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Performance of Feed Barley Genotypes Assessed by AMMI Mixed with BLUP for North Western Plains Zone of the India

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ABSTRACT

AMMI analysis for feed barley genotypes evaluated North Western Plains Zone of India had expressed highly significant effects of environments (E), GxE interaction and genotypes (G). Interaction effects GxE accounted for 23.4 and 26.9%, while environment explained up to tune of 63.4 and 61.4%; during cropping seasons of 2018-19 and 2019-20, respectively. ASTAB measure achieved the desirable lower values for PL906, DWRB137, UPB1080. Composite measure MASV1 found PL906, DWRB137, RD2552, and as per MASV ranks desired PL906, DWRB137, and UPB1080 genotypes would be of choice for these locations of the zone. Superiority index while weighting 0.65 and 0.35 for average yield & stability found KB1707, PL906, RD2994 as of stable performance with high yield. Biplot graphical analysis as per 73.7% of variation of the measures exhibited MASV1 clubbed with ASTAB, EV, SIPC, Za, W3, WAASB and MASV measures. For the second-year lower value of WAASB measure had observed for KB1707, RD2994. Barley genotypes DWRB137, PL906 were selected as per values of ASTAB measure. MASV1 selected PL906, DWRB137 while PL906, DWRB137 identified by MASV as genotypes of choice. Superiority index pointed towards PL906, DWRB137 feed barley genotypes. About 64.3% of variation among the measures under biplot analysis seen AMMI based IPCA1, Za, W1, W2, W3, ASTAB, WAASB measures grouped in quadrant. Simultaneous utilization of AMMI and BLUP of genotypes would be more appropriate to recommend high-yielding stable genotypes.

Keywords**:** AMMI, ASV, ASV1, HMGV, GAI, HMPRVG, biplot, barley

Introduction

Barley represents one of the ancient grain crops cultivated worldwide owing to its high adaptability; this plant grows in different global climates where common cereals fail to survive (Karkee et al. 2020). Barley plants are used for forage, pasture, or hay, as per the harvested stage (Badr et al. 2000). Straw after grain harvesting is a good source of fibre for animal feeding (Kendel et al. 2019). Since a long time by products of malting and brewing industries were used in animal feed (Newton et al. 2011). Multi-environment trials (MET) had been advocated to retrieve the maximum information from the best estimator of each genotype's performance in a given environment (Bocianowski et al. 2019). AMMI (additive main-effects and multiplicative interaction) is popular for analyzing MET data with fixed effect (Agahi et al. 2020). The genotypic effects regarded as random may be preferable and the assessment of it may be viewed as a problem of prediction rather than estimation (Piepho et al. 2008). The prediction of the outcome of random variables is commonly done by Best Linear Unbiased Prediction (BLUP). Advantages of both methods are combined in Superiority Index put forward by assigning weights to high yield and stability of genotypes as per the breeding objectives in crop improvement program (Olivoto et al. 2019).

Materials and Methods

The mega wheat growing area of the country comprises of parts of sub-humid Sutlej-Ganga Alluvial Plains and arid western plains, which comprises Punjab, Haryana, Delhi, Rajasthan (except Kota and Udaipur divisions), Western Uttar Pradesh (except Jhansi division and hilly areas), parts of Jammu and Kashmir (Jammu and Kathua districts) and parts of Himachal Pradesh (Paonta Valley and Una districts). Twenty-one feed barley genotypes at six locations and eight genotypes at eight locations were evaluated under research field trials during 2018-19 and 2019-20 cropping seasons, respectively. Field trials were conducted at research centres in randomized complete block designs with four replications. Recommended agronomic practices were followed to harvest good yield. Details of genotype parentage along with environmental conditions were reflected in Table 1 and Table 2 for ready reference.

Stability measure as Weighted Average of Absolute Scores calculated as

$$\mathrm{WAASB} = \sum_{k=1}^{p} |IPCA_{ik} \times EP_k| \,/\, \sum_{k=1}^{p} EP_k$$

Where, WAASB_i was the weighted average of absolute scores of the *i*th genotype (or environment); IPCA_{ik} the score of the *i*th genotype (or environment) in the *k*th IPCA, and EP_k was the amount of the variance explained by the *k*th IPCA. Superiority index allowed variable weightage between yield and WAASB to select genotypes that combined high performance and stability as

$$\mathrm{SI} = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(\theta_Y + \theta_S)};$$

where rG_i and rW_i were the rescaled values for yield and WAASB, respectively, for the *i*th genotype; G_i and W_i were the yield and WAASB for *i*th genotype. SI superiority index for the *i*th genotype weighted between yield and stability, and θY and θS were the weights for yield and stability would be of order 65 and 35 respectively for present study,

