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AMMI model to analyse GxE for dual purpose barley in multi-environment trials

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ABSTRACT

The highly significant effects of environments, genotypes and interactions were observed for forage and grain yield. The environmental effects explained the major portion of the total variance as of 82.3% and 58.8% respectively. Indicated that the environments were diverse and a major part of variation in yield resulted from environmental changes. The highly significant interaction effects partitioned into IPCA1, IPCA2 and IPCA3, IPCA4; which explained 30.4, 19.4, 14.8 & 13.2% for forage and 37.0, 17.2, 16.1 and 12.5% for harvested grain yield. AMMI stability value(ASV) identified promising genotypes G12(UPB 1035), G6(UPB 1034), G7(BH 971) and G13(RD 2857), G7 (BH 971) & G11(NDB 1570) for forage and grain respectively. AMMI distance (D) marked G3(RD 2035) G9(BH 970) & G13(RD 2857) for former while genotypes G15(RD 2856) G11(NDB 1570) & G7(BH 971) for grain yield. GSI score advocated G13(RD 2857), G11(NDB 1570) G3(RD 2035),G5(RD 2715) and G7(BH 971), G2(RD 2552) G14(AZAD) desirable genotypes for selection with forage and grain yield. Genotypes with IPCA-1 scores close to zero identified G4(UPB 1036), G7(BH 971), G16(NDB 1566) and G11(NDB 1570), G2(RD 2552) for forage and yield respectively would have wider adaptation to the tested environments as per AMMI graphical plots.

Key words : AMMI models, AMMI stability value (ASV), Biplot analysis, D(AMMI distance), GxE interaction, Genotypic Selection Index(GSI).

INTRODUCTION

The Barley (*Hordeum vulgare* L.) cereal has been cultivated as grain crop for human consumption and as fodder for animal feed in our country (Verma *et al*., 2011). In the recent years barley can be utilized as green fodder with very limited water supply or less rainfall in these areas (Kumar *et al*., 2014). Green forage and grain can be utilized for animal fodder/ feed purposes; the barley has shown advantage over oats, because of its dual utilization, faster early growth as well as less water requirement. Dual barley cultivation provides nutrition to the livestock through its green fodder and grains harvested from regenerated crop (Kharab *et al*., 2013)

The GxE interaction study has recognized as an important aspect for barley improvement programmes as well as the promotions of new cultivars (Bavandpori *et al*., 2015). Large number of statistical methods are available for analysis of interaction by subdividing the information contained in GxE interaction data matrix into more meaningful components representing real responses of genotypes vis-a-vis locations (Bose *et al*., 2014). Methods varied from univariate parametric to multivariate models such as the additive main effect and multiplicative interaction (AMMI) analysis (Mohammadi *et al*., 2013). More over the static stability is defined by Becker and Leon (1988) as a stable genotype possessing unchanged performance regardless of variation of the environments. Wricke (1962) based on quantifying G x E interaction effects put forward dynamic stability concept. Lin and Binns (1988) proposed the cultivar performance measure (Pi). The better the genotype judged by the smaller the value of Pi. AMMI model is a hybrid model separates the additive variance from the multiplicative variance. The principal component analysis (PCA) applied to the interaction portion to a new set of coordinate axes that explains in more detail the interaction pattern (Mortazavian *et al*., 2014).

The objectives of the present work have been: (i) compare different measures of the AMMI model, environmental variance and PI statistics, of dual purpose barley genotypes for forage as well as for grain yield (ii) to explore the advantages AMMI graphical biplots to stratify the better-adapted genotypes based on PC1 and PC2 scores.

MATERIALS AND METHODS

The AMMI model for the main and GE interaction effects defined as (Silveira *et al*., 2013):

$$Y_{ij} = \mu + g_{i.} + e_{.j} + \sum_{k=1}^{n} \lambda_k \gamma_{ik} \delta_{jk} + \rho_{ij} \qquad \text{(i)}$$

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where Y_{ij} is the yield of the i-th genotype in the j-th environment; µ is the grand mean; gi. and e.j are the genotype and environment deviations from the grand mean, respectively; l_k is the eigen value of the Principal Component analysis axis k; g_{ik} and d_{jk} are the genotype and environment principal component scores (eigenvectors) for axis k; n is the number of principal components retained in the model and p_{ij} is the error term.

