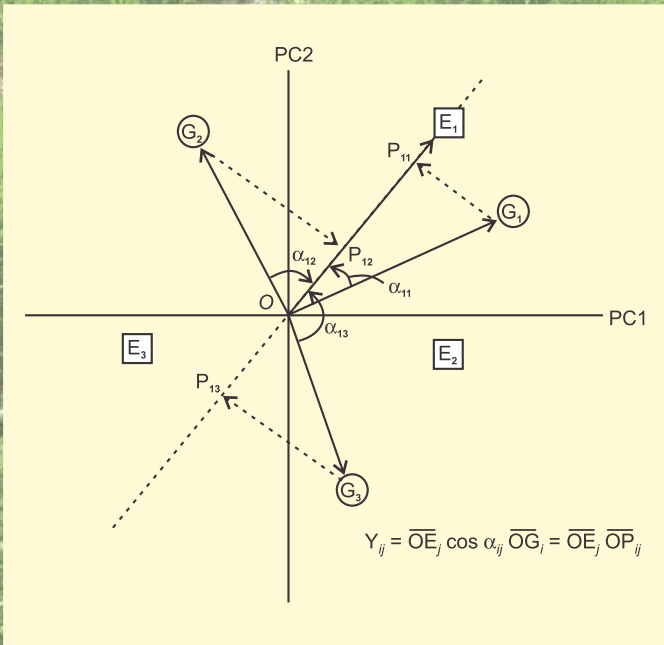


GGE BIPLLOT ANALYSIS for COORDINATED TRIALS: BARLEY



भा.कृ.अनु.प.- भारतीय गेहूँ एवं जौ अनुसंधान संस्थान

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Preface

In AICW&BIP programs, barley genotypes are evaluated at number of funded and non-funded centers in multi environment trials (METs) for testing the relative behavior of promising genotypes across environments. This helps to recommend the good genotypes in terms of yield for suitable environments. Genotype \times environment (GE) interaction is an important issue particularly for breeders in barley improvement programs. A significant GE interaction for a quantitative trait such as yield can seriously limit progress in selection. Variance due to GE interaction is an important component of the variance of phenotypic means. GE interactions complicate the identification of superior genotypes but their interpretation can be facilitated by the use of several statistical modeling methods. These methods may use linear models, such as joint regression analysis, multivariate analytical methods such as AMMI (additive mean effects and multiplicative interaction) analysis, or GGE (genotype plus GE interaction) biplot analysis. The GGE biplot method is effective for identifying the really good cultivars across environments, and evaluating the yield and stability of genotypes. According to the GGE biplot, a stable genotype draws a shorter projection on to the average environment coordinate abscissa, irrespective of the direction.

More recently, various biplot visualization methods have been developed to address the specific questions relative to genotype by environment data analysis. The GGE concept is based on the assumption that genotype main effect (G) and genotype by environment interaction (GE) are the two sources of variation relevant to genotype evaluation and needs to be considered simultaneously, not alone or separately.

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The support provided by Dr A Sarkar, ICARDA New Delhi and Dr Murari Singh, Senior Biometrician, ICARDA Jordan sincerely acknowledged by authors. The multi-environment testing of barley genotypes was performed within the AICW&BIP project at centers across the country. Authors are grateful to all the staff of centers under AICW&BIP for their hard work to carry the field evaluation and data recording.

Barley Network (AICW & BIP)

Funded Centres

BHU, Varanasi (UP)
CCSHAU, Hisar (Haryana)
CSAUA & T, Kanpur (UP)
CSK HPKV, Bajaura (HP)
JNKV, Rewa (MP)
NDUA & T, Faizabad (UP)
SKNAU, Durgapura (Rajasthan)
PAU, Ludhiana (Punjab)

Voluntary Centres

GBPUA & T, Pantnagar (Uttarakhand)
IARI, Shimla (HP)
VPKAS, Almora (Uttarakhand)

Contents

S.No	Index	Page no.
	Introduction	
	GGE Biplot	
	MET's	
	Mathematical presentation for Biplot	
	Advantages of GGE Biplot analysis	
	GGE Biplot Analysis :	
	Feed Barley	
	Dual purpose barley: Forage yield	
	Salinity tolerance barley	
	Further considerations	
	Bibliography	

INTRODUCTION

Biplot is an analysis tool to present the output from principal component analysis (PCA) of multi location trials which was proposed by Gabriel in the year 1971. Basically it is a scatter plot that graphically displays a rank-2 matrix by both the entries and the testers. The term "bi" means "both". A rank - 2 matrix is resulted from multiplying a matrix with 2 columns by a matrix with 2 rows. The two dimensional biplots used effectively for two-way tables that easily approximated by rank two matrix.

The first application of biplot analysis to agricultural data analysis was shown by Bradu and Gabriel, 1978 who used a cotton performance trial dataset to illustrate the diagnostic role of biplots in model selection. Other early work of analyzing genotype by environment tables using biplots includes Kempton, 1984, Gauch, 1992, and Cooper and DeLacy in the year 1994.

The biplot has become a popular data visualization tool in many researchable areas under agricultural sciences. This tool has been used by plant breeders and agronomists for cultivars evaluation and megaenvironment investigation under coordinated system. Biplot analysis considers the relevance of genotypes effects and Gx E interaction effects and considered simultaneously both effects for evaluating cultivars. The graphic axes of such analysis are the first two principal components of multivariate analysis and account for most of the data variance.

GGE Biplot

The term "GGE biplot" first coined by Yan et al. in the year 2000. It refers to a biplot that displays the G and GE of a genotype-by-environment data. The key property of a GGE biplot is that it is based on Tester-Centered data, whereby the tester (environment) main effects (E) are removed, and the entry main effect (G) and the entry by tester interaction (GE) are retained and combined. A biplot based on tester-centered data contains only G+GE, represented in short as GGE.

The GGE biplot methodology was developed for graphical analysis of genotype by environment data for multi-environment trials (MET). It is a general method that can be applied to many other types of two-way data generated under research. GGE biplot is the most commonly used type of biplot.

Basically GGE biplot was originally designed to analyze complex interaction pattern between genotypes and environments. More over it complements the results of the significant mean squares for interactions in ANOVA (Analysis of variance). The concept of crossover interaction patter in agricultural research has made interaction study more interesting and opened new avenues of GGE biplot analysis.