Zobel	Averages of the squared eigenvector values	$\mathrm{EV} = \sum_{n=1}^{N} \lambda_{in}^2 \,/n$
Sneller et al.	Sums of the absolute value of the IPC scores	$\mathrm{SIPC} = \sum_{n=1}^{N} \lambda_n^{0.5}\, \gamma_{in}$
Rao and Prabhakaran	AMMI based stability parameter	$ASTAB = \sum_{n=1}^{n} \lambda_n \gamma_{ni}^2$
Zali et al.	Modified AMMI stability value	$MASV = \sqrt{\sum_{n=1}^{N-1} \frac{SSIPC_n}{SSIPC_{n+1}} (PC_n)^2 + (PC_{n+1})^2}$
Zali et al.	Absolute value of the relative contribution of IPCs to the interaction	$\mathrm{Z_a} = \sum_{n=1}^{N} \lvert \lambda_n \gamma_{in} \rvert$
Ajay et al.	MASV1	$\mathrm{MASV1} = \sqrt{\sum_{n=1}^{N-1} (\frac{SSIPC_n}{SSIPC_{n+1}} PC_n)^2 + (PC_{n+1})^2}$
Olivato	Superiority Index	$\mathrm{SI} = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(\theta_Y + \theta_S)}$

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.

Results and Discussion

AMMI analysis of barley genotypes

In first year (2018-19), highly significant GxE interaction, environment (E) and genotypes (G) effects had observed by AMMI analysis. Environment accounted for 63.4% of the total sum of squares due to treatments indicating that diverse environments caused most of the yield variations (Table 3). Genotypes explained only 9.1% of total sum of squares, whereas GxE interaction contributed about 23.4% of treatment variations in yield. Significant GxE interaction demanded the stable estimation of genotypes yield over the studied environments (Ajay et al. 2020). Larger magnitude of GxE interaction sum of squares as compared to genotypes indicated the presence of genotypic differences across environments and complex GxE interaction for yield (Gauch 2013). GxE interaction further revealed that the first four multiplicative terms (IPCA1, IPCA2, IPCA3, and IPCA4) of AMMI were highly significant and explained 37.6%, 25.8%, 19.1%, and 10.7% of interaction sum of squares, respectively. Total of the significant multiplicative components were

93.2% and remaining 6.8% was the discarded residual (Oyekunle et al. 2017).

In second year (2019-20), highly significant effects of environment (E), GxE interaction and genotypes (G) had been achieved by analysis for multi-location evaluation of feed barley genotypes. Environment contributed maximum to the tune of 61.4%; GxE interaction accounted for 26.9% whereas genotypes contributed only 3.6% of total treatment variations in yield (Table 4). Further GxE interaction observed only two out of six multiplicative terms had explained about 39.3%, 27.8%, 14.4%, 11.6%, 4.4% and 2.4% of interaction sum of squares, respectively. Moreover, the total of these components were to the tune of 99.8% and remaining was noise that was discarded.

Ranking of barley genotypes as per AMMI based stability measures

In first year (2018-19), least value of absolute IPCA1 expressed by NDB1723, NDB1709, HUB266 and higher value achieved by KB1707 and RD2991 (Table 5). Low values of (EV) associated with stable behaviour of the barley genotypes NDB1723 followed by DWRB137, NDB1709 and unstable yield by RD2899, BH 946 genotype. Measure SIPC identified NDB1723 followed by NDB1709, DWRB137 as of stable nature, whereas RD2899, DWRB205 would be of least stable type. Za measure considered absolute value of the relative contribution of IPCs to the interaction revealed NDB1723, NDB1709, and DWRB137 as genotypes with descending order of stability, whereas DWRB205, KB1707 genotype with the least stability. ASTAB measure observed genotypes NDB1723, NDB1709 and DWRB137 as stable and KB1707, RD2899 was least stable in this study (Rao and Prabhakaran 2005). MASV1 and MASV measures considered all the significant IPCAs. Values of MASV1 showed that the genotypes, NDB1723, NDB1709 and BH1024 were most stable and RD2899, BH 946 would express unstable while, NDB1723, NDB1709 and BH1024 would be stable and RD2899 along with DWRB205 by MASV measure respectively (Ajay et al. 2019). Measure W1 favoured KB1707, RD2991, RD2786 while as per W2, genotypes identified were KB1707, DWRB205, RD2991while W3 favoured DWRB205, RD2991, RD2899 whereas finally lower values of WAASB associated with stable nature of DWRB205, KB1707, RD2991genotypes as for considered locations of the zone at the same time maximum deviation from the average performance across environments obtained by NDB1723, NDB1709 genotypes.

