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AMMI Appended with BLUP to Assess the Superiority of Hullness Barley Genotypes Evaluated under Coordinated System of the Country

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Authors' contributions

This work was carried out in collaboration among all authors. Author AV performed the statistical analysis and wrote the draft of the manuscript. Author RPSV designed the study and corrected the manuscript. Authors JS and LK managed the research field data of the study. Author GPS managed the overall resources for successful completion of the study. All authors read and approved the final manuscript.

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Original Research Article

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ABSTRACT

Highly significant effects of environments (E), G×E interaction and genotypes (G) had expressed by AMMI analysis for hulless barley genotypes under coordinated barley improvement program. Environment effects explained 69.9% and 59.7% whereas Interaction effects accounted for 17% and 20.9% during cropping seasons of 2018-19 and 2019-20, respectively. Stability measure WAASB based on all significant interaction principal components ranked suitability of DWRB204, K1149 genotypes. Superiority index while weighting 0.65 and 0.35 for mean yield & stability ranked DWRB204, Karan 16 as of stable performance with high yield barley genotypes. Ranks as per composite measures MASV1 and MASV found NDB943, KB1750 as desirable genotypes. Lower values ASTAB measure achieved by Karan 16, NDB943. Biplot graphical analysis as per 40.4% of variation of the measures exhibited MASV1 clubbed with ASTAB, EV, SIPC, Za, W6, WAASB and MASV measures observed in different group. For the second-year lower value of WAASB measure had observed for PL891, KB1843, NDB943. Ranking of genotypes as per Superiority index found Karan16, DWRB216 genotypes of choice for these locations. Barley genotypes Karan16,

DWRB216 were selected as per values of ASTAB measure accounted AMMI analysis with BLUP of genotypes yield values. About 78.1% of variation of the measures under biplot analysis observed MASV1 grouped with ASTAB, EV, SIPC, and MASV. While Za joined together with W2, W3, W4, W5, W6, WAASB to form separate group.

Keywords: AMMI; MASV; ASTAB; WAASB; SSI.

1. INTRODUCTION

Hulless barley (Hordeum vulgare var. nudum L.) contains loose husk cover may be separated from the caryopsis during the process of threshing [1]. Earlier cultivated in the highaltitude Himalaya areas to supplement the food of tribal people [2]. Grains possess the ample quantity of ß-glucan and therapeutic uses of ßglucan to lower the sugar level of diabetic patients and helps to reduce the serum cholesterol of heart patients received much attention [3]. Good number of statistical measures has been developed to estimate G×E interactions under multi-location trials [4]. Still AMMI analysis had been widely utilized as analysis retained most of the G×E pattern in the first interaction principal component axis (IPCA), while most of the random error had been explained by the last IPCAs [5]. BLUP proved the potential to improve the predictive accuracy of random effects [6]. BLUP and AMMI, two distinct approaches, utilized to distinguish the pattern from the random error components in G×E interactions. Taking into account the importance of AMMI and BLUP, the benefits of these two important techniques incorporated into a measure Superiority Index for stability and adaptability of genotypes [7]. The performance of Superiority measures had been compared with AMMI based measures for hulless barley genotypes evaluated under the coordinated barley improvement program of the country.

2. MATERIALS AND METHODS

Nine genotypes at thirteen locations and ten genotypes at fourteen locations were evaluated under research field trials during 2018-19 and 2019-20 cropping seasons, respectively. Field trials were conducted at research centers 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 Tables 1 and 2 for ready reference.