MET's

Multi-environment trials (MET) are conducted under barley network to evaluate yield performance of the promising genetic materials under varying environmental conditions across the country. Large numbers of promising genotypes are grown in different environmental conditions to select high yielder genotypes under all India coordinated system of research. More over the fluctuations in the biological yield are influenced by number of environmental factors and known as genotype-by-environment (GE) interaction. However, GE interaction reduces the genetic progress in plant breeding programs through minimizing the association between phenotypic and genotypic values. Hence, GE interaction must be either exploited by selecting superior genotypes for each specific target environment or avoided by selecting widely adapted and stable genotype across wide range of environments. Numerous methods are cited in literature to be useful for analyzing MET data.

Recently developed methodology GGE-biplot has been used extensively for graphical display of GE interaction pattern with many additional advantages. GGE biplot analysis considers both genotype (G) and GE interaction effects and graphically displays GE interaction in a two way manner. GGE biplot has been found an effective method based on the principal component analysis (PCA) to fully explore MET data. The visual examination of the relationships among the test environments, genotypes and the GE interactions is possible with GGE biplot.

Mathematical presentation for Biplot

The biplot technique makes it possible to display of the performance of each genotype at each location in a single graph. The singular value decomposition (SVD), a $g \times e$ matrix of mean yield of g cultivars in e environments can be approximated as the product of a genotype matrix and an environment matrix, so that the yield of genotype i at environment (location) j , Y_{ij} , is approximated as

$$\hat{Y}_{ij} = \sum_{n=1}^r \lambda_n \xi_{in} \zeta_{jn} \quad (\lambda_1 \geq \lambda_2 \geq \lambda_3 \dots \geq \lambda_r)$$

where r is the number of PCs required to approximate the original data, with condition $r \leq \min(g, e)$; λ_n is the singular value of PC_n , the square of which is the sum of squares explained by PC_n . ξ_{in} and ζ_{jn} are the i th genotype score and the j th environment score, respectively, for PC_n . The SVD allows the two way $g \times e$ table of means to be displayed in a plot having g points for the genotypes plus e points for the environments. Each genotype is represented by a point, called a marker, defined by the genotype's scores on all PCs, and each environment is represented by a marker defined by the environment's scores on all PCs. Biplots can be multidimensional, but two-dimensional biplots, using only the first and the second PCs, are most common, both for biological reasons as well as for easy comprehension.

GGE biplot displays the genotype main effect and the genotype-environment interactions of two-way table simultaneously and assist in studying relative performance of the cultivars as well as test environments graphically. The cultivars have been evaluated for their yield performance in an individual environment and across all environments. Simultaneously environments can be judged and grouped on the basis of their ability to discriminate among genotypes. Redundant environments as well as those that are most appropriate for selecting superior genotypes or discarding inferior genotypes can be visually identified through GGE biplots.

Advantages of GGE biplot analysis

The widely used GGE biplot methodology comprised with two concepts i.e. biplot and GGE to analyze the results of MET data. This methodology uses a biplot to show the two factors (G plus GE) that are important in cultivar evaluation and are the sources of variation in MET data analysis. The GGE biplot shows the first two principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from environment-centered data. This analysis is an effective tool for: (i) “which-won-where” pattern analysis, the specific genotypes can be recommended for particular environments, (ii) mean and stability performance of genotypes and (iii) discriminate tested genotypes in target environments.

The first is the polygon (“which-won-where”) view of the GGE biplot consists of an irregular polygon and a set of lines drawn from the biplot origin to intersect the sides of the polygon at right angles. The vertices of the polygon are the genotype markers away from the biplot origin in various directions, in such a manner to accommodate all genotype markers. A line that starts from the biplot origin and perpendicularly intersects a polygon side represents the set of environments in which the two cultivars occupied at side ends perform equally; the relative ranking of the two cultivars would be reversed in environments on opposite sides of the line (“crossover GE”). The perpendicular lines to the polygon sides divide the biplot into sectors, each having its own winning cultivar. The winning cultivar for a sector is the vertex cultivar at the intersection of the two polygon sides. It is positioned usually, within its winning sector. The environment markers fall into different sectors, indicates different cultivars won in different sectors contrary to a situation with all environment markers fall into a single sector, this indicates a single cultivar would have the maximum yield in all environments.

Next is the average tester coordination view, this ranks entries along the average-tester axis (ATC abscissa), with an arrow pointing to entry with greater average performance across all testers. A vertical line (average-tester coordinate [ATC] y axis) divides the abscissa into two halves in order to separate out entries with below and above average means. The average performance of an entry is approximated by the projection on the abscissa while stability is measured by projection onto the double-arrow line. The less stable entry show largest projection length.

Finally the third view displays the discriminating ability and representativeness of the tester. The discriminating power of a tester, its ability to differentiate among tested entries is displayed by the length of the vector, which proportionate the standard deviation of the tester. Testers with shorter vectors provide little or no information about the entries evaluated compared to those with longer vectors. The small circle located on the abscissa represents the average-tester axis (AEA). The cosine of the angle between two testers approximates the correlation coefficient. Testers that have small angles with AEA are more representative than those with large angles.

Feed Barley

Barley is considered suitable under diverse production conditions for its tolerance to biotic and abiotic stresses. Many parts of the world including Indian sub-continent cultivate barley as feed crop. The most prime objectives of the barley improvement programmes are high fodder and grain yield. Multi-location yield trials are conducted by the Barley Network under All India Coordinated Wheat and Barley Improvement Programme (AICW&BIP) to develop new cultivars to sustain barley cultivation of the country. Twenty eight feed barley genotypes were evaluated under national varietal trials. The experiments were conducted across 12 environments, throughout crop seasons, 2013-2014 as the characteristics of these sites and pedigrees of investigated genotypes are listed in table 1. The randomized complete block design experimental design employed, with three replications. All the cultural practices were carried out as recommended to harvest good yield. The GGE biplot analysis was performed to quantify the interaction using Genstat 17.1 version software.

