing date, seed rate, and weed management were adopted across all locations. Randomization was done for individual location in each year. The four middle rows were harvested from each plot. Data were recorded on grain yield, heading days, maturity days, plant height, 1000-grain weight (TGW) and number of tillers per meter (TLN). The analysis of variance (ANOVA) for individual trials and combined analysis across locations over years and zones was done using GenStat 14 software. The biplot was used to identify superior genotypes. It provides a reference "*ideal*" genotype in the biplot having the highest average value of all genotypes across locations and is stable with no genotype by environment interaction. A set of concentric circles are created using the *ideal* genotype at the center. The ideal genotype is used to rank other genotypes by drawing a performance line, going through the origin of the biplot to determine mean performance of a genotype. The arrow indication on the performance line represents increasing mean. Another line perpendicular to the performance line, called stability line also passes through the origin of the biplot with arrows in both directions which represent decreasing stability. A genotype lying farther on either side on the stability line of the biplot origin has a relatively lower stability. The GGE biplot analysis was also used to study relationship among locations using five common checks included in all locations in each year. Each environment in the biplot is connected to the origin with a line, called a vector. The cosine of the angle between the vectors of two environments approximates the correlation coefficients between them. The environments with longer vectors length are more discriminative of the genotypes; the short vectors are less discriminative. The closely associated environments suggest redundant locations. On the other hand, a large gap between environments suggests that additional testing locations are needed to fully sample the target environments. The "which-won-where" pattern of MET data shows the possible existence of different mega-environments. The polygon view of a biplot is the best way to visualize the interaction patterns between genotypes and

Table 1.   Name and origin of the experimental genotypes used in the study in different years at multi-locations in India

Origin	Genotypes contributed in different years			
	2008	2009	2010	2011
HAU, Hisar	BH910, BH911, BH912, BH913	BH920, BH922, BH923	BH932, BH933, BH934	BH946, BH947, BH948, BH902(C)
BHU, Varanasi HUB198	HUB196, HUB197,	HUB199, HUB200 HUB210	HUB208, HUB209,	HUB113, HUB114
JNKVV, Rewa	JB149	JB125, JB129	JB186, JB187, JB188	JB217, JB224, JB225
CSAUA&T, Kanpur	K890, K892, K894, K898, JYOTI(C)	K909, K916, K917, JYOTI(C)	K944, K958, JYOTI(C)	K1055, K1076, K1077, K1078, JYOTI(C)
NDUA&T, Faizabad	NDB1431, NDB1434	NDB943, NDB1458, NDB1470	NDB1475, NDB1476	NDB1506
PAU, Ludhiana	PL816, PL817, PL818, PL819	PL830, PL831, PL832, PL751(C)	PL841, PL842, PL843, PL844, PL751(C)	PL853, PL854, PL855, PL751(C)
ARS, Durgapura	RD2740, RD2741, RD2742, RD2743, RD2035(C), RD2552(C)	RD2763, RD2764, RD2765, RD2035(C), RD2552(C)	RD2784, RD2785, RD2786, RD2787, RD2035(C), RD2552(C)	RD2808, RD2809, RD2810, RD2811, RD2552(C)
GBPUA&T, Pantnagar	UPB1004, UPB1005, UPB1006	UPB1001, UPB1003	UPB1002, UPB1013, UPB1014	UPB1018, UPB1019, UPB1020

environments. The vertex genotype for each sector is the one that give the highest yield for the environments that fall within that sector. Thus, it indicates environmental groupings, which suggests the possible existence mega-environments.

Results and discussion

The analysis of variance for individual location showed significant variances due to genotype (data not presented). The combined ANOVA showed that zone, genotype, location within zone, genotype × zone and genotype × location within zone effects were highly significant for grain yields in all years of evaluation (Table 2). The relative magnitudes of the G, E and GE interaction are presented in Table 3. The result revealed that E was the most important source of variation in all the years contributing 37.6, 67.4, 58.6 and 32.9% of the total variation in 2008, 2009, 2010 and 2011 respectively. The contributions of G were 20.4, 4.7, 14.4 and 15.9% while the proportions of variation explained by GE were 42.0, 27.9, 27.0 and 44.0% during 2008, 2009, 2010 and 2011 respectively. The location means, grand mean of all locations for each year, range and coefficient of variation (CV) for grain yield are given in Table 4. There were arrays of variation in grain yield across the locations with the values ranging from 2.12 t/ha at Ranchi in 2009 to 5.36 t/ha at Ludhiana in 2010. Mean grain yield varied significantly between years with values of 3.94, 3.25,

3.68 and 4.08 t/ha in 2008, 2009, 2010 and 2011 respectively. The mean of individual genotype evaluated across locations in different years (data not presented) for yield, days to flowering, number of tillers per plant, plant height at maturity and thousand grain weights showed high variation among the materials. Based on the mean performance of the 98 genotypes across the years, JB188 (2.6 t/ha) and RD2743 (4.7 t/ha) were the lowest and highest yielders, respectively.