In second year (2019-20), genotypes UPB1080, PL906 expressed least absolute values of IPCA1 measure and higher value achieved by KB1707 (Table 6). Stable behaviour of PL906, UPB1080 genotypes anticipated as per minimum values of EV measure and maximum value had by KB1707, genotype. PL906, followed by UPB1080 identified for the lower value SIPC measure, whereas KB1707 would be of least stable behaviour. Preference order of genotypes PL906, UPB1080 revealed by Za measure in descending order of stability, whereas KB1707 would express the least stability. ASTAB measure observed genotypes PL906, and UPB1080 as the stable whereas RD2552 genotype was of least stable performance (Rao and Prabhakaran 2005). PL906, UPB1080 genotypes were of choice by of MASV1 and MASV measure pointed for PL906, RD2994 as the stable genotypes while BH946 would be unstable. W1 measure selected KB1707, RD2994 while measure W2 favoured KB1707, BH946 whereas genotypes KB1707, UPB1080 selected by W3 measure. Lower value of WAASB measure had observed for KB1707, RD2994 whereas large value by PL906.

Superiority indexes as per AMMI and BLUP barley genotypes

In first year (2018-19), average yield of genotypes as per BLUP values selected KB1707, HUB266, RD2994 where PL906, KB1707, RD2994 selected by Geometric adaptability index while Harmonic mean of genotypic values pointed for PL906, RD2994, and UPB1080 as suitable genotypes as far as higher production are concerned. More yields alone is not a desirable selection criterion as high yielders genotypes may not be of stable performance, simultaneous use of yield and stability in a single measure has considered by (Kang 1993; Farshadfar et al. 2008). Simultaneous Selection Index also referred to as genotype stability index (GSI) or yield stability index (YSI) (Farshadfar et al. 2011) was computed by adding the ranks of mean yield of genotypes and ranks of stability measure. Least ranks for IPCA1 measure exhibited by DWRB137, PL906, HUB266 were considered as stable with high yield, whereas high values suggested as least stable high yield of RD2991 genotype (Table 7). EV measure identified PL906, DWRB137 and PL909 whereas ranks as per SPIC measure favoured DWRB137, PL906&PL909 genotypes. Genotypes DWRB137, PL906&UPB1080 possessed lower value of Za measure. ASTAB measure achieved the desirable lower values for PL906, DWRB137, UPB1080. Composite measure MASV1 found PL906, DWRB137, RD2552, and as per MASV ranks desired PL906, DWRB137, UPB1080 genotypes would be of choice for these locations of the zone. Superiority index while weighting 0.65 and 0.35 for average yield and stability found

KB1707, PL906, RD2994 as of stable performance with high yield. Least magnitude of SIgm ranked PL906, KB1707, RD2994 as desirable genotypes while values of SIhm measure favoured PL906, RD2994, KB1707 feed barley genotypes.

In second year (2019-20), simultaneous ranking of barley genotypes as per IPCA1 measure favoured DWRB137, PL906 as per the least values, whereas large values of KB1707 suggested unstable high yield (Table 8). EV measure ranked for PL906 and BH946 barley genotypes. Minimum ranks as per SPIC favoured PL906 and DWRB137 genotypes. Lower value of Za ranks possessed by PL906 and DWRB137 genotypes for stable higher yield as compared to other genotypes. Barley genotypes DWRB137, PL906 were selected as per values of ASTAB measure accounted the AMMI analysis with BLUP of genotypes yield values. Composite measure MASV1 selected PL906, DWRB137 while PL906, DWRB137 identified by MASV as genotypes of choice for these locations of the zone. Maximum average yield expressed by DWRB137, PL906 genotypes and good variation had been observed from 45.5 to 50.9 q/ha among feed barley genotypes. Higher value of genotypes adaptability index achieved by DWRB137, PL906 whereas harmonic mean of genotypic values ranked DWRB137, PL906 barley genotypes. Superiority index measures pointed towards PL906, DWRB137 and large value by KB1707. Superiority index while weighting 0.65 and 0.35 for GAI and stability found PL906, DWRB137 as of stable performance with high yield. While considering harmonic mean and stability corresponding ranks identified DWRB137, PL906 genotypes.