The AMMI distance statistic coefficient (D) (Zang *et al.*, 1998) was calculated where D is the distance of the interaction principal component (IPC) point from the origin in space, n is the number of significant IPCs, and γ_{is} is the score of genotype i in IPC. The genotype with the lowest value of D statistic considered as the most stable. Purchase et al., 2000 developed the AMMI stability value (ASV) based on the AMMI model's IPC1 and IPC2 scores for each genotype. The genotypes with the lowest ASV value would be more stable.

AMMI Stability Value (ASV) =

$$\sqrt{[\frac{SSIPCA1}{SSIPCA2} * IPCA1\ score]^2 + IPCA2\ score^2} \qquad \text{(ii)}$$

where SSIPCA1 and SSIPCA2 are sum of squares by the IPCA1, IPCA2 respectively

AMMI Distance (D_i)=

$$\sqrt{\sum_{i=1}^{n} \gamma_{is}^2} \qquad \text{(i= 1,2,3,.. n)} \qquad \text{(iii)}$$

Stability *per se* might not be the only selection parameter because the most stable genotypes would not necessarily give the best yield performance (Mohammadi *et al.*, 2007). The need was felt to incorporate both yield and stability in a single index. Cause to it various authors had advocated the different selection criteria for simultaneous selection of yield and stability (Kang, 1993; Farshadfar *et al.*, 2011). Genotypic stability index (GSI) considered the rank of yield of genotypes across environments and rank of AMMI stability value. This index incorporate mean and stability index in a single criteria and calculated as:

$$GSI = RASV+RY \qquad \text{(iv)}$$

where, RASV is the rank of AMMI stability value and RY is the rank of mean yield of genotypes (RY) across environments. Low values show desirable genotypes with high mean yield and stability.

Sixteen barley genotypes were evaluated under national varietal trials carried out under the All India coordinated wheat and barley improvement programme at eleven locations. The experiments were conducted during crop season 2012-13 across locations, viz: Banswara, Bikaner, Durgapura, Faizabad, Hisar, Jalore, Kanpur, Kota, Udaipur, Varanasi and Vijapur. The details of pedigrees for studied genotypes and characteristics of environments are presented in Table 1 for ready reference. The randomized complete block design employed, with four replications. All the cultural practices were carried out as per zone recommendations to harvest good forage and grain yield. Genstat software version 17.1 (VSN) applied to calculate AMMI analysis of data.

RESULTS AND DISCUSSION

AMMI analysis of variance: The main effects of genotypes, environments and GxE interaction were highly significant for forage yield at 1% level of significance (Table 2a). The highly significant GxE interaction ranked genotypes differently studied environments. Large portion of total variance was described by the environmental main effect (82.3%) while the genotypes accounted for 3.0% of total variation. A large yield variation, explained by environments, indicated that the environments were diverse and a major part of variation in yield resulted from environmental changes

TABLE 1: Details of barley genotypes, parentage and environments

Code	Genotype	Parentage	Code	Locations	Latitude	Longitude	Mean Sea Level (m)
G1	RD 2859	K-551/PL-604//RD2552	E1	Banswara	23° 55' N	74° 45' E	216.4
G2	RD 2552	RD2035/DL472	E2	Bikaner	28° 02' N	73° 31' E	225.3
G3	RD 2035	RD103/PL101	E3	Durgapura	26° 51 'N	75 °47 ' E	390
G4	UPB 1036	JYOTI/(CABUYA/JAZMIN//PETUNIA. 1)	E4	Faizabad	26° 47 °N	82° 12 ‘E	113
G5	RD 2715	RD387/BH602//RD2035	E5	Hisar	29° 10'N	75° 46 ' E	215.2
G6	UPB 1034	RD2624/DWR46	E6	Jalore	25° 34' N	72° 62' E	170.5
G7	BH 971	HBL 405/RD/2683	E7	Kanpur	26° 29 ' N	80° 18 ' E	125.9
G8	KB 1238	K603 /RD2552	E8	Kota	25° 21' N	75° 86' E	259.7
G9	BH 970	HBL 276/RD/2683	E9	Udaipur	24° 34 ' N	70° 42 ' E	582
G10	RD 2858	RD2035/UBL-9//VMORALIS	E10	Varanasi	25° 20 ' N	83° 03 ' E	75.5
G11	NDB 1570	NDB1020/LAKHAN	E11	Vijapur	23° 35 °N	72° 55 ‘E	41.1
G12	UPB 1035	LAKHAN/ (GIORIA-BAR/4/SOTOL//2762/BC-B/3/11012.2/…)					
G13	RD 2857	RD2620/NDB1173//RD2522					
G14	AZAD	K12/K19					
G15	RD 2856	RD2620/NDB1173//RD2634					
G16	NDB 1566	BCB128/NDB940					