Mean performance and stability of the genotypes across locations

Mean performance and stability of genotypes have been presented graphically through GGE biplot (Fig. 1). In 2008, the genotypes BH910, RD2742, RD2743 and cultivar Jyoti were closer to the point of ideal genotype (Fig. 1a). The only genotype NDB1470 was superior in 2009 (Fig. 1b). The genotypes BH933, NDB1475 and check variety RD2552 were superior performers (Fig. 1c) in 2010, while RD2811, RD2808, RD2809, BH946 and BH948 were superior to others in 2011 (Fig. 1d). The mean grain yield, days to heading, maturity days, tiller numbers per meter and TGW of these superior genotypes are given in Table 5. Among all, the genotype BH933 outperformed and was selected for evaluation in the subsequent years for considerations as a new cultivar. However, it could not be released due to lack of other important traits like resistance to diseases. BH933 can be used as an

Table 2. Combined ANOVA for grain yield and their level of significance for different years of evaluation

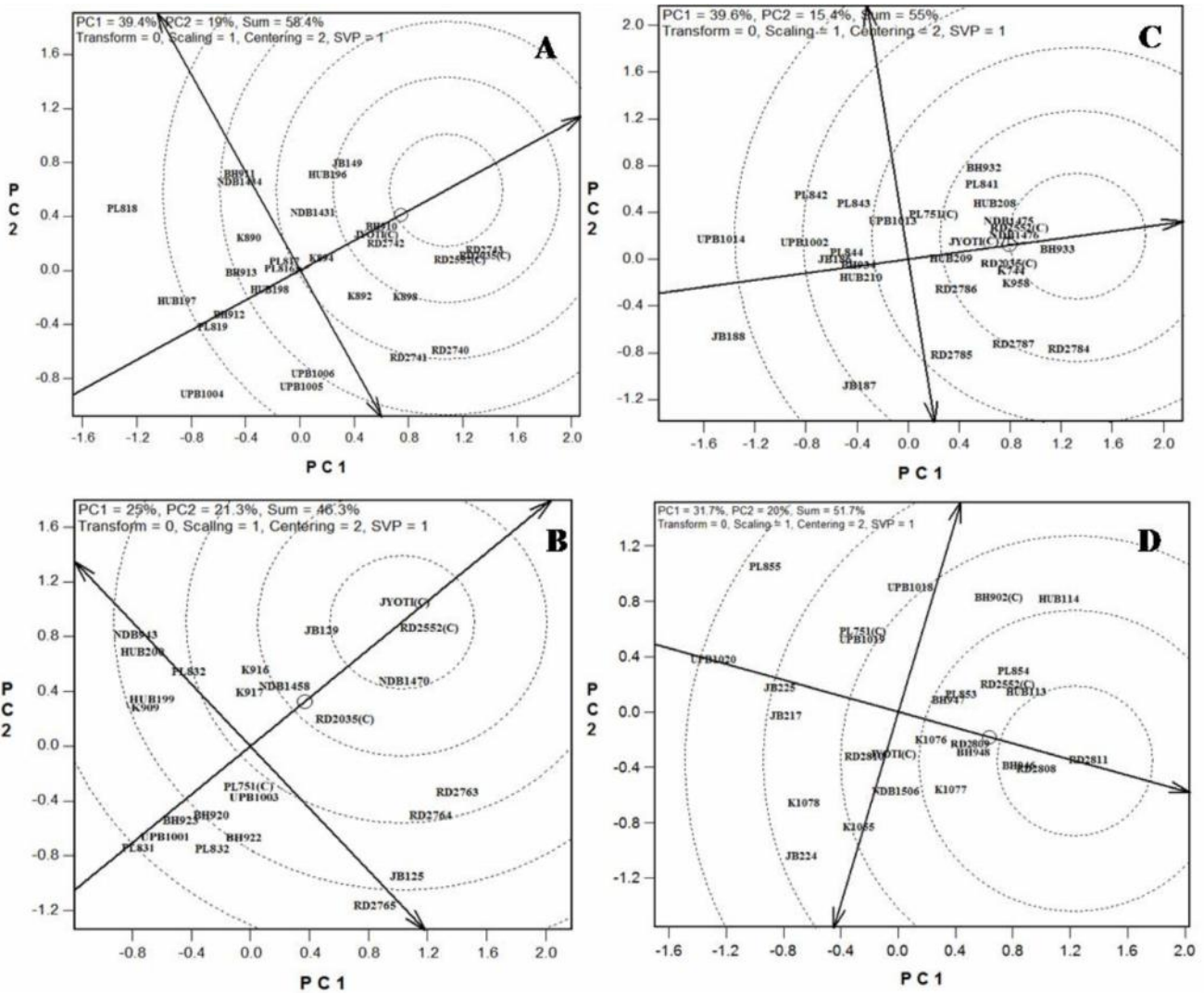| Source of Variation	2008		2009		2010		2011	
	df	Mean square	df	Mean square	df	Mean square	df	Mean square
Zone	2	14.1**	2	252.8**	2	80.6**	2	43.5**
Location/zone	6	41.4**	7	26.2**	8	108.0**	6	29.4**
Replication/(loc/zone)	27	0.2	30	0.3	33	0.2	27	0.3
Genotype	27	6.2**	24	2.0**	27	9.5**	26	3.6**
Genotype × zone	54	1.2**	48	1.8**	54	2.3**	52	1.4**
Genotype × (loc/zone)	162	1.5**	168	1.2**	216	1.6**	156	1.4**
Error	729	0.2	720	0.1	891	0.2	702	0.2
CV (%)		10.1		10.2		10.8		10.4