Which-Won-Where Pattern

The polygon view of the GGE biplot indicates the best genotype(s) in each environment and possible similarity among studied environments. The polygon is formed by connecting the genotypes that are farthest away from the origin in such a manner to include all other genotypes in the polygon. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 accounted for 25.8% and 19.4% of the total GGE sum of squares, respectively, explaining a total of 45.2% variation. The eight rays divide the biplot into eight sectors. Major locations fall in the two sectors. Genotypes located on the vertices of the polygon reveal the best or poor behavior in one or other environment. The fourth sector had locations Hisar, Varanasi and Ludhiana with high yielder genotypes G14, G4, G28, G2, G27, G23, G1 and G8, while sixth sector showed Faizabad, Kanpur, Navgaon, Udaipur,

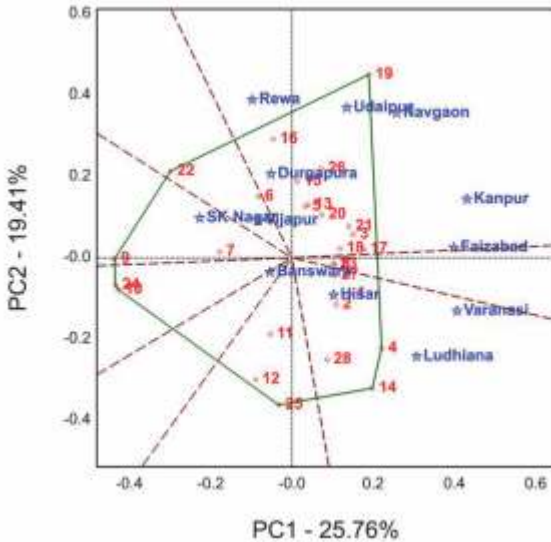


Figure 1. Polygon view of 28 feed barley lines over 12 test environments

Genotypes denoted by numbers (red colour)

G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14
HUB 236	KB 1353	NDB 580	BH 981	KB 1369	HUB 237	BH 982	BH 980	RD 2875	RD 2876	UPB 1040	UPB 1042	JB 291	PL 880
G15	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26	G27	G28
BH 902	PL 881	JYOTI 881	PL 751	RD 2552	BH 946	HUB 113	RD 2786	JB 290	RD 2877	UPB 1041	RD 2874	NDB 1578	KB 1367

Rewa and Durgapura environments as well as quite large number of genotypes. The eight sector with environment S K Nagar showed advantage for genotype G9. The other genotypes G24 and G25 lying on the vertices did not respond at any of the locations.

In this graphic presentation the first principal component (PC1) represents cultivar productivity, and the second principal component (PC2) cultivar stability. The ideal genotype would show a high PC1 value (high productivity) and low PC2 value near to zero (more stable). The present study showed genotype G17 had the largest PC1 score and had the highest average grain yield. The PC2 value of G19 genotype was the largest indicating its specific adaptation. In contrast, G9 yielded poorly at all sites but was relatively stable, as indicated by its small PC1 scores (low yielding) and relatively small PC2 scores (stable). Genotypes with PC1 scores more than zero were identified as higher yielding and those

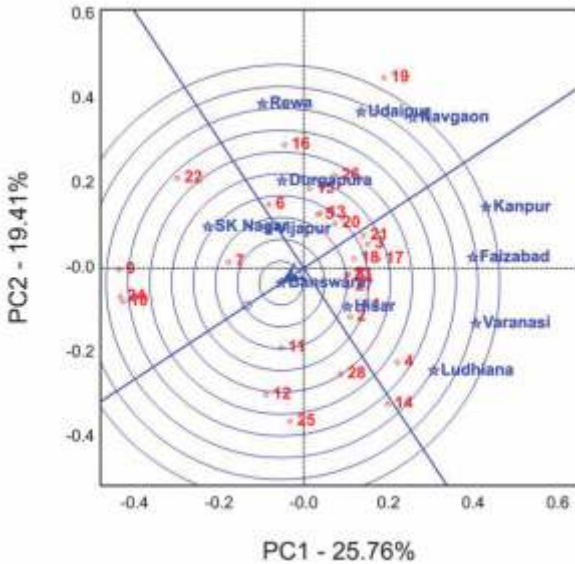


Figure 2. Relative ranking of environments

Genotypes denoted by numbers (red colour)

1	2	3	4	5	6	7	8	9	10	11	12	13	14
HUB 236	KB 1353	NDB 1580	BH 981	KB 1369	HUB 237	BH 982	BH 980	RD 2875	RD 2876	UPB 1040	UPB 1042	JB 291	PL 880
15	16	17	18	19	20	21	22	23	24	25	26	27	28
BH 902	PL 881	JYOTI	PL 751	RD 2552	BH 946	HUB 113	RD 2786	JB 290	RD 2877	UPB 1041	RD 2874	NDB 1578	KB 1367

with PC1 scores < 0 were identified as lower yielder. Accordingly, the average yield of G11, G12 and G25 were below average and highly unstable (large absolute PC2 scores). In contrast, genotypes G18, G17, and G21 had positive PC1 scores and were identified as high yielder genotypes.

Stratification of test environments

The figure 2 presents the biplot with an Average-Environment Axis (AEA) represented by the small circle at the end of the arrow and has the average coordinates of all test environments. This line passes through the average environment and the biplot origin. The concentric circles on the biplot help to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environments and is a measure of the discriminating ability of the environments. An environment that has a smaller angle with the AEA is

more representative of other test environments. Thus, Udaipur, Navgaon, Kanpur and Faizabad are representative. Test environments that are both discriminating and representative are good test environments for selecting generally adapted genotypes.

