

Biplot Analysis of Adaptability Measures of Barley Genotypes Evaluated under Salinity and Alkalinity Conditions

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ABSTRACT: Analytic measures of adaptability had been defined recently for efficient estimation of GxE interaction under multi environment trials. Highly significant effects of the environment (E), genotypes (G), and GxE interaction had been observed by AMMI analysis. GxE interaction accounted for 38.4% whereas Environment explained 31.7% of treatment variations in yield during first year. Harmonic Mean of Genotypic Values (HMGV) expressed higher values for NDB1445, RD2552, DWRB201 genotypes. Ranking of genotype as per IPCA-1 were HUB268, DWRB201, RD2999. While IPCA-2, selected RD2907, DWRB201, HUB267 genotypes. Values of Measures ASV1 and ASV identified DWRB201, HUB267, HUB268 barley genotypes. Adaptability measures Harmonic Mean of Relative Performance of Genotypic Values (HMPRVG) and Relative Performance of Genotypic Values (RPGV) identified NDB1445, RD2552, DWRB201 as the genotypes of performance among the locations. Biplot graphical analysis exhibited PRVG, HMPRVG clustered with mean, GM, HM IPC2, IPC5 measures. During 2019-20 cropping season Environment effects accounted 42.5% whereas GxE interaction contributed for 30.2 % of treatment variations in yield. HMGV expressed higher values for RD3016, KB1822, RD3017. IPCA-1 scores, desired ranking of genotypes was RD2907, HUB274, KB1845. While IPCA-2 pointed towards RD2907, RD3015, KB1815, as genotypes of choice. Analytic measures ASV and ASV1 selected PL908, RD2849, DWRB123 barley genotypes. HMPRVG along with PRVG settled for RD3016, KB1822, RD3017. Measures ASV, ASV1 expressed bondage with adaptability measures PRVG, HMPRVG, mean, GM along with IPC3 as observed in different quadrant of biplot analysis. Selection of barley genotypes by the harmonic mean of genotypic values allow to identify the stable and productive genotypes for problem soils of the country.

Keywords: AMMI, ASV, ASV1, HMGV, GAI, HMPRVG, Biplots

INTRODUCTION

Barley (*Hordeum vulgare* L.), an ancient cereal crop, domesticated about 10,000 years ago mentioned as the fourth important crop in the world agriculture scenario (Kendall *et al.*, 2019). Mainly cultivated not only for food, bio-fuel and animal feed but used as raw material for malt and malt-based products (Kharub *et al.*, 2017). A target to restoring 26 million ha of degraded lands, including salt-affected soils, had been fixed by the year 2030 to ensure food security for the people (Kumar & Sharma, 2020). Grains consist β -glucan, an important constituent of human diets. β -glucan plays a critical role in decreasing the sugar of diabetic patients, reduce the serum cholesterol of heart patients and decrease the risk of coronary heart disease (Shimizu *et al.*, 2008). Now a days more emphasis given to consume barley and barley-based products by the health-conscious consumers (Karkee *et al.*, 2020). AMMI analysis had been established as an efficient analytic tool for GxE interaction analysis under multi location trials (Ajay *et al.*, 2019; Agahi *et al.*, 2020). Researchers identify barley genotypes would possess stable yield along with broad or narrow adaptation of the genotypes (Bocianowski *et al.*, 2019).

AMMI based stability and adaptability measures had observed in literature (Tekdal & Kendal, 2018). Analytic measure of adaptability as the harmonic means of the relative performance of the predicted genotypic values (MHPRVG) utilized productivity, stability, and adaptability simultaneously of genotypes (Resende & Durate, 2007). Comparative performance of AMMI based measures had been studied with relatively new adaptability measures for barley genotypes evaluated under multi location research trials under coordinated barley improvement program of the country.

MATERIAL AND METHODS

During cropping seasons of 2018-19 and 2019-20 sixteen promising genotypes in advanced trials evaluated at seven major locations of the zone and eighteen genotypes at five locations respectively. Field trials were conducted at research centers in randomized complete block designs with three replications. Recommended agronomic practices were followed to harvest good yield. Details of locations and genotype parentage were reflected in Tables 1 & 2 for ready reference.

Mohamadi & Amri 2008	Geometric Adaptability Index	$GAI = \sqrt[n]{\prod_{k=1}^n \bar{X}_k}$
Purchase 1997	AMMI stability value	$ASV = [(\frac{SSIPC 1}{SSIPC 2} PCI)^2 + (PC2)^2]^{1/2}$
Zali <i>et al.</i> , 2012	AMMI stability value	$ASV1 = [(\frac{SSIPC 1}{SSIPC 2} (PCI)^2 + (PC2)^2)]^{1/2}$
Resende & Durate 2007	Harmonic mean of Genetic Values	$MHV G_i = \text{Number of environments} / \sum_{i=1}^k \frac{1}{X_i}$
Resende & Durate 2007	Relative performance of genotypic values across environments	$PRV G_{ij} = VG_{ij} / VG_i$
Resende & Durate 2007	Harmonic mean of Relative performance of genotypic values	$MHPRV G_i = \text{Number of environments} / \sum_{j=1}^k \frac{1}{PRV G_{ij}}$

Table 1: Parentage details of barley genotypes and environmental conditions (2018-19).