TABLE 2 a: AMMI analysis of barley genotypes over locations for forage yield

Source of variation	Degree of freedom	Mean Sum of squares	Variance ratio	% TSS	% GxE
Treatments	175	14983	67.97***	95.47	
Genotypes	15	5454	24.74***	2.98	
Environments	10	226077	487.68***	82.31	
Block	33	464	2.10		
Interactions	150	1863	8.45***	10.18	
IPCA 1	24	3537	16.04***		30.37
IPCA 2	22	2465	11.18***		19.40
IPCA 3	20	2063	9.36***		14.76
IPCA 4	18	2046	9.28***		13.18
Residuals	66	944	4.28		
Error	495	220			
Total	703	3907			

%TSS, percentage of total sum of squares, % GxE, percentage of GxE total sum of squares
*** denotes significant at 0.001 level of significance

TABLE 2 b: AMMI analysis of barley genotypes over locations for grain yield

Source of variation	Degree of freedom	Mean Sum of squares	Variance ratio	% TSS	% GxE
Treatments	175	358.6	32.55***	90.68	
Genotypes	15	501.8	45.55***	10.88	
Environments	10	4065.3	134.44***	58.75	
Block	33	30.2	2.74	1.44	
Interactions	150	97.1	8.82***	21.06	
IPCA 1	24	224.7	20.40***		37.01
IPCA 2	22	113.9	10.34***		17.20
IPCA 3	20	117.5	10.66***		16.12
IPCA 4	18	100.8	9.15***		12.46
Residuals	66	38.0	3.45		
Error	495	11.0			
Total	703	98.4			

%TSS, percentage of total sum of squares, % GxE, percentage of GxE total sum of squares
*** denotes significant at 0.001 level of significance

(Abdipur and Vaezi, 2014). The multiplicative variance of the treatment sum of squares due to interaction was partitioned into the IPCA1, IPCA2, IPCA3 and IPCA4; which explained 30.4, 19.4, 14.8 and 13.2% of the interaction sum of squares, respectively. More over the first two interaction principal components explained 49.8% of the interaction sum of squares as reported by Anandan *et al.*, 2009.

The highly significant effects of environments, interactions and genotypes were observed for grain yield. GxE interaction explained 21.1% of the total variance (Table 2b). Of the total variance, a larger portion was described by the environmental main effect (58.8%) while the genotypes accounted about 10.9% of total variation. The significant interaction components i.e. IPCA1, IPCA2 and IPCA3, IPCA4; explained 37.0, 17.2, 16.1 and 12.5% of the interaction sum of squares, respectively. The first two interaction principal components explained 54.2% of the interaction sum of squares.

Average yield: The forage yield of dual purpose barley genotype ranged from 169.8 to 127.5 q/ha with genotype RD2715 recorded highest yield closely followed by RD2857 and RD2859 (Table 3a). The lowest yield shown by UPB 1035, UPB 1034 and BH 971.

The grain yield varied from 34 to 23.4 q/ha with genotype RD2035 recorded highest yield closely followed by Azad and RD2552 (Table 3b). The lowest yielder genotypes were RD2857, RD2856 and KB1238.