Where ** = significant at p = <0.01

Fig. 1. GGE biplots for grain yield for different years where A, B, C and D is mean versus stability biplots of the genotypes for years 2008, 2009, 2010 and 2011 respectively

Table 3. Mean sum of squares of variation explained by genotype (G), Environment and G×E interaction for grain yield

Year	Sources	Environment	Genotypes	G×E
2008	df	8.0	27.0	216.0
	MS	34.6**	5.54**	1.4**
	Proportion of G + L + GL (%)	37.6	20.4	42.0
2009	df	9.0	24.0	216.0
	MS	76.5**	2.0**	1.3**
	Proportion of G + L + GL (%)	67.4	4.7	27.9
2010	df	10.0	27.0	270.0
	MS	102.5**	9.3**	1.7**
	Proportion of G + L + GL (%)	58.6	14.4	27.0
2011	df	8.0	26.0	208.0
	MS	32.9**	3.7**	1.4**
	Proportion of G + L + GL (%)	41.1	14.9	44.0

** = significant at p= <0.01

Table 4. Locations yield means (t/ha), range, coefficient of variation (CV) of different years (2008-2011)

Locations	Grain yield (t/ha)				
	2008	2009	2010	2011	Overall location
Durgapura	3.66	4.23	3.82	4.28	4.00
Hisar	4.22	4.11	4.09	4.70	4.28
Ludhiana	4.39	4.47	5.36	#	4.74
Pantnagar	3.42	#	3.35	3.45	3.41
Faizabad	#	2.48	2.59	#	2.54
Kanpur	3.40	3.24	2.90	3.80	3.34
Rewa	4.15	3.61	4.27	4.00	4.01
Varanasi	3.75	2.43	2.63	3.46	3.07
Ranchi	#	2.12	4.69	3.46	3.42
SK Nagar	5.03	3.50	4.28	4.96	4.27
Vijapur	3.41	2.27	2.50	3.85	3.01
Year mean &	3.94	3.25	3.68	4.08	3.64
range	(3.41-5.03)	(2.12-4.47)	(2.50-5.36)	(3.41-4.76)	(2.54-4.74)
CV & range	10.11	10.24	10.84	10.40	-
	(2.4-19.0)	(3.3-14.6)	(2.7-19.3)	(2.7-16.8)	-

Where # = trials not conducted in this location on respective year

improved parent in barley crossing programs.