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	RD2794	RD2035/RD2683	E1	IIWBR Hisar	29°14' N	75°73' E	
G2	HUB267	BH 550 / RD 2624	E2	Faizabad	26° 46' N	82° 9' E	97
G3	RD2999	RD2592 / RD2830	E3	Khumer	25°42' N	93°96' E	
G4	NDB1708	3rd GSBYT-18 (2016)	E4	Dalipnagar	28°63' N	77°21' E	
G5	DWRB207	CDC MANLEY/BCU2881	E5	Banasthali	26°40' N	75°85' E	
G6	KB1762	PENCO/CHEVRON-BAR//KASOTA	E6	HAU Hisar	29°10' N	75° 46' E	215.2
G7	DWRB201	DWRUB52/BONMRA-73//Prestige/PL426	E7	Vallabh Nagar	24°67' N	74' E	
G8	KB1754	LIGNEE527/GERBEL/3/BOY-B*2/SURB//CI12225.2D/4/BBSC/CONG0NA					
G9	HUB268	YARADU / 22NDIBYT-01-2-2-4-2					
G10	KB1706	Jagriti/RD2785					
G11	NDB1173	BYTLRA 3-(1994-95)/NDB217					
G12	RD3000	DWRUB64 / RD2503					
G13	RD2552	RD2035/DL472					
G14	RD3002	RD2715 / RD2552					
G15	NDB1445	NDB940/Ratna					
G16	RD2907	RD103/RD2518//RD2592					

Table 2: Parentage details of barley genotypes and environmental conditions (2019-20).

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	KB1845	PETUNIA1/5/POST/COPAL//GLORIA-BAR/COME/3/SIND89A-148/4/CARD/6/GLORIA-BAR/COPAL//BLU/3/PETUNIA 1/7/PINON	E1	IIWBR Hisar	29°14' N	75°73' E	
G2	DWRB214	EC361898	E2	HAU Hisar	29°10' N	75° 46' E	215.2
G3	RD3017	RD 2552 / PL 419 // RD 2508	E3	Dalipnagar	28°63' N	77°21' E	
G4	HUB274	JB 18 / 31st IBON-4-02	E4	Faizabad	26° 46' N	82° 9' E	97
G5	BH1033	BH 942 / BH 393	E5	Fatehpur	25°93' N	80°81' E	
G6	RD2794	RD2035/RD2683					
G7	RD3018	RD 2592 / RD 2607					
G8	RD2907	RD103/RD2518//RD2592					
G9	NDB1730	Avt/Attiki//M-AH73-337-1/3/Aths/Lignee686/4/HB42					
G10	KB1822	K 996/K 508					
G11	NDB1742	Avt/Attiki //M-AH73-337-1/3/Aths/Lignee686/4/HB42					
G12	BH1032	BH 965 / BH 885					
G13	RD3016	RD 2715 / RD 2552					
G14	NDB1173	BYTLRA 3-(1994-95)/NDB217					
G15	HUB273	31st INBON-18/ RD 2508					
G16	KB1815	Ghinneri(smooth awns)/6/JLB70-01/5/DeirAlla106//DL70/Pyo/3/RM1508 /4/Arizona5908/Aths//Avt/Attiki/3/Ager (4thGSBSN2016-17-52)					
G17	RD3015	RD 2715 / RD 2552					
G18	RD2552	RD2035/DL472					

AMMI analysis was performed using AMMISOFT version 1.0, available at <https://scs.cals.cornell.edu/people/hugh-gauch/> and SAS software version 9.3. Simple and effective measure for adaptability is calculated as the relative performance of genetic values (PRVG) across environments and MHVG (Harmonic mean of Genetic Values), based on the harmonic mean of the genotypic values across in different environments. Lower the standard deviation of genotypic performance across environments, the greater is the harmonic mean of its genotypic values.

RESULTS AND DISCUSSION

A. AMMI analysis of barley genotypes

First year of study 2018-19. AMMI based measures evaluate the adaptability performance after reduction of the noise from the GxE interaction effects (Gauch, 2013). Highly significant effects of the environment (E), GxE interaction and genotypes (G), had been observed by AMMI analysis of barley genotypes evaluated under multi location trials for coordinated improvement program (Table 3). Analysis observed the greater contribution of GxE interactions, environments,

and of genotypes effects to the total sum of squares (SS) as compared to the residual effects (Hongyu *et al.*, 2014). Environment explained about significantly 31.7% of the total sum of squares due to treatments indicating that diverse environments caused most of the variations in genotypes yield. Genotypes explained only 9.3% of a total sum of squares, whereas GxE interaction accounted for 38.4% of treatment variations in yield. Further bifurcation of GxE interaction observed the significant four multiplicative terms out of five explained most of interaction sum of squares (Oyekunle *et al.*, 2017).