IPCAs Interaction (crossover and non-crossover interactions): Fifty per cent of genotypes showed positive and negative IPCA1values for forage yield. Genotype G14(AZAD) has large negative IPCA1 score also showed positive IPCA4 value. This type of response is referred to as crossover GxE interaction. On the other hand, same sign or near zero scores represent a non-crossover interaction or a proportionate genotype response (Silveira *et al.*, 2013). The genotypes with lower IPCA1 scores would produce a lower absolute G×E interaction effect than those with higher absolute IPCA1 scores and have less variable yields (more stable) across genotypes (Oliveira *et al.*, 2014). Genotypes G5(RD 2715) and G7(BH 971) with yields greater than the overall mean and low IPCA1 scores had a combination of high yield and stability performances (Table 3a). Genotypes G1(RD 2859) and G13(RD 2857) were similar to G9(BH

TABLE 3a: AMMI estimates and ranking of genotypes for forage yield

Code	Genotype	Gm	R_{Gm}	IPCA1	IPCA2	IPCA3	IPCA4	D	R_D	ASV	R_{ASV}	GSI	P	R_P	St	R_{St}	W	R_W
G1	RD 2859	162.5	3	3.876	2.204	1.678	4.275	6.40	13	6.45	13	16	761	4	4633	15	6024	14
G2	RD 2552	154.5	9	-4.153	1.717	2.348	-1.181	5.21	9	6.72	14	23	975	6	3783	7	5879	13
G3	RD 2035	158	6	-2.440	1.763	-0.409	0.434	3.07	1	4.21	6	12	805	5	4304	10	3214	5
G4	UPB 1036	146.7	11	-1.036	2.447	-5.457	3.563	7.04	14	2.94	4	15	1447	11	4341	12	5358	12
G5	RD 2715	169.8	1	3.276	1.649	3.520	1.485	5.30	10	5.39	11	12	566	1	4306	11	4185	9
G6	UPB 1034	141.3	15	1.211	0.127	-2.046	-2.954	3.79	5	1.90	2	17	1646	15	3213	3	2558	3
G7	BH 971	142.5	14	-0.077	-2.905	-2.554	3.423	5.17	8	2.91	3	17	1592	14	4380	13	3460	6
G8	KB 1238	152.8	10	3.195	-0.256	-0.404	-3.998	5.14	7	5.01	9	19	1122	10	3279	4	3563	7
G9	BH 970	144.4	12	-2.360	0.271	0.920	-2.175	3.35	2	3.70	5	17	1478	12	3136	1	2538	2
G10	RD 2858	156.6	7	3.730	-0.401	-4.231	-2.000	6.00	12	5.85	12	19	1108	9	3151	2	4479	10
G11	NDB 1570	162.4	4	-1.181	-4.021	3.741	1.415	5.79	11	4.43	7	11	728	3	4097	8	4923	11
G12	UPB 1035	127.5	16	0.341	0.956	0.309	-3.572	3.73	4	1.10	1	17	2508	16	3506	6	2237	1
G13	RD 2857	168.1	2	2.873	0.981	1.351	1.014	3.47	3	4.60	8	10	584	2	5160	16	3206	4
G14	AZAD	158.7	5	-7.033	-1.785	-1.281	0.447	7.38	16	11.15	16	21	1050	7	4288	9	8189	16
G15	RD 2856	156.3	8	1.506	-6.989	0.729	0.052	7.19	15	7.38	15	23	1087	8	3451	5	6434	15
G16	NDB 1566	144.2	13	-1.728	4.241	1.785	-0.228	4.92	6	5.03	10	23	1478	13	4480	14	3635	8

Gm-Genotype mean yield, ASV-AMMI stability value, D- AMMI Distance, GSI -Genotypic Stability Index, P - Cultivar superiority, St - Static stability, W- Wricke's ecovalence