Environment evaluation

The relationship among the test environments based on grain yield is shown in Fig. 2. The environments differed in terms of discriminating ability for individual traits, as shown by their distance from the centre of the biplot. The Varanasi, Kanpur, Vijapur and Durgapura greatly discriminated the genotypes. Similar trends were observed for other traits i.e., days to heading, maturity days, plant height, tiller number and TGW (graphs are not presented). The locations showed different levels of association for individual traits. The angle of the location vector represents their degree of association. For example in case of grain yield the vector angle between Rewa and Pantnagar is obtuse which indicates that this two locations fall into two different contrasting environments. Pantnagar is closer to the foothill in Himalaya which is cooler during the crop season while Rewa is in the state of Madhya Pradesh under central India and mostly remains dry and warmer during the crop season.

Analysis of common checks

The GGE biplot (Fig. 3) showed that the equality lines divided the biplot into 4 sectors, where 3 checks retained the 10 locations out of 11 where feed barley trials were conducted. The testing locations may be divided into three mega-environments: one with Pantnagar, Vijapur, Hisar, SK Nagar, Rewa and Varanasi with BH902 as the winning genotype. The second mega-environment includes Ranchi and Faizabad with RD2552 as the winning genotype, while third mega-environment was represented by Durgapura and Kanpur with RD2035 as the winning genotype.

The GGE biplot can graphically detect the genotype by environment interaction pattern; identify winning genotype and delineate mega-environments among the testing locations [9]. However, this potential tool has not been exploited to analyze the multi-location trials data of barley improvement programme in India. The GGE biplots analysis on barley having
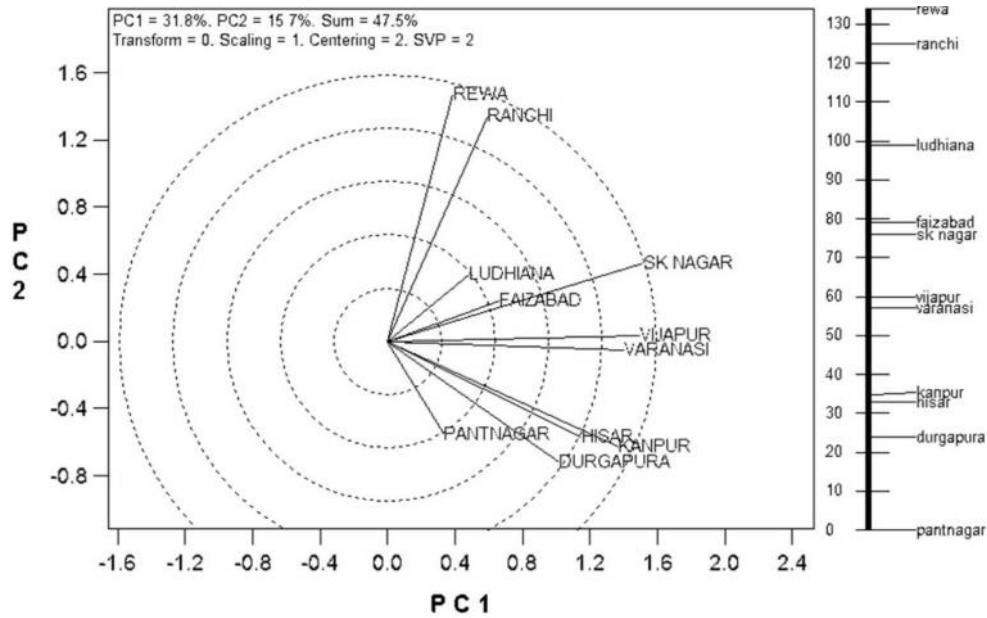
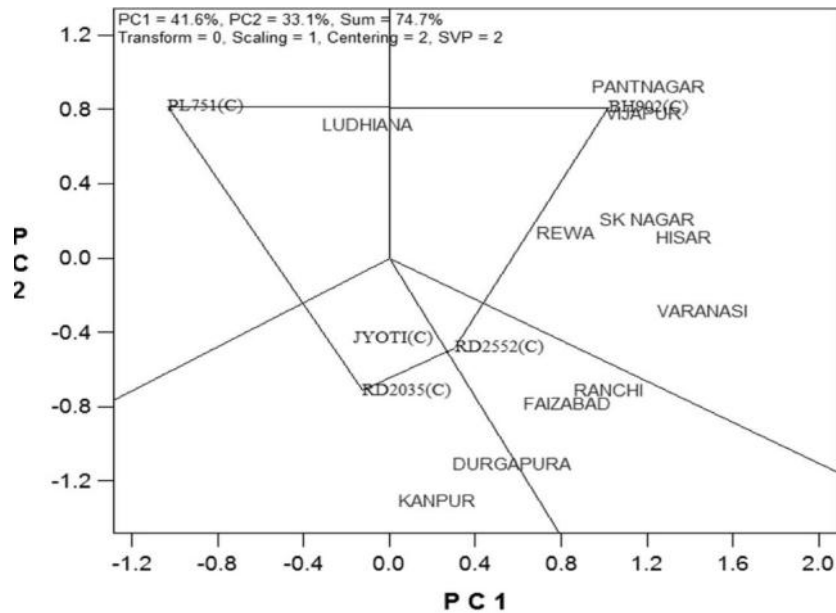**Fig. 2. Relation among 11 test locations for grain yield evaluated over 4 years**