Biplot graphical analysis

In first year (2018-19), loadings of studied measures as per first two significant principal components were reflected in Table 9. Biplot graphical analysis considered these PCAs as accounted for 73.7% of variation of the measures (Bocianowski et al. 2019). Three major clusters of the studied measures observed in graphical analysis (Figure 1). MASV1 clubbed with ASTAB, EV, SIPC, Za, W3, WAASB and MASV measures. Yield based measures clubbed with corresponding SI measures. Measure IPCA1 and W2 maintained distance from measures and observed as outliers in different quadrant. Nearly right angles between group of AMMI based and Superiority Index had reflected all together performance of these measures.

The second year (2019-20**)** results are given in Table 10 which reflected the loadings of the measures as per first two significant principal components. Graphical Biplot analysis as per these PCAs accounted for 64.3% of the total variation among the measures (Figure 2). Measures had grouped all together into three major clusters. MASV1 clubbed with ASTAB, EV, SIPC, and MASV measures. Average yield measures clubbed with corresponding SI measures. Others AMMI based measures IPCA1, Za, W1, W2, W3, ASTAB, WAASB observed in adjacent quadrant.

Conclusions

Simultaneous utilization of AMMI and BLUP of genotypes would be more appropriate to recommend high-yielding stable genotypes. The main advantages of AMMI and BLUP had been combined to increase the reliability of multi-locations trials analysis by Superiority Indexes. An additional advantage was to assign desirable weights to the yield and stability performance based on the goal of crop breeding trials.

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Conflict of interest

The authors declared no conflict of interests.

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

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	RD2991	RD2592 /RD2503//RD 2715	E1	Karnal	29°43'N	70°58’E	245
G2	KB1707	Manjula/DWRUB52	E2	Hisar	29°10'N	75°46’E	229
G3	RD2994	RD2624 / NDB1173	E3	Durgapura	26°51'N	75°47’E	390
G4	RD2992	RD2660 /13thEMBGSN-4	E4	Ludhiana	30°54'N	75°48’E	247
G5	KB1713	IBON-19 (2011-12)/RD2885	E5	Pantnagar	29°02'N	79°48’E	243.8
G6	UPB1077	AHOR1489.58//GLORIA-BAR/ COPAL/3/PRO-/4/CAPUL/TOCTE/5/ ICARO	E6	Tabiji	26°35'N	74°61’E	508
G7	UPB1080	AHOR1489.58//GLORIA-BAR/ COPAL/3/PRO-/4/CAPUL/TOCTE/5/ ICARO					
G8	HUB266	DL 70 / 25th IBYT-22-1					
G9	PL906	RD2503/WSA353 (*H. spontaneum*)					
G10	DWRB205	CDC MANLEY/BCU2881					
G11	NDB1709	INBYT-HI-2 (2016)					
G12	PL909	RD2740/BL194					
G13	BH 946	BHMS22A/BH549//RD2552					
G14	NDB1723	3rd GSBSN-35 (2016)					
G15	DWRB203	P.STO/3/LBIRAN/UNA80// LIGNEE640/4/BLLU/5/PETUNIA 1/6/ M111					
G16	RD2552	RD2035/DL472					
G17	BH1023	NBGSN-4 (2011-12)/RD 2552					
G18	RD2786	RD2634/NDB1020//K425					
G19	DWRB137	DWR28/DWRUB64					
G20	BH1024	NBGSN-12 (2011-12)/BH 393					
G21	RD2899	RD2592/RD2035//RD2715					

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

Code	**Genotype**	**Parentage**	**Code**	**Location**	**Latitude**	**Longitude**	**Altitude (m)**
G1	BH946	BHMS22A/BH549//RD2552	E1	Durgapura	26°51'N	75°47'E	390
G2	RD2994	RD2624 / NDB1173	E2	Hisar	29°10'N	75°46'E	229
G3	DWRB137	DWR28/DWRUB64	E3	Karnal	29°43'N	70°58'E	245
G4	PL906	RD2503/WSA353 *(H. spontaneum)*	E4	Ludhiana	30°54'N	75°48'E	247
G5	BH902	BH495/RD2552	E5	Modipuram	29°05'N	77°70'E	226
G6	RD2552	RD2035/DL472	E6	Pantnagar	29°02'N	79°48'E	243.8
G7	UPB1080	AHOR1489.58//GLORIA-BAR/ COPAL/3/PRO-/4/CAPUL/ TOCTE/5/ICARO	E7	Tabiji	26°35'N	74°61'E	508
G8	KB1707	Manjula/DWRUB52	E8	Udaipur	24°34'N	73°41'E	585

Table 3. AMMI analysis and percentage contribution of significant interaction principal components (2018-19).