With respect to the contribution of testing locations towards the interaction effects, location Banswara had least contribution as it lied closest to the origin, but locations Vijapur and SK nagar were made the highest contribution. The biplot in this trial also indicated that genotype G15 and G26 were performed above average in location Durgapura, while G16 at Rewa, and G19 in Udaipur, and Navgaon. Meanwhile, discriminating ability was an important measure of a test environment. Another equally important measure of a test environment was its representativeness of the target environment. An ideal environment

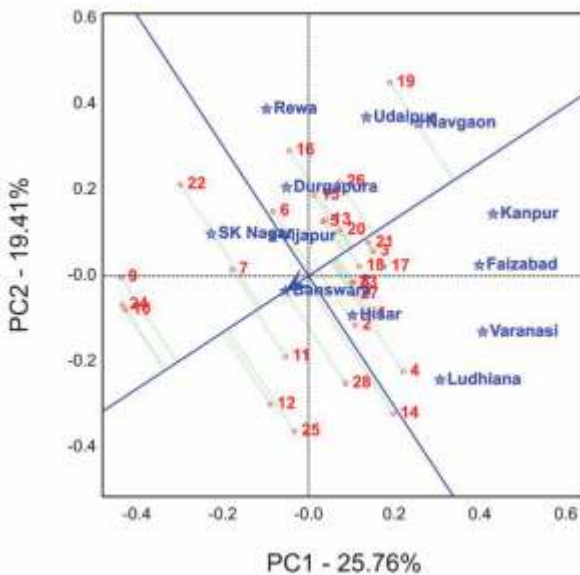


Figure 3. Projection of genotypes on AEC

Genotypes denoted by numbers (red colour)

1	2	3	4	5	6	7	8	9	10	11	12	13	14
HUB 236	KB 1353	NDB 1580	BH 981	KB 1369	HUB 237	BH 982	BH 980	RD 2875	RD 2876	UPB 1040	UPB 1042	JB 291	PL 880
15	16	17	18	19	20	21	22	23	24	25	26	27	28
BH 902	PL 881	JYOTI	PL 751	RD 2552	BH 946	HUB 113	RD 2786	JB 290	RD 2877	UPB 1041	RD 2874	NDB 1578	KB 1367

should be highly differentiating of the genotypes and at the same time representative of the target environment. Hence in the current experiment, locations Kanpur and Navgaon were most discriminating of the entries as indicated by the longer distance between their markers and the origin. However, due to relatively large PC2 score, genotypic differences observed at both locations did not exactly reflect the genotypes in average yield over all sites. On the other hand, location Vijapur was not actually the most discriminating as distance of its vector was the smallest, but varietal difference at this site was highly consistent with those averaged over all sites because it had almost zero PC2 scores and lowest PCI.

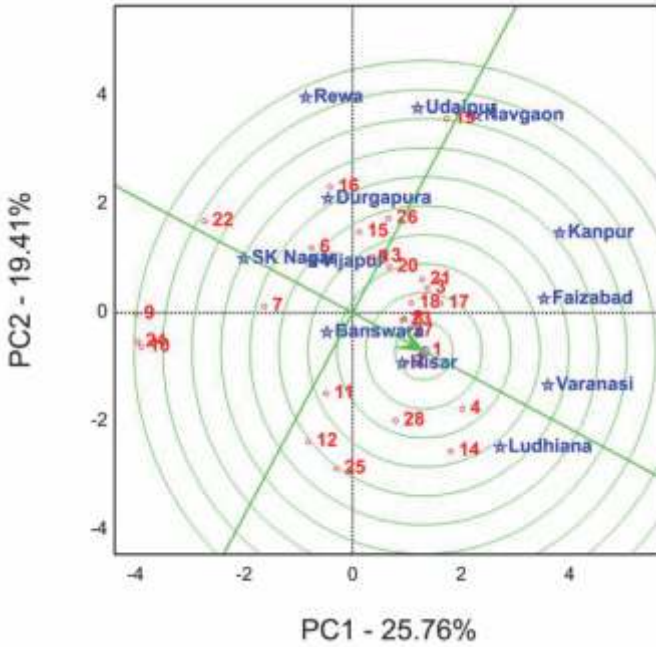


Figure 4. Genotypes ranking in relation to ideal genotype

Genotypes denoted by numbers (red colour)

1	2	3	4	5	6	7	8	9	10	11	12	13	14
HUB 236	KB 1353	NDB 1580	BH 981	KB 1369	HUB 237	BH 982	BH 980	RD 2875	RD 2876	UPB 1040	UPB 1042	JB 291	PL 880
15	16	17	18	19	20	21	22	23	24	25	26	27	28
BH 902	PL 881	JYOTI	PL 751	RD 2552	BH 946	HUB 113	RD 2786	JB 290	RD 2877	UPB 1041	RD 2874	NDB 1578	KB 1367

Genotypes behavior relative to highest yielding environment

The figure 3 denotes the graphic comparison for the relative performance of genotypes in respect to the Banswara environment (highest yielding location). A line was drawn that passed through the biplot's origin and the E12 marker to make an E12-axis, and then a line was perpendicularly drawn from each genotype toward this axis. The genotypes were ranked on the basis of their projections onto the E12-axis, with rank increasing in the direction toward the positive end. From the graph, genotypes ranging from G5, G3, G20, G15 and G26 on the right side of the perpendicular line to the axis had higher than the average yield in Durgapura environment, while genotype G7, G11, G10, G24, G12 and G9 showed lower yield than average yield performance.

Ranking of genotypes in relation to ideal genotype

An ideal genotype would show the higher average yield and stable performance (figure 4). Such an ideal genotype has the highest yield and zero GE (or highest stability), as represented by the dot with an arrow pointing to it. Therefore, G1 and G2 can be regarded as ideal genotypes. The genotypes G23, and G27 were close to the ideal genotype. Ranking of other genotypes based on the ideal genotype was $G18 > G17 > G3 > G21 > G4 > G28 > G20 > G11 > G14$. In other words, the lower yielding genotypes (G22, G9, G24 and G10) were unfavorable because they are far from the ideal genotype. The genotypes located near the biplot origin are considered as widely adapted genotypes, while genotypes located far as specifically adapted. For broad adaptation, the ideal genotypes are those that have both high mean yield and high stability (closest to the ideal genotype marker). Genotypes G17, G18, G21, G3, G13, G20 and G5 can be regarded as genotypes with high mean yield and high stability in performance. For specific adaptation, the ideal genotypes are those with high mean yield but low stability that respond best to particular environments. In this study, genotypes G16 and G19 tended to be specifically adapted to Durgapura and Navgaon environments.