Second year 2019-20. Analysis observed the greater contribution of environments, GxE interactions, and genotypes to the total sum of squares (SS) as compared to the residual effects. Environment explained significantly about 42.5%, GxE interaction accounted for 30.2 % whereas Genotypes explained only 8.4% of the total sum of squares due to treatments (Table 7). Partitioning of GxE interaction revealed that only first three multiplicative terms were highly significant and explained most of the interaction sum of squares.

Table 3: Multi environment trials analysis by AMMI of barley genotypes (2018-19).

Source	Degree of freedom	Mean Sum of Squares	Significance level	% contributions of factors
Treatments	111	237.21	.0000000 ***	79.49
Genotypes (G)	15	205.41	.0000000 ***	9.30
Environments (E)	6	1753.76	.0000000 ***	31.77
Interactions (GxE)	90	141.40	.0000000 ***	38.42
IPC1	20	225.05	.0000000 ***	
IPC2	18	209.27	.0000000 ***	
IPC3	16	204.18	.0000000 ***	
IPC4	14	51.54	.0038716 **	
IPC5	12	30.26	0.2688757	
Residual	10	10.69	0.8241293	
Error	336	20.22		
Total	447	74.10		

B. Ranking of genotypes as per descriptive measures

First year of study 2018-19. An average yield of genotypes selected NDB1445, RD2552, DWRB201 genotypes (Table 5). This method is simple, but not fully exploiting all information contained in the dataset. Geometric mean is used to evaluate the adaptability of genotypes. Geometric mean observed NDB1445, RD2552, DWRB201 were top-ranked genotypes. Harmonic mean of genetic values (HMGV) of yield expressed higher values for NDB1445, RD2552, DWRB201 genotypes.

Consistent yield performance judged by lower values of Coefficient of Variation and genotypes RD2907, DWRB207, HUB268 would be suitable for considered locations of this zone of the country. Minimum values of standard deviation of yield values selected RD2907, RD3002, RD2794 barley genotypes. Analytic measures PRVG, MHVG, and MHPRVG, had showed consensus for classification of genotypes as per raking of genotypes vis-à-vis analytic measures (Table 4).

Presence of significant cross over interactions has been validated by differences among ranks of genotypes vis-à-vis locations of the zone.

Second year 2019-20. An average yield of genotypes selected RD3016, KB1822, RD3017 genotypes (Table 9). Geometric mean observed RD3016, KB1822, RD3017, were with top-rank. Harmonic mean of genetic values (HMGV) expressed higher values for RD3016, KB1822, RD3017 genotypes.

Consistent yield performance of RD3016, RD2552, NDB1173 judged by lower values of Coefficient of Variation. Minimum values of standard deviation of yield values selected RD2552, KB1845, NDB1173 barley genotypes. Analytic measures PRVG, MHVG, and MHPRVG, had showed consensus for classification of genotypes as per raking of genotypes vis-à-vis analytic measures (Table 6). Presence of significant cross over interactions has been validated by differences among ranks of genotypes vis-à-vis locations of the zone.

Table 4: Ranking of barley genotypes as per descriptive measures (2018-19).