TABLE 3b: AMMI estimates and ranking of genotypes for grain yield

Code	Genotype	Gm	R_{Gm}	IPCA1	IPCA2	IPCA3	IPCA4	D	R_D	ASV	R_{ASV}	GSI	P	R_P	St	R_{St}	W	R_W
G1	RD 2859	26.29	10	-2.387	1.003	0.618	0.498	2.71	10	5.23	13	23	102.74	13	96.09	11	292.5	13
G2	RD 2552	32.13	3	-0.001	-1.747	-1.722	0.042	2.45	8	1.75	6	9	35.21	4	96.25	12	207.7	9
G3	RD 2035	34.03	1	1.151	-1.334	2.330	-0.534	2.97	13	2.81	9	10	14.42	1	110.32	15	281.6	11
G4	UPB 1036	30.93	5	2.505	0.603	-0.535	-1.008	2.82	11	5.42	14	19	43.42	6	103.62	14	299.5	14
G5	RD 2715	26.67	8	-1.260	1.458	1.014	-0.343	2.20	6	3.08	10	18	90.90	10	56.80	2	174.3	6
G6	UPB 1034	30.36	6	1.422	0.556	0.070	-1.582	2.20	5	3.11	11	17	43.22	5	79.14	5	203.5	8
G7	BH 971	32.08	4	0.256	-0.741	1.519	1.202	2.09	3	0.92	2	6	25.29	2	98.31	13	133.8	3
G8	KB 1238	25.42	14	-2.897	0.327	-1.087	0.395	3.14	15	6.24	16	30	121.68	15	77.12	4	383.8	15
G9	BH 970	30.17	7	0.980	0.434	-1.486	1.331	2.26	7	2.15	7	14	51.00	7	95.36	10	166.9	4
G10	RD 2858	26.13	11	-2.140	0.556	0.700	-1.044	2.54	9	4.63	12	23	99.40	12	90.85	9	236.1	10
G11	NDB 1570	26.05	12	0.213	-0.877	-1.788	-0.078	2.00	2	0.99	3	15	89.68	8	118.52	16	170.0	5
G12	UPB 1035	26.55	9	2.219	2.603	0.836	1.387	3.78	16	5.44	15	24	97.57	11	85.24	8	430.4	16
G13	RD 2857	23.38	16	0.035	0.430	-0.962	-2.709	2.91	12	0.44	1	17	131.83	16	63.04	3	199.7	7
G14	AZAD	32.36	2	0.015	-2.699	1.404	0.014	3.04	14	2.70	8	10	26.44	3	80.80	6	285.4	12
G15	RD 2856	23.8	15	-0.703	-0.107	0.153	0.742	1.04	1	1.51	5	20	120.17	14	46.94	1	61.1	1
G16	NDB 1566	25.9	13	0.591	-0.466	-1.066	1.687	2.13	4	1.35	4	17	90.70	9	82.18	7	116.5	2

Gm-Genotype mean yield, ASV-AMMI stability value, D- AMMI Distance, GSI -Genotypic Stability Index, P - Cultivar superiority, St - Static stability, W- Wricke's ecovalence

970) in the main effect but tended to contribute more to GxE interaction.

Only 10 and 6 genotypes showed positive IPCA1 scores and negative values respectively. Genotype G1(RD 2859) has large negative IPCA1 score also showed positive IPCA3 and IPCA4 values. Genotypes G5(RD 2715) and G7(BH 971) with yields greater than the overall mean and low IPCA1 scores had a combination of high yield and stability performances (Table 3b).

AMMI stability index (D) incorporates: The scores of significant IPCA towards the interaction SS and the lower D associated high stability across the tested environments and vice versa (Zang *et al*, 1988). The ranking of genotypes in ascending order of D values are those in G3(3.07) < G9(3.35) < G13(3.47) < G12(3.73) (Table 3a). Genotypes G12(UPB 1035) and G6(UPB 1034) with lowest yield exhibited D values 3.73 and 3.79 respectively. Genotype G14(AZAD) showed smallest negative IPCA1 score (-7.03).

The ranking of genotypes for grain yield in ascending D values are G15(1.04) <G11(2.00) < G7 (2.09) < G16(2.13). Genotypes G13(RD 2857) and G8(KB 1238) with lowest yield exhibited D values 2.91 and 3.14 respectively (Table 3b). Genotype G8(KB 1238) showed lower yield and smallest negative IPCA1 score (-2.89) as well as larger D (3.14) value. This genotype recognized with stable yield of lower magnitude.