Table I . Details of feed barley genotypes, parentage and environments

Codes	Genotype	Parentage	Codes	Environments	Latitude	Longitude
G1	HUB 236	DL88/22nd IBYT15	E1	Durgapura	26° 51 'N	75° 47 'E
G2	KB 1353	K508/RD2676	E2	Navgaon	18° 70 'N	72° 86 'E
G3	NDB 1580	NB3/HUB114	E3	Hisar	29° 10 'N	75° 46 'E
G4	BH 981	RD2660/RD2683	E4	Ludhiana	30° 56 'N	75° 52 'E
G5	KB 1369	Jaqruti/K169	E5	Varanasi	25° 20 'N	83° 03 'E
G6	HUB 237	EIBGNOT-18/RD250B	E6	Rewa	24° 31 'N	81° 15 'E
G7	BH 982	'13" EMBSN-14/RD2683	E7	Faizabad	26°47 'N	82°12 'E
G8	BH 980	NBD1276/8H393	E8	Kanpur	26° 29 'N	80° 18 'E
G9	RD 2875	RD2552/PL419//RD2508	E9	Vijapur	23° 35 'N	72° 55 'E
G10	RD 2876	RD2660/PENCO/CHEVRON-BAR	E10	Udaipur	24° 34 'N	70° 42 'E
G11	UPB 1040	IBON-LRA-M-31 (EIBGN 2010-11-30)	E11	SK Nagar	24° 19 'N	72° 19 'E
G12	UPB 1042	INBYT-LRA-M-17 (EIBGN 2010-11)	E12	Banswara	23° 55 'N	74° 45 'E
G13	JB 291	DL88/K633				
G14	PL 880	PL426/BC473				
G15	BH 902	BH495/RD2552				
G16	PL 881	PL426/K537				
G17	JYOTI	K 12/C 251				
G18	PL 751	K226/PL226				
G19	RD 2552	RD2035/DL472				
G20	BH 946	BHMS22A/BH549 //RD2552				
G21	HUB 113	KARAN2BO/C138				
G22	RD 2786	RD2634/NDB1020//K425				
G23	JB 290	JB58/RD250B				
G24	RD 2877	RD2052/DWR64//RD2660				
G25	UPB 1041	IBON-HI-33 (EIBGN 2012-13-45)				
G26	RD 2874	NDB 1173 /BH902// RD2715				
G27	NDB 1578	BCB128/NDB940				
G28	KB 1367	PFCBO23/MSEL				

Dual purpose barley: Forage yield

Traditionally barley has been used as a grain crop for human consumption and feed for animals in the country. It is grown during the winter season (Rabi) in the northern plains as well as in northern hills, mostly under rainfed or limited irrigation condition on poor to marginal soils. In the recent years it has been observed that in the drier parts of northern plains there is an acute shortage of green fodder in the months of November to January. Barley possesses high total biomass, thus the small and marginal farmers of our country use green barley as fodder to feed milch animals. Other popular forage crops i.e. berseem oat and sugarcane are not available due to water shortage, in such areas, barley can be utilized as green fodder with very limited water supply or less rainfall in these areas. In drier parts of Northern plains (Rajasthan, Madhya Pradesh, Southern Haryana, South West Punjab and Western U.P.) during November to January, farmers grow dual purpose barley over other forage crops because of its dual utilization and less water requirement. In these regions, animal husbandry occupies an important role and there is a big gap between demand and supply of forage. Since both the green forage and grain can be utilized for animal fodder/ feed purposes, the crop can be advantageous over oats, because of its dual utilization, faster early growth as well as less water requirement.

The materials comprised of nineteen genotypes including advanced breeding lines and released checks of dual purpose barley developed at various centers under all India coordinated wheat and barley improvement programme. Field trials were conducted at ten locations representing typical conditions of the country. More details are given in table 2 for ready reference. The data were recorded for all morphological traits but grain yield were subjected to GGE analysis.

Polygon view for forage yield

The polygon view of a biplot (figure 5) is the best way to visualize the interaction patterns to show the presence of cross over GE interaction if any. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 accounted for 46.3% and 12.5% of GGE sum

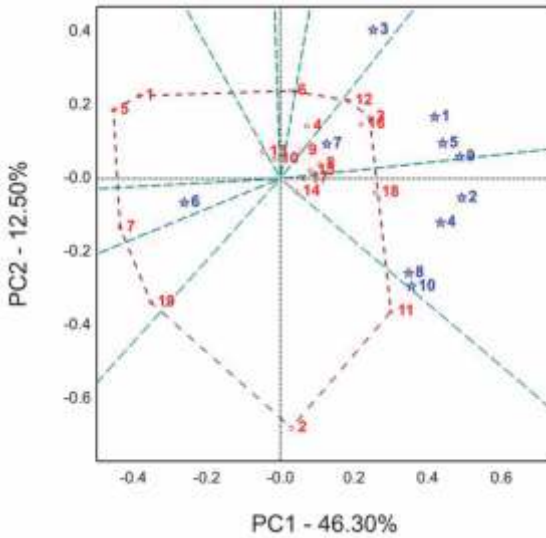


Figure 5. Which won where pattern of genotypes

Legends for figure (Genotypes depicted by red colour circles and environments by blue colour stars)

G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14
UPB 1040	NDB 1585	HUB 238	BH 980	UPB 1041	BH 983	UPB 1042	AZAD	KB 1369	NDB 1584	RD 2880	RD 2881	RD 2552	KB 1347
G15	G16	G17	G18	G19									
RD 2879	RD 2715	RD 2035	RD 2878	HUB 239									
E1	E2	E3	E4	E5	E6	E7	E8	E9	E10				
Hisar	Durgapura	Modipuram	Ludhiana	Varanasi	Kanpur	Faizabad	Rewa	Udaipur	Jabalpur				

of squares, respectively, explaining a total of 58.8% variation. Specifically, lines are drawn to connect the markers of the furthest genotypes in the biplot in a manner to occupy the corners (i.e., vertices) of an irregular polygon and, for each side of the polygon, drawing a line segment perpendicular to that side of the polygon so as to pass through (or, more commonly, to stop at) the origin. These line segments subdivide the polygon into sectors involving different subsets of environments and genotypes. The genotype, the marker for which is at the corner of one sector, is the best performer in the environments included in that sector. Environment markers which are located far away from the origin, discriminate the genotypes more than those near the origin. The vertex genotypes in this study were G2, G19, G7, G5, G1, G3 and G11. These genotypes were the best or the poorest genotypes in some or all of the environments as observed farthest from

the origin. From the polygon view , the genotypes fell in eight sections and the test environments fell in four sections. The largest section contains the test environments E2, E8, E4 which had the genotypes G14,G17 and G18 as the winner; the second section contains the environments E9,E5,E7 and E1 with G8, G13,G9,G12,G3 and G16 as the best yielder. The test environment E6 was fallen in a separate section with G7 as highest yielder. The vertex genotype G2,G11,G19,G5 and G1 were not the top-yielding genotypes in any test environment.