Genotype	Hisar	Faizabad	Khumer	Dalipnagar	Banasthali	Hisar	Vallabhagar	Mean	R _k	GM	R _k	HM	R _k	CV	R _k	Sdev	R _k
RD2794	37.92	25.06	26.06	34.24	38.41	26.95	33.57	31.74	15	31.30	13	30.87	12	0.1783	5	5.66	3
HUB267	28.75	33.21	33.56	35.51	37.32	24.95	43.14	33.78	9	33.33	8	32.88	7	0.1738	4	5.87	5
RD2999	31.46	31.10	43.86	29.35	32.61	20.87	34.01	31.89	14	31.26	14	30.59	13	0.2131	9	6.80	8
NDB1708	33.15	24.76	45.47	28.80	34.78	25.47	39.79	33.17	10	32.45	10	31.76	10	0.2292	10	7.60	10
DWRB207	36.29	32.31	43.63	42.76	38.77	26.38	33.04	36.17	5	35.70	5	35.21	4	0.1698	2	6.14	6
KB1762	36.11	31.40	46.83	36.24	38.04	20.67	48.91	36.89	4	35.71	4	34.38	5	0.2569	12	9.48	13
DWRB201	38.71	37.02	36.12	42.03	36.59	23.82	45.53	37.12	3	36.50	3	35.79	3	0.1825	6	6.78	7
KB1754	21.92	36.90	22.94	36.96	38.41	18.90	48.13	32.02	13	30.39	15	28.79	15	0.3385	16	10.84	16
HUB268	37.86	31.40	39.58	38.77	36.23	23.67	30.31	33.97	8	33.51	7	32.99	6	0.1703	3	5.79	4
KB1706	26.45	25.97	31.50	42.76	38.77	20.29	41.06	32.40	12	31.37	12	30.32	14	0.2664	14	8.63	11
NDB1173	32.67	42.15	32.81	28.99	39.13	22.66	41.37	34.25	6	33.57	6	32.84	8	0.2076	8	7.11	9
RD3000	31.70	17.57	36.86	48.55	37.68	25.41	40.62	34.06	7	32.56	9	30.88	11	0.3000	15	10.22	15
RD2552	35.81	24.76	43.54	51.09	39.13	26.39	48.33	38.44	2	37.19	2	35.90	2	0.2652	13	10.19	14
RD3002	32.43	31.89	21.26	27.72	36.59	23.73	27.18	28.68	16	28.25	16	27.82	16	0.1854	7	5.32	2
NDB1445	34.78	42.88	52.38	35.51	35.51	22.89	45.47	38.49	1	37.41	1	36.24	1	0.2455	11	9.45	12
RD2907	39.73	35.51	27.82	32.61	35.51	27.11	28.57	32.41	11	32.11	11	31.82	9	0.1473	1	4.77	1

Table 5: Adaptability measures of barley genotypes evaluated under MET (2018-19).

Genotype	IPC1	IPC2	IPC3	IPC4	IPC5	ASV1	R _{ASV1}	ASV	R _{ASV}	PRVG	R _{PRVG}	HMPRVG	R _{HMPRVG}
RD2794	-0.978	-1.386	-1.469	1.467	0.497	1.81	5	1.75	5	0.9416	12	0.9163	14
HUB267	-0.240	-0.333	1.098	0.434	-0.712	0.44	2	0.42	2	0.9922	8	0.9859	7
RD2999	0.214	2.060	-0.383	-0.085	-0.599	2.08	9	2.07	10	0.9349	14	0.9208	13
NDB1708	1.033	1.674	-0.535	2.115	-0.668	2.08	10	2.02	9	0.9746	10	0.9515	9
DWRB207	0.405	0.417	-1.480	-1.491	-0.908	0.64	4	0.61	4	1.0652	5	1.0531	4
KB1762	1.309	1.281	0.922	0.917	1.042	2.02	8	1.92	7	1.0682	4	1.0513	5
DWRB201	-0.187	-0.314	0.605	-0.582	1.997	0.39	1	0.37	1	1.0863	3	1.0800	3
KB1754	-0.851	-1.742	3.237	-0.318	-0.448	2.02	7	1.97	8	0.9298	15	0.8735	15
HUB268	-0.160	0.505	-1.694	-1.252	0.089	0.54	3	0.53	3	1.0005	7	0.9875	6
KB1706	0.950	-1.603	0.708	-0.536	-0.776	1.96	6	1.91	6	0.9395	13	0.9225	12
NDB1173	-1.933	0.731	1.414	0.277	-0.115	2.42	11	2.24	11	1.0081	6	0.9848	8
RD3000	2.399	-1.921	-0.985	0.084	-0.307	3.45	16	3.25	16	0.9922	9	0.9348	11
RD2552	2.524	-1.144	-0.152	-0.135	0.627	3.23	15	2.99	15	1.1177	2	1.0884	2
RD3002	-2.551	-0.781	-0.857	0.361	-0.526	3.15	14	2.90	14	0.8556	16	0.8202	16
NDB1445	0.377	2.766	1.146	-0.967	0.127	2.80	13	2.80	13	1.1246	1	1.0966	1
RD2907	-2.311	-0.210	-1.576	-0.288	0.682	2.77	12	2.53	12	0.9689	11	0.9366	10

Table 6: Loadings of adaptability measures as per Principal Components (2018-19).