Source	**Degree of Freedom**	**Mean Sum of Squares**	**Level of Significance**	**Proportional Contribution of Factors**	**GxE Interaction Sum of Squares (%)**	**Cumulative Sum of Squares (%) by IPCA's**
Treatments	125	638.79	0.0000000***	95.94		
Genotype (G)	20	378.02	0.0000000***	9.08		
Environment (E)	5	10555.55	0.0000000***	63.42		
GxE interactions	100	195.11	0.0000000***	23.44		
IPC1	24	305.44	0.0000000***		37.57	37.57
IPC2	22	228.62	0.0000000***		25.78	63.35
IPC3	20	186.59	0.0000000***		19.13	82.48
IPC4	18	116.28	0.0000000***		10.73	93.21
Residual	16	82.85	0.0000000***			
Error	252	13.40				
Total	377	220.75				

***=Highly significant effects, IPC1, IPC2, IPC3=Interaction Principal Components 1 , 2 and 3

Table 4. AMMI analysis and percentage contribution of significant interaction principal components (2019-20).

Source	**Degree of Freedom**	**Mean Sum of Squares**	**Level of Significance**	**Proportional Contribution of Factors**	**GxE Interaction Sum of Squares (%)**	**Cumulative Sum of Squares (%) by IPCA's**
Treatments	63	425.98	***	91.93		
Genotype (G)	7	150.36	***	3.61		
Environment (E)	7	2559.33	***	61.37		
GxE interactions	49	160.59	***	26.95		
IPC1	13	237.81	***		39.29	39.29
IPC2	11	198.94	**		27.81	67.10
IPC3	9	126.06	0.613385		14.42	81.51
IPC4	7	130.13	0.96681		11.58	93.09
IPC5	5	68.54	0.973109		4.36	97.45
IPC6	3	63.48	0.904934		2.42	99.87
Residual	1	10.58	0.739886			
Error	128	18.42				
Total	191	152.85				

Table 5. AMMI stability measures and Weighted average of absolute scores for barley genotypes (2018-19).

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	W1	W2	W3	WAASB
RD2991	2.72	0.040	5.923	20.00	104.23	5.72	4.76	2.7154	2.0018	1.9058	1.7306
KB1707	3.63	0.047	5.494	20.06	140.86	5.86	4.95	3.6299	2.7088	1.6174	1.7986
RD2994	1.72	0.041	6.321	19.15	82.17	4.80	4.21	1.7214	1.6838	1.4834	1.5885
RD2992	0.55	0.027	4.384	13.31	55.27	5.07	4.23	0.5487	0.8536	1.4376	1.0881
KB1713	2.13	0.029	5.154	17.09	72.68	4.91	4.09	2.1333	1.6306	1.6327	1.4672
UPB1077	1.40	0.038	6.008	17.88	71.98	4.69	4.08	1.3988	1.4137	1.4442	1.4680
UPB1080	1.36	0.020	3.845	13.15	51.14	3.95	3.51	1.3591	1.6186	1.1236	1.1416
HUB266	0.20	0.016	3.501	10.27	32.37	3.55	3.09	0.2037	0.7371	0.9570	0.8295
PL906	1.06	0.014	3.730	11.58	30.39	2.95	2.60	1.0628	1.1184	0.9058	0.9700
DWRB205	2.10	0.043	6.506	21.35	107.62	5.91	5.12	2.1002	2.2141	1.9171	1.8227
NDB1709	0.11	0.012	2.020	4.88	16.19	1.64	1.61	0.1113	0.2463	0.1526	0.3645
PL909	1.01	0.014	3.571	11.35	32.56	3.10	2.77	1.0110	1.2197	0.8806	0.9598
BH 946	0.69	0.047	5.963	17.10	86.07	6.10	5.11	0.6854	0.9000	1.6655	1.3688
NDB1723	0.02	0.003	1.298	3.39	4.24	1.14	1.00	0.0211	0.1402	0.2602	0.2602
DWRB203	0.96	0.037	5.581	16.18	66.61	4.28	3.87	0.9644	1.3227	1.1716	1.3143
RD2552	1.04	0.016	3.672	11.21	33.21	2.91	2.63	1.0373	1.1489	0.7496	0.9356
BH1023	1.02	0.018	3.607	10.37	32.30	3.10	2.66	1.0209	0.6227	0.8385	0.8415
RD2786	2.21	0.033	5.339	16.82	74.39	4.15	3.62	2.2089	1.7508	1.1666	1.4278
DWRB137	0.73	0.010	3.069	9.69	22.50	2.74	2.41	0.7316	0.9435	0.8383	0.8136
BH1024	1.20	0.015	3.392	10.04	28.83	2.65	2.30	1.2039	0.7679	0.7386	0.8295
RD2899	0.51	0.058	6.884	19.79	110.92	6.44	5.59	0.5141	1.3199	1.7525	1.5864

IPCA1=Interaction Principal Components Axis 1 used for stabe performance of genotypes, MASV=Modified AMMI Stability Value, WAASB=Weighted Average of Absolute Scores

Table 6. AMMI stability measures and Weighted average of absolute scores of barley genotypes (2019-20).