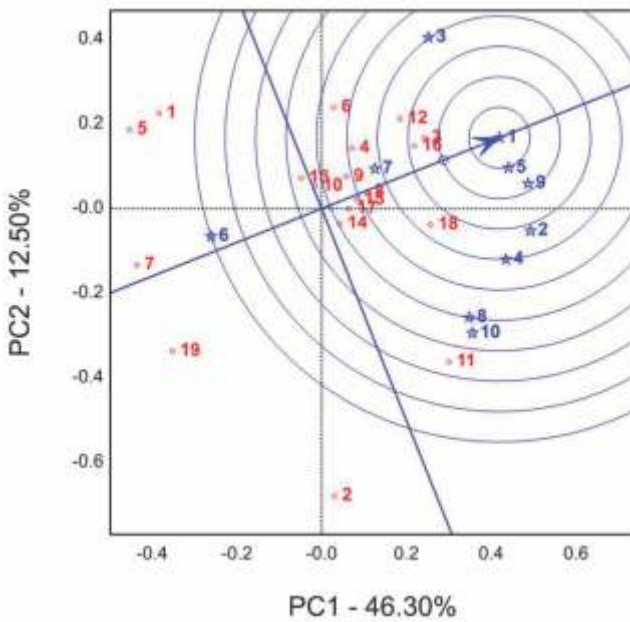


Figure 6. Discrimination of genotypes relative to ideal environment

Legends for figure (Genotypes depicted by red colour circles and environments by blue colour stars)

G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14
UPB 1040	NDB 1585	HUB 238	BH 980	UPB 1041	BH 983	UPB 1042	AZAD	KB 1369	NDB 1584	RD 2880	RD 2881	RD 2552	KB 1347
G15	G16	G17	G18	G19									
RD 2879	RD 2715	RD 2035	RD 2878	HUB 239									
E1	E2	E3	E4	E5	E6	E7	E8	E9	E10				
Hisar	Durgapura	Modipuram	Ludhiana	Varanasi	Kanpur	Faizabad	Rewa	Udaipur	Jabalpur				

Performance relative to ideal environment

The graphical interpretation showed that the genotypes G3 and G16 followed by G12, with high mean yield and stability performances may be considered as ideal genotypes. The genotypes lying on the right side of the line had yield greater than the overall mean whereas genotypes on the left side had yields lower than the mean. Genotypes with high yield but low stability were G14, G11 and G2, while those with average yield and highest stability were G17, G9, and G8. Since GGE represents $G + GE$ and since the AEC abscissa approximates the genotypes' contributions to G , the AEC ordinate approximates the genotypes' contributions to GE , which is a measure of their stability or instability. Genotypes G16, G9 and G10 were the most stable as located almost on the AEC abscissa and had a near-zero projection onto the AEC ordinate, indicating their consistent ranks across environments. In contrast, G8, G6, and G9 were among the genotypes with the lowest stability and

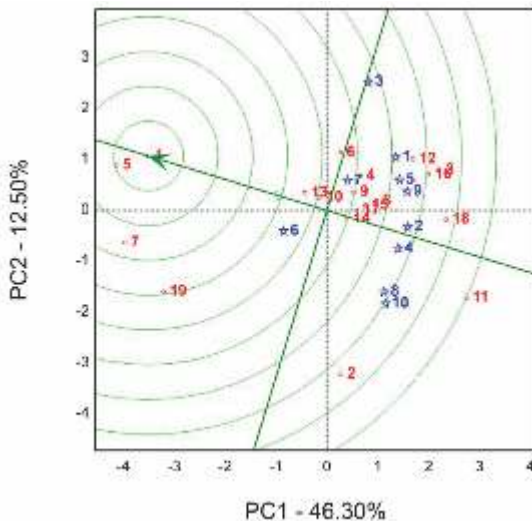


Figure 7. Classification of genotypes relative to ideal genotype

Legends for figure (Genotypes depicted by red colour circles and environments by blue colour stars)

G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14
UPB 1040	NDB 1585	HUB 238	BH 980	UPB 1041	BH 983	UPB 1042	AZAD	KB 1369	NDB 1584	RD 2880	RD 2881	RD 2552	KB 1347
G15	G16	G17	G18	G19									
RD 2879	RD 2715	RD 2035	RD 2878	HUB 239									
E1	E2	E3	E4	E5	E6	E7	E8	E9	E10				

Hisar Durgapura Modipuram Ludhiana Varanasi Kanpur Faizabad Rewa Udaipur Jabalpur

with higher (G8) and lower (G6 and G9) mean yield performances than the overall mean.

Relationship of genotypes in relation to ideal genotype

The ideal genotype is stable because its projection on the ATC y-axis is near zero as represented by genotype G1. Genotype G5 is more favorable as it is closer to the ideal genotype. Ranking of other genotypes based on the ideal genotype was $G7 > G19 > G13 > G10 > G6$. In other words, the lower yielding genotypes (G18, G2, and G11) were unfavorable as observed far from the ideal genotype.

Identification of an ideal genotype procedure by GGE biplot are similar to those found in other crop stability studies (Samonte et al., 2005; Fan et al., 2007).