Component	PC1	PC2
IPC1	-0.2246	-0.2025
IPC2	-0.1230	0.1762
IPC3	-0.0568	-0.2970
IPC4	0.1167	-0.0526
IPC5	-0.1751	0.1066
CV	-0.0460	-0.4430
Sdev	-0.1535	-0.4056
GM	-0.3631	0.0597
HM	-0.3492	0.1318
Hisar	-0.1373	0.3506
Faizabad	-0.0561	0.1136
Khumer	-0.2826	0.0372
Dalipnagar	-0.2082	-0.1541
Banasthali	-0.0655	-0.1696
Hisar	-0.0359	0.2560
Vallabh Nagar	-0.2287	-0.2991
Mean	-0.3666	-0.0072
ASV1	0.0670	-0.2083
ASV	0.0634	-0.2173
PRVG	-0.3635	0.0344
MHPRVG	-0.3595	0.0851
% variation	35.13	22.61

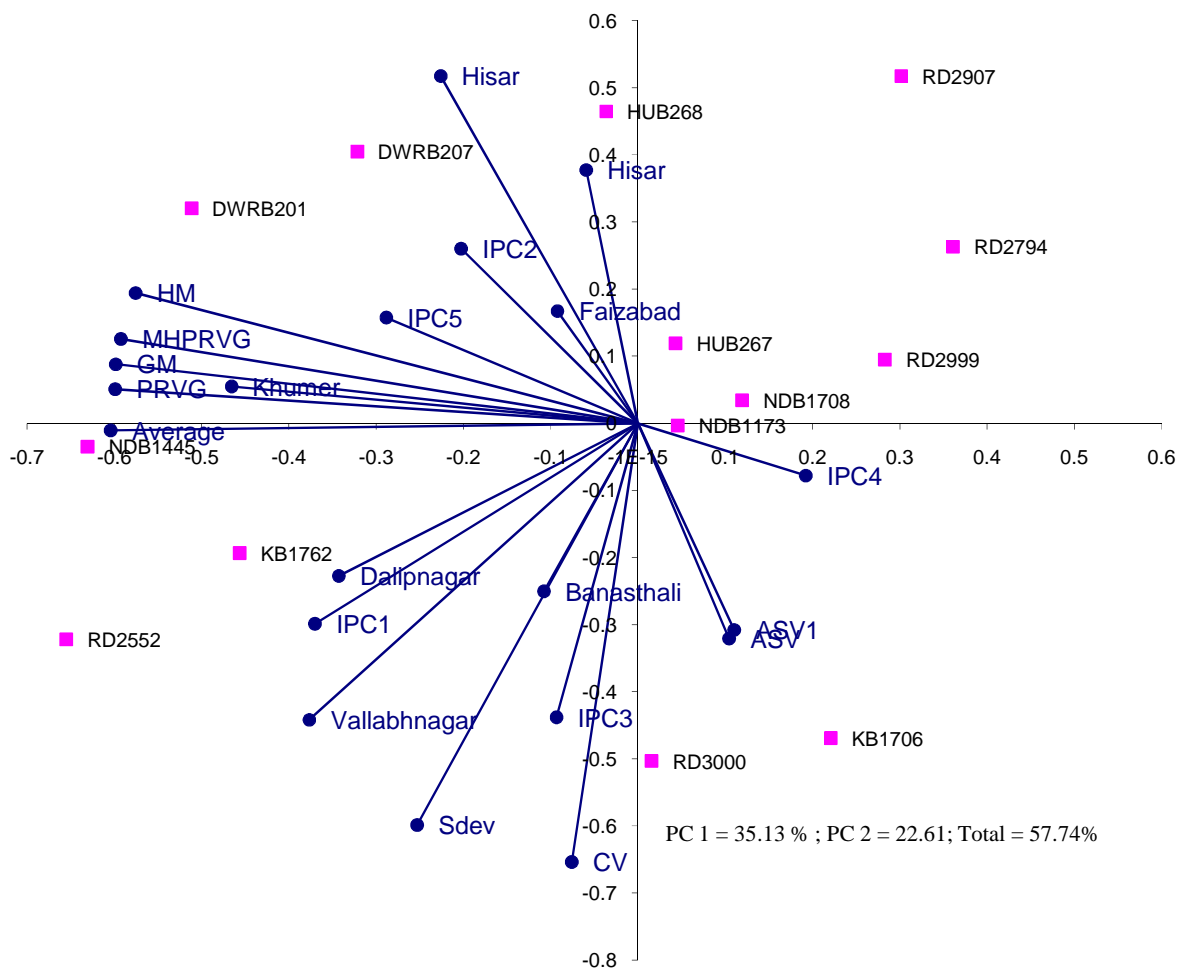


Fig. 1. Biplot analysis of adaptability measures for barley genotypes (2018-19).

C. Adaptability behaviour of genotypes

First year of study 2018-19. The IPCA scores of a genotype in AMMI analysis indicate the stability or adaptation over environments. The greater the IPCA scores, either negative or positive (as it is a relative value), the more specifically adapted is the genotype to certain environments. The more the IPCA scores approximate zero, the more stable or adapted the genotypes are over the entire environments sampled (Ajay *et al.*, 2019). Kendal and Tekdal (2016) stated that genotypes having PC1 scores > 0 were recognized as high-yielding and those having PC1 scores < 0 were regarded as low-yielding.