Genotype	IPCA1	MASV1	MASV	Za	EV	SIPC	ASTAB	W1	W2	W3	W4	WAASB
BH946	0.83	8.27	6.58	23.20	0.078	7.898	95.89	0.829	1.879	1.677	1.482	1.435
RD2994	3.04	6.96	5.40	24.21	0.082	8.002	100.72	3.041	1.788	1.563	1.595	1.509
DWRB137	0.19	7.56	6.07	18.02	0.084	6.635	71.37	0.194	1.153	1.108	0.995	1.058
PL906	0.11	5.65	3.89	9.34	0.025	3.480	23.68	0.111	0.110	0.209	0.530	0.509
BH902	1.67	8.21	5.88	21.90	0.057	6.991	73.82	1.673	1.474	1.390	1.603	1.382
RD2552	0.51	8.26	6.31	23.42	0.084	7.944	88.26	0.515	1.510	1.437	1.511	1.402
UPB1080	0.05	6.31	5.83	15.30	0.083	5.888	87.38	0.047	0.194	0.989	0.902	0.852
KB1707	4.36	7.31	6.08	26.73	0.084	7.782	167.15	4.365	3.144	2.493	2.074	1.837

Table 7. Superiority index measures and corresponding ranking of genotypes (2018-19).

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	Mean	R_k	SIam	R_k	GM	R_k	SIgm	R_k	HM	R_k	SIhm	R_k
RD2991	40	36	36	39	38	37	37	41.34	20	6.98	20	38.81	20	9.57	20	36.31	20	11.77	20
KB1707	22	20	15	21	22	19	19	55.97	1	65.63	1	52.86	2	64.74	2	50.14	4	63.01	3
RD2994	19	20	22	20	19	17	18	54.07	3	57.96	3	52.08	3	61.60	3	50.17	2	63.06	2
RD2992	26	32	32	32	32	37	37	39.75	21	0.38	21	36.53	21	0.38	21	33.30	21	0.38	21
KB1713	32	26	26	28	28	29	28	47.18	16	30.30	15	46.67	12	40.31	11	46.24	10	48.43	10
UPB1077	32	32	35	33	30	30	30	46.50	17	27.58	17	44.84	17	33.13	17	43.28	16	37.49	16
UPB1080	18	14	14	14	14	14	14	53.94	4	57.28	4	51.96	4	60.96	4	50.14	3	62.80	4
HUB266	15	19	17	17	19	21	21	47.85	12	32.76	12	46.72	11	40.30	12	45.71	12	46.26	12
PL906	14	6	11	11	7	8	7	55.35	2	62.88	2	53.09	1	65.34	1	50.85	1	65.34	1
DWRB205	33	34	36	37	35	35	36	47.26	14	30.72	14	46.15	14	38.41	14	45.07	13	44.22	13
NDB1709	17	18	17	17	17	17	17	47.18	15	29.93	16	45.78	15	36.43	15	44.50	15	41.63	15

Continuing Table 7

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	Mean	R$_k$	SIam	R$_k$	GM	R$_k$	SIgm	R$_k$	HM	R$_k$	SIhm	R$_k$
PL909	16	12	13	15	15	14	15	51.57	7	47.71	7	49.68	7	51.97	7	47.92	6	54.49	6
BH 946	17	31	28	26	28	31	30	48.40	11	35.13	11	45.48	16	35.63	16	42.68	17	35.21	17
NDB1723	20	20	20	20	20	20	20	44.82	19	20.42	19	43.40	18	27.06	18	42.07	18	32.59	18
DWRB203	18	24	25	22	22	22	22	49.18	10	38.26	10	47.53	10	43.62	10	45.95	11	47.32	11
RD2552	19	16	16	15	17	13	14	49.73	8	40.34	8	48.07	9	45.62	9	46.44	9	49.00	9
BH1023	19	18	16	15	15	17	16	49.57	9	39.64	9	48.32	8	46.55	8	47.08	8	51.35	8
RD2786	25	19	19	19	21	17	17	52.21	6	50.45	6	49.97	6	53.25	6	47.85	7	54.41	7
DWRB137	12	7	8	8	8	9	9	52.47	5	51.27	5	50.55	5	55.33	5	48.76	5	57.55	5
BH1024	31	24	22	22	22	21	21	45.00	18	21.34	18	43.33	19	26.97	19	41.75	19	31.59	19
RD2899	17	34	34	31	33	34	34	47.69	13	32.37	13	46.25	13	38.71	13	44.82	14	43.22	14