Table 2 . Details of dual purpose barley genotypes, parentage and environments

Codes	Genotype	Parentage	Codes	Environments	Latitude	Longitude
G1	UPB 1040	IBON-LRA-M-31 (EIBGN 2010-11-30)	E1	Hisar	29°10'N	75°46'E
G2	NDB 1585	31 st IBON-MRA-96/NDB21 7	E2	Durgapura	26°51'N	75°47' E
G3	HUB 238	DL88/RD2508	E3	Modipuram	29°06' N	77°69' E
G4	BH 980	NBD1276/BH393	E4	Ludhiana	30°54' N	75°52' E
G5	UPB 1041	IBON-HI-33 (EIBGN 2012-13-45)	E5	Varanasi	25°20' N	83° 03' E
G6	BH 983	NDB1289/JB42	E6	Kanpur	26°29'N	80°18'E
G7	UPB 1042	INBYT-LRA-M-17 (EIBGN 2010-11)	E7	Faizabad	26°47' N	82°12' E
G8	AZAD	K12/K19	E8	Rewa	24° 31' N	81° 15' E
G9	KB 1369	Jaqrithi/K169	E9	Udaipur	24° 34' N	70°42'E
G10	NDB 1584	IBCB-S(2008-09)-39	E10	Jabalpur	23°90' N	79°58' E
G11	RD 2880	SARA-1 -BAR/CAPU CON A20// RD2592				
G12	RD 2881	RD2634/N DB1 020/RD2660				
G13	RD 2552	RD2035/DL472				
G14	KB 1347	Jagrithi/K614				
G15	RD 2879	RD2624/RD2715//RIHANE03				
G16	RD 2715	RD387/BH602//RD2035				
G17	RD 2035	RD103/PL101				
G18	RD 2878	RD2618/RD2620//RD2552				
G19	HUB 239	26th IBYT19-3/RD2615				

Salinity tolerance barley

In our country, barley is cultivated in harsh environments viz drought, salinity/alkalinity and marginal lands. Soil salinity is a major abiotic stress which delays and reduces flowering cause to it yield reductions. Many workers in wheat and barley have reported reduction in yield under salinity conditions. Grow salinity tolerant varieties is one of the economical efforts to mitigate the ill effects. Under AICWBIP system the efforts of barley research workers have resulted in the development and release of many tolerant varieties, which give good yield level under unfavourable conditions. Twenty barley genotypes were studied at major six locations and details were mentioned in table 3.

Polygon view of salinity tolerant barley genotypes

The polygon view of twenty barley is developed by connecting the vertex genotypes to visualize the interaction effects between salinity tolerance genotypes and six environments to quantify the cross over GE interaction. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 accounted for 30.9% and 29.4% of GGE sum of squares, respectively, explaining a total of 60% variation. The vertex genotypes in this study were G20, G6, G7 and G16. The genotypes fell in four sectors and the test environments fell in two sectors. The first sector contains the no test environments; the second sector contains the environments E3 and E5 with G6 and G13 close to E3. The four test environments fall together in fourth sector while first and third sectors do not have any test environments. The vertex genotype G16 and G20 were not the top-yielding genotypes in any environment.

Accordingly, statistically stable genotypes and locations were located near to the bi plot origin, with scores practically null for the two interaction axis (PC1 and PC2). The genotype, which lie near the origin and practically stable was G10, and had wide adaptability; and G8 is located a little bit farther from the origin hence had medium stability across the five locations. On the other hand, genotypes G1, G2, G3, G4,

and G7 were located far away from the origin, which were more responsive to environment change and are considered as specifically adapted genotypes. The genotype which was located near the origin was less responsive than the corner genotype.

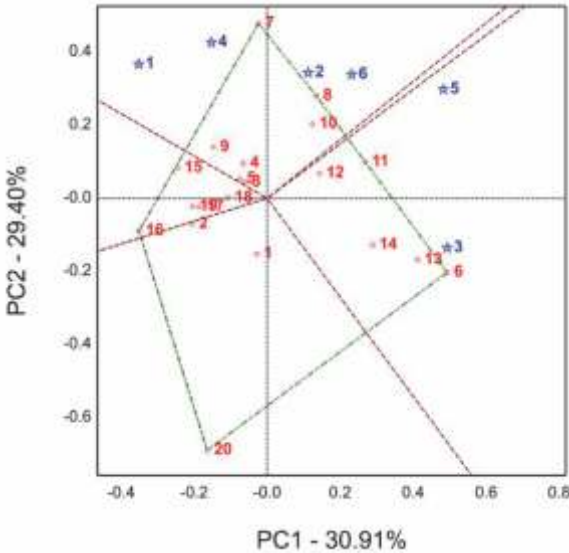


Figure 8. Polygon view of salinity tolerance barley genotypes

Legends for figure (Genotypes depicted by red colour circles and environments by blue colour stars)

G1	G2	G3	G4	G5	G6	G7	G8	G9	G10
NDB 1592	KB 1370	RD 2552	DWRB 31	NDB 1586	RD 2886	NDB 1173	RD 2888	BH 984	BH 972
G11	G12	G13	G14	G15	G16	G17	G18	G19	G20
RD 2860	RD 2889	RD 2890	RD 2887	NDB 1600	BH 986	BH 985	RD 2794	NDB 1587	KB 1375
E1	E2	E3	E4	E5	E6				
Hisar	Faizabad-1	Faizabad-2	Rampura	Bawal	DWR Hisar				

Ranking of genotypes relative to highest yielding environment

The comparison of the relative performance of all genotypes relative to the environment E1 is illustrated in following figure 9. A line was drawn that passed through the biplot's origin and the E1 marker to make an E1-axis. The genotypes were ranked on the basis of their projections onto the E1-axis. From the graph, genotypes ranging from G11, G12, G14, G13 and G6 on the right side of the perpendicular line to the axis had higher than the average yield in this environment, while genotype G20

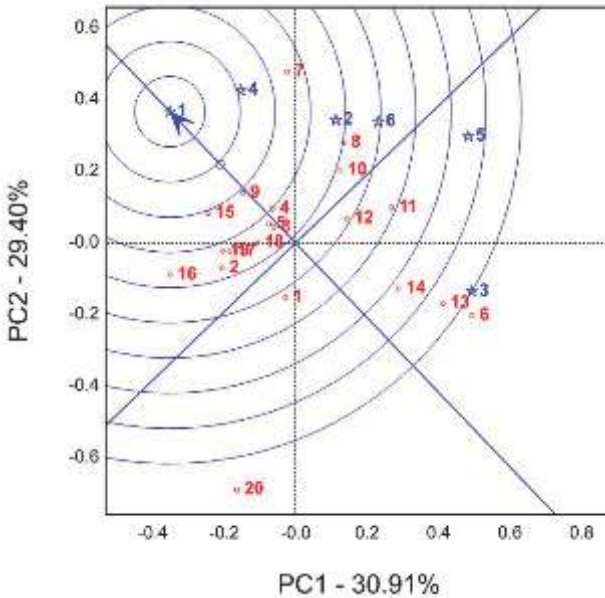


Figure 9. Genotypes ranking for ideal environment

Legends for figure (Genotypes depicted by red colour circles and environments by blue colour stars)

G1	G2	G3	G4	G5	G6	G7	G8	G9	G10
NDB 1592	KB 1370	RD 2552	DWRB 131	NDB 1586	RD 2886	NDB 1173	RD 2888	BH 984	BH 972
G11	G12	G13	G14	G15	G16	G17	G18	G19	G20
RD 2860	RD 2889	RD 2890	RD 2887	NDB 1600	BH 986	BH 985	RD 2794	NDB 1587	KB 1375
E1	E2	E3	E4	E5	E6				
Hisar	Faizabad-1	Faizabad-2	Rampura	Bawal	DWR Hisar				

to G1 showed lower yield that average yield performance.