The IPCA scores of genotypes in the AMMI analysis are an indication of stability or adaptability over environments. The ranking of genotype as per absolute IPCA-1 scores were HUB268, DWRB201, RD2999 (Table 4). While for IPCA-2, genotypes RD2907, DWRB201, HUB267 would be of choice. Values of IPCA-3 favoured RD2552, RD2999, NDB1708 barley genotypes. While RD3000, RD2999, RD2552 by IPCA-4 and IPCA-5 settled for HUB268, NDB1173, NDB1445 barley genotypes for the considered locations of the zone.

Analytic measures of adaptability ASV and ASV1 consider first two significant IPCAs of the AMMI analysis for adaptability behaviour. Values of ASV1 selected DWRB201, HUB267, HUB268 and ASV identified DWRB201, HUB267, HUB268 barley genotypes (Ajay *et al.* 2019). Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) method, the genotypes can be simultaneously sorted by genotypic values (yield) and stability using the harmonic means of the yield so that the smaller the standard deviation of genotypic performance among the locations. Values of HMRPGV ranked NDB1445, RD2552, DWRB201 as the performance of the genotypes among the locations. When considering the yield and adaptability simultaneously, the recommended approach is the relative performance of genetic values (RPGV) over crop years. Relative Performance of Genotypic Values had settled for NDB1445, RD2552, DWRB201 genotypes.

Second year 2019-20. RD2907, HUB274, KB1845 were the top ranked genotype as per absolute IPCA-1 scores (Table 8). While for IPCA-2 identified RD2907,

RD3015, KB1815 genotypes would be of choice. Values of IPCA-3 favoured RD3017, KB1822, NDB1173 barley genotypes.

Two significant IPCAs of the AMMI analysis considered by ASV and ASV1 for adaptability behaviour. Values of ASV1 selected RD2907, NDB1173, NDB1742 and ASV identified RD2907, NDB1173, RD2552 barley genotypes. Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) values ranked RD3016, KB1822, RD3017 as of stable performance among the locations. Relative Performance of Genotypic Values (RPGV) had settled for RD3016, KB1822, RD3017 genotypes.

D. Biplot analysis

First year of study 2018-19. Biplot analysis based on first two highly significant Interaction Principal Components exploited to understand the association if any among adaptability measures. First two significant interaction principal components contribute to the tune of 35.1 & 22.6 to the total for 57.7 % of total GxE interaction sum of squares (Fig. 1). Loadings of adaptability measures based on two interaction principal components had mentioned in table 6. CV clustered with Sdev, Average, IPC1 and IPC3 measures in one quadrant and adaptability measures PRVG, HMRPGV along with mean, GM, HM IPC2, IPC5 grouped in nearby cluster. Clustering of analytic measures ASV and ASV1 observed with IPC4 where close proximity of average yield among adaptability measures of genotypes was of more concern.

Second year 2019-20. First two significant interaction principal components accounted a total for 60.7 with respective % share of 37.9 & 22.7 of total GxE interaction sum of squares (Fig. 2). Loadings of adaptability measures based on two interaction principal components had mentioned in table 10. Measure CV clustered with Sdev & IPC2 in one quadrant while ASV, ASV1 expressed bondage with adaptability measures PRVG, HMRPGV, mean, GM along with IPC3 in separate quadrant. Measures IPC1, and HM clustered in nearby quadrant. Clustering of analytic measures expressed close proximity among themselves; this implies mean yield of genotypes would be suitable to express adaptability of genotypes as far this zone is concerned.

Table 7: Multi environment trials analysis by AMMI of barley genotypes (2019-20).

Source	Degree of Freedom	Mean Sum of Squares	Significance level	% contributions of factors
Treatments	89	160.59	.0000000 ***	81.17
Genotypes (G)	17	87.44	.0000000 ***	8.44
Environments (E)	4	1868.68	.0000000 ***	42.45
Interactions (GxE)	68	78.40	.0000000 ***	30.28
IPC1	20	131.18	.0000000 ***	
IPC2	18	71.82	.0000000 ***	
IPC3	16	65.62	.0000721 ***	
Residual	14	26.06	0.150117	
Error	180	18.42		
Total	269	65.46		

Table 8: Ranking of barley genotypes as per descriptive measures (2019-20).