AMu, GMu, HMu=Arithmetic, Geometric, Harmonic Mean for BLUP values; SI au, SI gu, SI hu=Superiority index as per Arithmetic, Geometric, Harmonic Mean; RPGVu, MHRPGVu=Relative performance and Harmonic mean of Relative Performance as per BLUP of genotypes; R$_k$=Rank of genotypes

Table 8. Superiority index measures and corresponding ranking of genotypes (2019-20).

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	MEAN	R$_k$	SIam	R$_k$	GM	R$_k$	SIgm	R$_k$	HM	R$_k$	SIhm	R$_k$
BH946	8	6	9	8	9	11	11	49.84	3	62.14	3	49.11	3	69.15	3	46.96	4	55.53	4
RD2994	12	9	13	12	12	8	7	48.54	5	44.55	5	47.55	4	48.18	5	46.72	5	51.81	5
DWRB137	4	8	4	4	3	6	6	50.95	1	85.54	2	49.64	1	85.54	2	49.66	1	85.54	1
PL906	4	3	3	3	3	3	3	50.38	2	93.11	1	49.31	2	95.98	1	47.18	2	81.59	2
BH902	10	6	8	8	7	10	8	48.78	4	50.78	4	47.54	5	51.39	4	42.47	7	23.50	7
RD2552	11	15	14	13	12	14	14	46.89	7	27.43	6	45.28	7	23.31	8	40.93	8	11.48	8
UPB1080	9	13	10	10	12	10	11	45.57	8	25.98	7	44.31	8	25.98	6	45.49	6	59.94	3
KB1707	14	12	11	14	14	10	12	47.45	6	22.71	8	46.3	6	24.27	7	46.96	3	44.95	6

Table 9. Loadings of measures as per two Principal Components (2018-19).

Measure	**PC1**	**PC2**
Karnal	0.0473	0.2939
Hisar	0.1332	0.1144
Durgapura	0.0490	0.2393
Ludhiana	0.0736	0.3190
Pantnagar	0.0632	0.0544
Tabji	-0.0667	0.1624
Mean	0.0772	0.3989
IPCA1	0.2553	0.0513
MASV1	0.2894	-0.1353
MASV	0.2915	-0.1241
Za	0.3128	-0.0667
EV	0.2857	-0.1078
SIPC	0.2945	-0.0899
ASTAB	0.3089	-0.0710
WAASB	0.3162	-0.0533
W1	0.2553	0.0513
W2	0.2949	0.0566
W3	0.3112	-0.0543
Siam	0.0800	0.3980
Sigm	0.0657	0.4014
Sihm	0.0513	0.3955
73.69	45.92	27.77