Evaluation of genotypes relative to an ideal genotype

An ideal genotype G1 is located at the center of the concentric circles in figure 10, has both high mean yield and high stability. Genotypes closer to the ideal genotype are more favourable. The G2 was near to the ideal genotype. Ranking of other genotypes based on the ideal genotype was $G19 > G7 > G18 > G4$ and $G5$. The lower yielding genotypes far from the ideal genotype were unfavorable (G7, G20 and G6).

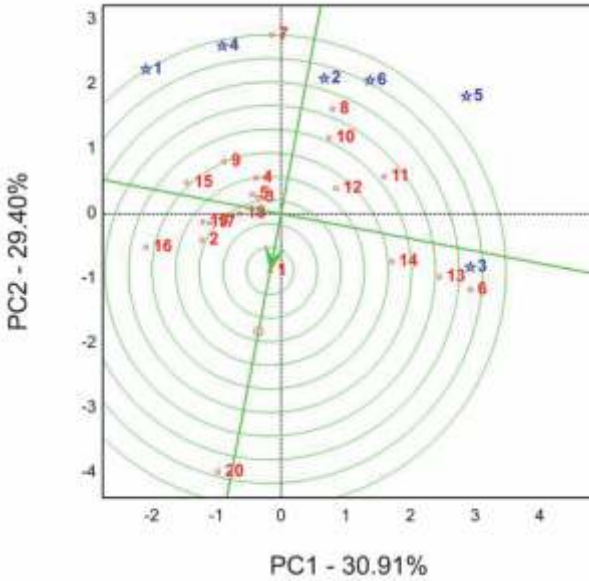


Figure 10. Relative ranking of genotypes

Legends for figure (Genotypes depicted by red colour circles and environments by blue colour stars)

G1	G2	G3	G4	G5	G6	G7	G8	G9	G10
NDB 1592	KB 1370	RD 2552	DWRB 131	NDB 1586	RD 2886	NDB 1173	RD 2888	BH 984	BH 972
G11	G12	G13	G14	G15	G16	G17	G18	G19	G20
RD 2860	RD 2889	RD 2890	RD 2887	NDB 1600	BH 986	BH 985	RD 2794	NDB 1587	KB 1375
E1	E2	E3	E4	E5	E6				
Hisar	Faizabad-1	Faizabad-2	Rampura	Bawal	DWR Hisar				

Table 3. Details of barley genotypes, parentage and environments

Codes	Varieties	Parentage	Codes	Environments	Latitude	Longitude
G1	NDB1592	IBCB-S(2008-09)-31	E1	Hisar	29° 10'N	75° 46'E
G2	KB 1370	JYOTI/RD2552	E2	Faizabad-1	26° 87'N	80° 98'E
G3	RD 2552	RD2035/DL472	E3	Faizabad-2	26° 87'N	80° 98'E
G4	DWRB 131	IBYT-LRA-M -11 (2011 -12)	E4	Rampura	24° 47'N	75° 44'E
G5	NDB 1586	(IBYT-MRA-24-2008-09)	E5	Bawal	28° 10'N	76° 59'E
G6	RD 2886	RD2715 / K750 // PETUNIA- 1	E6	DWR Hisar	29° 18'N	75° 68'E
G7	NDB 1173	BYTLRA 3-(1 994-95)/NDB217				
G8	RD 2888	RD2683/RD2503//RD2683				
G9	BH 984	2005EIBGN-4/BH646				
G10	BH 972	29" EIBGN-22/BH 646				
G11	RD 2860	RD2552/ADABELLA/M-1 1 1 /CANELA				
G12	RD 2889	RD2552 /UBL-9//GLORIA-BAR				
G13	RD 2890	BH393/RD2360//RD271 5				
G14	RD 2887	R D2670/RD2683// BLLU / PINON				
G15	NDB 1600	NDB2OB/ALFA93				
G16	BH 986	RD2670/K792				
G17	BH 985	JB47/K792				
G18	RD 2794	RD2035/RD2683				
G19	NDB 1587	IBON-HI-31(2008-09)				
G20	KB 1375	K551/HUB158				

Further considerations

The GGE biplot analyses allowed a meaningful and useful summary of GE interaction in MET data and assisted in examining the relationships/variations in genotype performance across various test environments. Now a biplot had established as, an useful visualization technique to study hidden patterns of similarity or dissimilarity among genotypes or environments, and retrieve information about interactions under coordinated system. The recent reviews advocated for the visual interpretation of complex GE (e.g., Yan and Tinker, 2006; Gauch, 2006; Yan et al., 2007; Gauch et al., 2008) information displayed by biplot in comparison to tabular numerical information.

Two major messages for the future endeavors with biplot analyses had suggested in literature. First, a biplot is a descriptive, graphical tool and cannot be used for hypothesis testing because there is no measure to estimate uncertainty in results. Selection of superior genotypes during breeding or recommendation of best cultivars from MET data are critical decisions for plant breeders and agronomists which require appropriate scientific support along with visualization of data points. The parametric as well as the non parametric bootstrapping approach to obtaining uncertainty measures for genotypic and environmental effects will help to consolidate the decisions as per sound statistical base. The application of parametric and bootstrapping non parametric approaches should be advocated to improve inference of the biplot analysis. Second, for detailed understanding of the GE structure additional information on the number of multiplicative terms being retained, features of different biplots, genetic and environmental covariates and correlation analysis among environments as well as between genotypes also considered.

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