AMMI Stability Value (ASV): ASV is the distance from origin in a two dimensional scatter graph of IPCA1 against IPCA2 scores. The IPCA1 score contributes more to GE sum of scores, weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 towards total GxE sum of squares. Genotype with least ASV score is the most stable, accordingly genotype G12(UPB 1035), followed by G6 (UPB 1034), G7 (BH 971) and G4(UPB 1036) were the most stable, while genotypes G14(AZAD), G15(RD 2856) and G2(RD 2552) were undesirable for forage yield (Table 3a). The ranking of genotypes G12 and G6 also supported by criteria based on Static and dynamic stability as per Wricke ecovalence (Mohammadi *et al*., 2013). However, the genotype G9 ranked as fifth desirable genotype by ASV stood at first and second place by static and dynamic respectively.

Genotypes with lower ASV score, were G13 (RD 2857), followed by G7 (BH 971), G11 (NDB 1570) were the most stable, while genotypes G8(KB 1238), G12(UPB 1035) and G4(UPB 1036) were undesirable (Table 3b). G15 genotype got first place of choice by static and dynamic concepts irrespective of fifth position by ASV. Genotype G7 got second rank by ASV and Pi values as well as third by dynamic stability (Mohammadi *et al*., 2013). G13 identified as most desirable by ASV got supported by third position by static stability.

Genotype Selection Index (GSI): The least GSI is considered as the most stable with high yield. Based on the GSI the most desirable genotype for selection is G13(RD 2857), G11(NDB 1570) followed by G3(RD 2035), G5(RD 2715) (Table 3a). The recommendation of genotype G13 was also supported by cultivar superiority and dynamic stability.

The desirable genotype for high grain yield is G7(BH 971), G2(RD 2552) followed by G3(RD 2035), G14(AZAD) as reflected by table 3b. The desirable genotype as per GSI value G7 also got positive weights by cultivars superiority and dynamic stability criteria.

Biplot analysis (Forage harvested): AMMI analysis plots the mean effects of genotypes and locations on the abscissa and IPCA1 scores of both effects, simultaneously on the ordinate (Figure 1). The differences in main effects reflected by displacement along the abscissa, whereas the positions along the ordinate differentiates the interaction effects (Rodriguez *et al*., 2007). Genotypes G4(UPB 1036), G7(BH 971) and G12(UPB 1035) with IPCA1 scores close to zero have small interactions and have wider adaptation to the tested environments (Mohamadi *et al*., 2010). The environments showed variability in both main effects and interactions as scattered in all quadrants (Figure 1). The high yielder environments Banaswara observed in quadrant-IV, with maximum interaction effects, negative IPCA1 scores. The high potential environment Jalore and Kota was in quadrant- I, with positive IPCA1 and yield. Hisar environment showed lower yield with largest negative IPCA1.

The discriminating ability of the environments can be judged by calculating the distance of each environment from the biplot origin (Oliveira *et al*., 2014). In this regard, the environments Banswara, Jalore and Hisar are most discriminating as indicated by long distance from the biplot origin. Genotypes with IPCA1 scores >0 G13(RD 2857), G5(RD 2715), G8(KB 1238), G10(RD 2858) responded positively (adaptable) to the environments Kota and Jalore that had IPCA1 scores > 0 (positive interaction), but responded negatively to the environments Bikaner and Hisar that had IPCA1 scores <0. The reverse applies for the genotypes G4(UPB 1036), G1(RD 2859), G16(NDB 1566), G9(BH 970) that had IPCA1 scores < 0 (Silveira *et al*., 2013).

IPCA scores were plotted in the x-axis and the y-axis respectively (Figure 2). The AMMI analysis for the first Interaction Principal Component (IPC1) captured 30.4% and the second interaction principal component explained 19.4% as the first two interaction principal components cumulatively captured 49.8% of the interaction sum of square. The closer the genotypes to the center the more stable is the genotype and vice versa for unstable genotypes (Purchase *et al.,* 2000). The G6(UPB 1034) and G12(UPB 1035) located near to the origin implies its