Genotype	IIWBR Hisar	HAU Hisar	Dalipnagar	Faizabad	Fatehpur	Mean	R _k	GM	R _k	HM	R _k	CV	R _k	Sdev	R _k
KB1845	24.00	18.30	27.17	19.87	17.66	21.40	18	21.10	18	20.83	18	0.1899	4	4.06	2
DWRB214	30.63	32.19	34.42	17.82	16.04	26.22	14	24.96	15	23.67	14	0.3285	14	8.61	13
RD3017	30.79	31.64	35.33	18.00	31.43	29.44	3	28.70	3	27.81	3	0.2255	10	6.64	11
HUB274	30.30	31.34	31.70	18.12	32.04	28.70	4	28.08	4	27.34	5	0.2074	6	5.95	9
BH1033	26.45	39.01	20.38	20.47	25.21	26.31	13	25.53	12	24.87	12	0.2894	12	7.61	12
RD2794	28.90	32.31	34.42	20.23	26.81	28.53	7	28.07	5	27.57	4	0.1927	5	5.50	5
RD3018	28.71	35.51	35.33	13.98	27.54	28.21	8	26.82	9	25.11	11	0.3106	13	8.76	14
RD2907	28.64	30.01	24.46	20.29	35.84	27.85	9	27.34	6	26.84	6	0.2107	8	5.87	7
NDB1730	27.28	30.37	46.20	18.66	20.83	28.67	5	27.20	7	25.93	8	0.3796	15	10.88	15
KB1822	25.64	40.10	30.80	31.55	23.85	30.39	2	29.88	2	29.40	2	0.2089	7	6.35	10
NDB1742	29.27	32.67	40.76	8.94	31.19	28.57	6	25.54	11	21.43	15	0.4136	16	11.81	17
BH1032	26.50	33.52	44.39	10.69	19.23	26.86	11	24.08	16	21.22	16	0.4822	18	12.95	18
RD3016	27.60	36.96	36.23	27.54	35.45	32.75	1	32.47	1	32.17	1	0.1455	1	4.76	4
NDB1173	27.26	25.84	34.42	23.55	24.30	27.08	10	26.82	8	26.59	7	0.1606	3	4.35	3
HUB273	31.74	28.75	31.70	18.72	22.47	26.67	12	26.12	10	25.54	9	0.2188	9	5.84	6
KB1815	29.21	32.61	16.31	11.96	38.41	25.70	17	23.48	17	21.20	17	0.4345	17	11.17	16
RD3015	33.35	30.25	23.55	18.96	22.68	25.76	16	25.23	14	24.71	13	0.2284	11	5.88	8
RD2552	26.95	27.24	19.38	29.59	25.76	25.78	15	25.53	13	25.25	10	0.1489	2	3.84	1

Table 9: Adaptability measures of barley genotypes evaluated under MET (2019-20).

Genotype	IPC1	IPC2	IPC3	ASV1	R _{ASV1}	ASV	R _{ASV}	PRVG	R _{PRVG}	HMPRVG	R _{HMPRVG}
KB1845	0.233	1.385	-2.030	1.46	8	1.42	10	0.7951	18	0.7635	18
DWRB214	-0.572	1.415	-0.141	1.83	11	1.63	11	0.9421	14	0.8981	14
RD3017	-0.565	0.778	-0.025	1.39	7	1.12	6	1.0636	3	1.0558	3
HUB274	0.181	-1.181	-0.624	1.24	5	1.21	8	1.0411	4	1.0332	5
BH1033	0.491	-0.944	-0.506	1.37	6	1.17	7	0.9636	13	0.9207	12
RD2794	1.922	-0.616	0.763	3.95	14	2.81	14	1.0370	5	1.0362	4
RD3018	1.464	0.362	1.673	2.99	12	2.12	12	1.0027	8	0.9761	9
RD2907	0.018	-0.060	-0.772	0.07	1	0.07	1	1.0262	7	0.9940	6
NDB1730	-0.605	-1.005	1.181	1.59	10	1.32	9	1.0269	6	0.9848	7
KB1822	1.494	-1.334	-0.025	3.31	13	2.51	13	1.1349	2	1.0759	2
NDB1742	0.335	-0.692	-1.780	0.97	3	0.84	4	0.9987	10	0.8723	15
BH1032	-2.139	1.204	0.086	4.50	17	3.28	17	0.9354	16	0.8448	16
RD3016	1.657	2.253	1.609	4.05	15	3.26	16	1.2094	1	1.1881	1
NDB1173	-0.332	-0.548	-0.025	0.87	2	0.72	2	0.9999	9	0.9812	8
HUB273	-1.889	-1.715	1.020	4.20	16	3.19	15	0.9687	12	0.9606	10
KB1815	-2.881	0.291	0.669	5.85	18	4.11	18	0.9283	17	0.8081	17
RD3015	0.749	-0.137	0.066	1.53	9	1.08	5	0.9419	15	0.9214	11
RD2552	0.438	0.545	-1.137	1.04	4	0.83	3	0.9844	11	0.9048	13

Table 10: Loadings of adaptability measures as per Principal Components (2019-20).