Fig. 3. 'Which-won-where' pattern for different locations of four national checks evaluated across 11 locations for 4 years showing mega-environment

similar trends had also been reported by Dehghani *et al.* [15] in Iran. Previous reports suggest that normally in multi environment trials, the environment accounts for about 80% of the total variation [19]. In the present study it was observed that GE interaction explained higher proportion of the variation than G alone. The higher proportion of GE as compared to G is indicative of possible existence of different mega-environments among testing locations which has also been reported in previous studies [20].

The CV was low in all years across locations which indicated that the yield trials were properly conducted as per the recommended practices. The

Table 5. List of superior barley genotypes with the high and stable grain yields evaluated across different locations during 2008 to 2011 crop season

S.No.	Entry	Pedigree	Year of evaluation	Locations tested	Heading days	Maturity days	Tillers/ meter	Plant height	TGW	Yield (q/ha)
1.	BH910	RD2035/JB14	2008	9	76	120	111	96	41	4.27
2.	RD2742	RD2634/PL751	2008	9	78	120	104	101	41	4.29
3.	RD2743*	RD2503/RD2579 //RD2035	2008	9	83	123	110	102	42	4.67
4.	NDB1470	BHS519/Dolma	2009	10	79	119	122	85	43	3.67
5.	BH932	Sel from EC538158 (2005-06)	2010	11	84	119	140	83	34	4.13
6.	BH933**	13th EMBSN-4	2010	11	78	117	145	95	39	4.35
7.	NDB1475	NDB209 / NDB208	2010	11	78	117	139	84	35	4.13
8.	RD2808*	RD2706/RD2052 //RD2670	2011	9	76	115	101	83	43	4.18
9.	RD2809*	RD2503/RD2579 //RD2035	2011	9	80	118	104	87	41	4.11
10.	RD2811*	RD2579/JB26 //RD2552	2011	9	79	119	103	93	44	4.71
11.	BH946	BHMS 22A/BH549//RD2552	2011	9	79	118	111	92	43	4.4
12.	BH948	BHMS 21A/BH75//RD2552	2011	9	76	117	102	92	43	4.4

Where * = went up to first year of advance varietal trial, ** = evaluated in the final year of advance varietal trial.

complex GE interactions are simplified in different PC and the data are presented graphically. The use of GGE biplot in this study allowed identification of high yielding lines, stable across locations. These lines were superior to one or more checks used in the trials by being closer to the point of ideal genotype. Out of the 12 superior lines identified through GGE biplot, five lines (RD2743, BH933, RD2808, RD2809, RD2811) were promoted to advanced varietal trials while, BH933 went upto to final year of evaluation in the coordinated trials. These superior lines identified provided an option of introducing new materials into the production system in different barley growing regions in the country and can also be used in the hybridization programme for further improvement over the existing varieties. The finding of this study in terms of identifying superior genotypes using GGE biplot is in agreement with the previous users of this technique for similar objective in several crops including barley and wheat [13-15].

The GGE biplot analysis helped in understanding the usefulness of the different locations in their relative levels of discrimination among genotypes as well as relationship among them for various traits. The differences in association among different locations for different traits are suggestive of complex GE interactions for each trait. The locations such as Varanasi and Vijapur, although belonged to two different zones, close association between the two implies that only one of the two could be used under resource constraints. The large variation due to location indicated strong influence of environments and existence of mega-environment among trial conducting locations. This suggests the usefulness of GGE biplot technique for identifying mega-environments among barley growing locations. Our results suggested that there were three mega-environments for growing feed barley in India. Previous studies have reported the usefulness of GGE biplot in identifying superior genotypes and mega-environments [15, 19]. The present study provided new information on barley improvement programme in India.

Acknowledgements

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