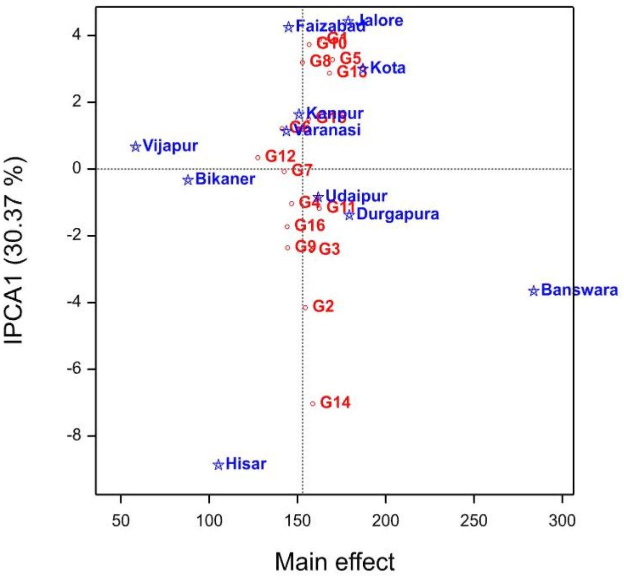

FIG 1: First principal axis of interaction (PCA1) versus forage yield of genotypes

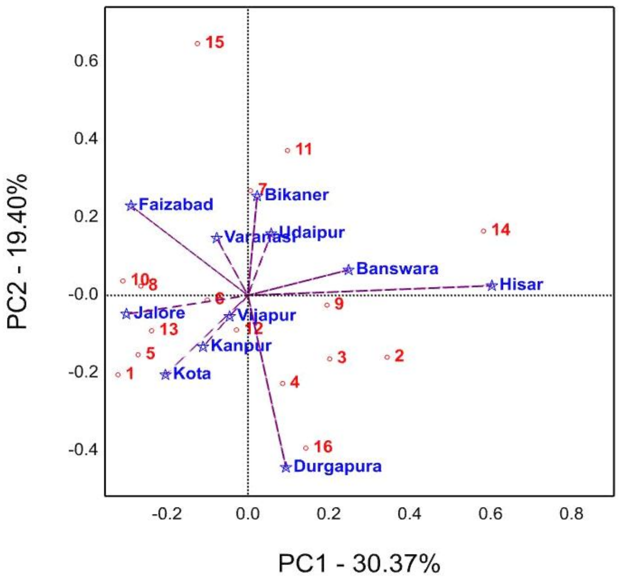

FIG 2: PCA1 versus PCA2 for forage yield of genotypes

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

G1	G2	G3	G4	G5	G6	G7	G8
RD 2859	RD 2552	RD 2035	UPB 1036	RD 2715	UPB 1034	BH 971	KB 1238
G9	G10	G11	G12	G13	G14	G15	G16
BH 970	RD 2858	NDB 1570	UPB 1035	RD 2857	AZAD	RD 2856	NDB 1566

stable behavior as compared to the barley genotypes G15(RD 2856), G11(NDB 1570), G14(AZAD), G16(NDB 1566), G1(RD 2859) located distant from the origin. The cosine of angle involving a pair of environment or genotype vectors approximates correlation between them (Mladenov *et al*., 2012). An acute angle (less than 90°) indicates a strong positive correlation between environments (Banswara, Hiar), (Bikaner, Udaipur), (Faizabad, Varanasi); an angle close to 90° indicates the environments are not correlated (Kota, Faizabad), (Jalore, Durgapura) ; whereas, an obtuse angle close to 180° represents a strong negative relationship (Varanasi, Durgapura) and (Jalore, Hisar). Vectors corresponding to (Faizabad, Hisar) showed angles more than 90° angle suggesting that these environments tend to discriminate among genotypes in a similar manner.

Biplot analysis (Grain yield): Genotypes G11(NDB 1570) and G2(RD 2552) with IPCA1 scores close to zero have small interactions and have wider adaptation to the tested environments (Figure 3). The environments were scattered in all quadrants. The high yielder environments Udaipur and Hisar were seen in quadrant-IV, with maximum interaction effects, high negative IPCA-1 scores. The low potential environment Banswara was in quadrant-III, with low negative IPCA1 and yield. Kota environment showed higher yield potential with highest positive IPCA1.

The environments Bikaner, Hisar and Vijapur are most discriminating as indicated by long distance from the biplot origin. Genotypes G7(BH 971), G3(RD 2035), G9(BH 970), G6(UPB 1034), G4(UPB 1036) with IPCA1 scores >0 responded positively (adaptable) to the Kota & Jalore environments that had IPCA1 scores > 0 (positive interaction), but responded negatively to the environments Banswara, Bikaner, Faizabad with IPCA1 scores <0. More over the reverse behavior seen for the genotypes G15(RD 2856), G5(RD 2715),G10(RD 2858),G1(RD 2859) that had IPCA1 scores < 0.