Component	PC1	PC2
IPC1	0.2343	-0.2112
IPC2	-0.0381	0.0127
IPC3	0.1908	0.3060
ASV1	0.0166	0.3720
ASV	0.0222	0.3624
IWBR Hisar	0.0309	0.1038
HAU Hisar	0.2103	0.2830
Dalipnagar	0.0651	0.2097
Faizabad	0.2382	-0.2879
Fatehpur	0.1561	0.0949
Mean	0.3447	0.1913
GM	0.3872	0.0530
HM	0.3833	-0.0711
CV	-0.2129	0.3820
Sdev	-0.1570	0.4068
PRVG	0.3751	0.0960
MHPRVG	0.3867	0.0123
% variation	37.96	22.79

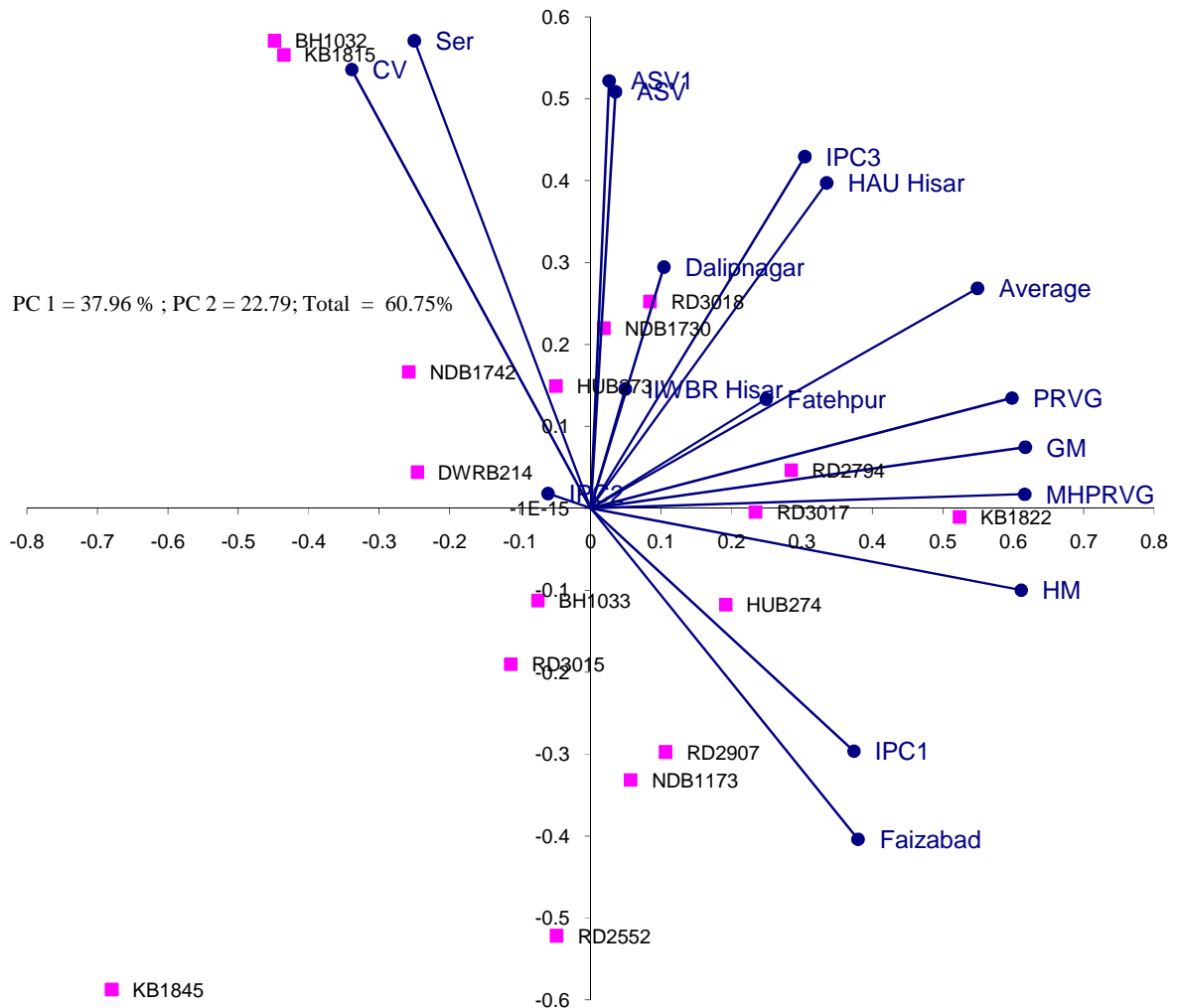


Fig. 2. Biplot analysis of adaptability measures for barley genotypes (2019-20).

CONCLUSIONS

Researchers concentrate on genotypes with high productive potential that respond to favourable environments. Often the occurrence of complex type G×E interaction leads to uncertainty in the identification of promising genotype; in this case, techniques exploit adaptability and stability can provide precise information about genotype performance. The identification of stable and highly productive genotypes between different environments remains a constant challenge for breeders of various crop species around the world. Selection of barley genotypes by the harmonic mean of genotypic values allow to identify the stable and productive genotypes for problem soils of the country.

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