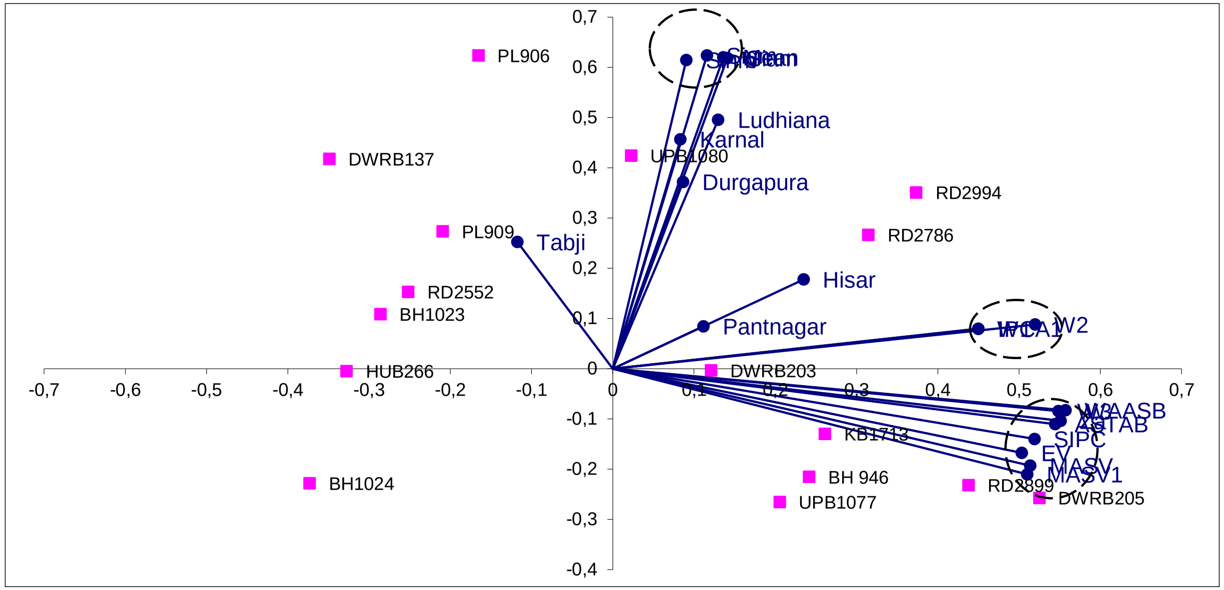

Figure 1. Biplot analysis of superiority index and other measures of barley genotypes 2018-19.

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

Measure	PC1	PC2
Durgapura	0.0407	0.2748
Hisar	0.0905	-0.4187
Karnal	0.1184	-0.1296
Ludhiana	-0.0598	-0.2978
Modipuram	0.1598	-0.2997
Pantnagar	-0.1372	-0.0706
Tabiji	0.0083	-0.0275
Udaipur	-0.1011	-0.3696
MEAN	0.1482	-0.3316
IPCA1	-0.2330	-0.1913
MASV1	-0.1708	0.0355
MASV	-0.2086	0.0670
Za	-0.2857	-0.0207
EV	-0.2152	0.1150
SIPC	-0.2636	0.0566
ASTAB	-0.2840	-0.1005
WAASB	-0.2888	-0.0751
W1	-0.2330	-0.1913
W2	-0.2690	-0.2059
W3	-0.2928	-0.1181
W4	-0.2892	-0.0648
Siam	0.2399	-0.2419
Sigm	0.2322	-0.2663
64.28	47.5	16.79

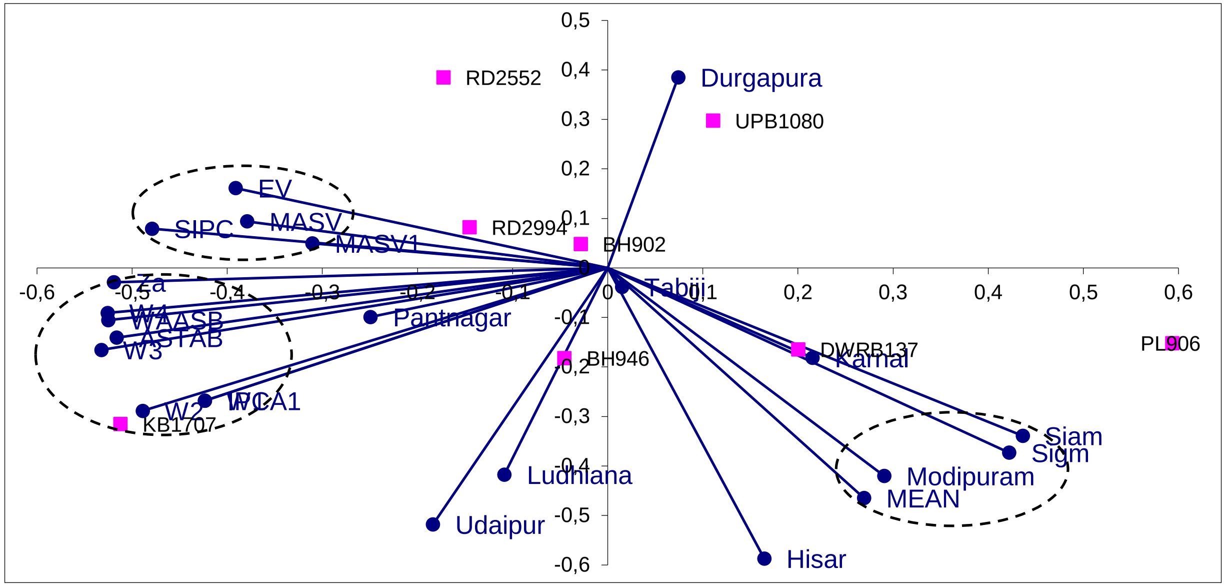

Figure 2. Biplot analysis of stability and adaptability measures of barley genotypes 2019-20.

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