First Interaction Principal Component (IPC1) captured 37% and the second interaction principal component explained 17.2% as the first two interaction principal components cumulatively captured 54.2% of the interaction sum of square (Figure 4). The G13(RD 2857), G15(RD 2856) and G16(NDB 1566) located near to the origin implies its stable behavior as compared to the barley genotypes G12(UPB 1035), G5(RD 2715), G8(KB 1238), G14(AZAD), G3(RD 2035) located distant from the origin. An acute angle (less than 90°) indicates a strong positive correlation between environments (Banswara, Durgapura), (Bikaner, Udaipur), (Kota, Jalore); an angle close to 90° indicates the environments are not correlated (Kanpur, Hisar) ; whereas, an obtuse angle close to 180° represents a strong negative relationship (Kanpur, Bikaner). Vectors

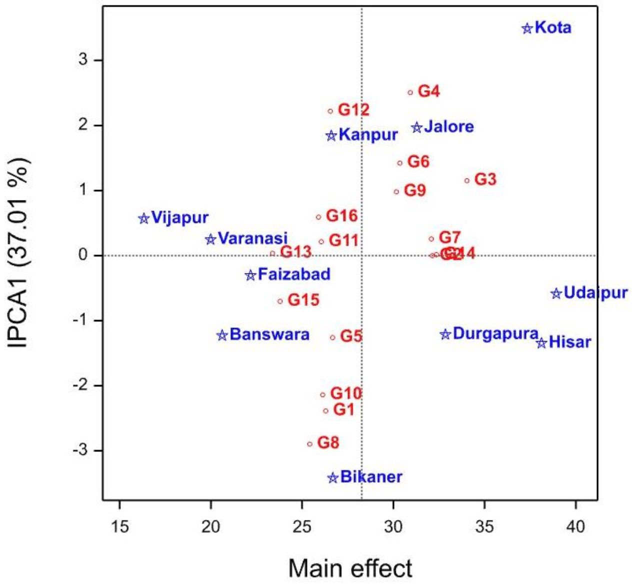

FIG 3: PCA1 versus mean yield

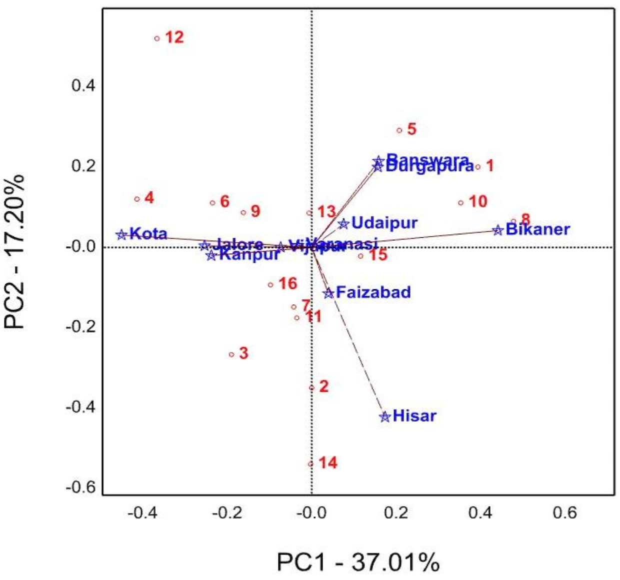

FIG 4: PCA1 versus PCA2 scores for yield

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

G1	G2	G3	G4	G5	G6	G7	G8
RD 2859	RD 2552	RD 2035	UPB 1036	RD 2715	UPB 1034	BH 971	KB 1238
G9	G10	G11	G12	G13	G14	G15	G16
BH 970	RD 2858	NDB 1570	UPB 1035	RD 2857	AZAD	RD 2856	NDB 1566

corresponding to (Kota, Hisar) showed angles more than 90^{o} angle suggesting that these environments tend to discriminate among genotypes in a similar manner.

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