Stability measure Weighted Average of Absolute Scores has been calculated as

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

where WAASB_i is the weighted average of absolute scores of the *i*th genotype (or environment); IPCA_{ik} is the score of the *i*th genotype (or environment) in the kth IPCA, and EP_k is the amount of the variance explained by the kth IPCA. Superiority index allows weighting between yield and stability measure (WAASB) to select genotypes that combine high performance and stability as SI = $\frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{rG_i}$; where rG_i $(\theta_Y + \theta_S)$ and rW_i are the rescaled values for yield and WAASB, respectively, for the *i*th genotype; G_i and W_i are the yield and the WAASB values for ith genotype. SI superiority index for the ith genotype that weights between yield and stability, and θ Y and θ S are the weights for yield and stability assumed to be of order 65 and 35 respectively in this study,

Zobel [8]	Averages of the squared eigenvector values	$\mathrm{EV} = \sum_{n=1}^{N} \lambda_{in}^2 / n$
Sneller et al. [9]	Sums of the absolute value of the IPC scores	$\text{SIPC} = \sum_{n=1}^{N} \lambda_n^{0.5} \gamma_{in}$
Rao and Prabhakar an [10]	AMMI based stability parameter	$ASTAB = \sum_{n=1}^{n} \lambda_n \gamma_{ni}^2$
Zali et al. [11]	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. [11]	Absolute value of the relative contribution of IPCs to the interaction	$Z_{\rm a} = \sum_{n=1}^{N} \lambda_n \gamma_{in} $
Ajay et al. [12]	MASV1	MASV1 = $\sqrt{\sum_{n=1}^{N-1} (\frac{SSIPC_n}{SSIPC_{n+1}} PC_n)^2 + (PC_{n+1})^2}$
Olivoto et al. 2019 [7]	Superiority Index	$\frac{SI}{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}}{(\theta_Y + \theta_S)}$

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.

3. RESULTS AND DISCUSSION

3.1 AMMI Analysis of Barley Genotypes

3.1.1 First year of study 2018-19

Highly significant effects of environment (E). G×E interaction and genotypes (G) had been observed AMMI analysis. Environment explained 69.9% of the total sum of squares due to treatments indicating that diverse environments caused most of the variations in yield of evaluated genotypes (Table 3). Significant proportion of G×E interaction deserves the estimation of genotypes stability over environments [4]. Genotypes explained only 2.8% of total sum of squares, whereas G×E interaction accounted for 17% of treatment variations in yield. More of G×E interaction sum of squares as compared to genotypes indicated the presence of genotypic differences across environments and complex G×E interaction for yield. Significant seven multiplicative terms of G×E interaction contributed about 28.2%, 23.9%, 17.5%, 11.2%, 8.5% , 5.9% and 3.9% of interaction sum of squares. Total of the components were to the tune of 99.1% and remaining 0.9% was the residual or noise that discarded [13].

3.1.2 Second year of study 2019-20

Highly significant effects of environment (E), $G \times E$ interaction and genotypes (G) had contributed 59.7%, 20.9% and 13.8%, respectively of the total sum of squares due to treatments indicated the diversity of environments caused most of the variations in yield of evaluated genotypes (Table 7). Seven multiplicative terms of $G \times E$ interaction explained significantly 33.4%, 24.3%, 12.6%, 10%, 8.3%, 5.9% and 3.1 % of interaction sum of squares. Total 97.6% of significant components and residual was only 2.4% that discarded.

3.2 Ranking of Barley Genotypes as per AMMI Based Stability Measures

3.2.1 First year of study 2018-19

Least value of absolute IPCA1 expressed by PL891, DWRB188 and higher value achieved by DWRB206 (Table 4). Low values of (EV) associated with stable behaviour, the genotypes KB1757 followed by DWRB206 expressed lower values and maximum value possessed by K1149 genotype. Measure SIPC identified KB1757 followed by DWRB206 as of stable nature, whereas DWRB204 would be of least stable type. Za measure considered absolute value of the relative contribution of IPCs to the interaction revealed KB1757 and DWRB206 as genotypes with descending order of stability, whereas UPB1077, DWRB204 genotype with the least stability. ASTAB measure observed genotypes KB1757 and PL891 as stable and DWRB204 was least stable in this study [10]. All significant IPCAs had been considered by MASV1 and MASV measures. Values of MASV1 showed that the genotypes, KB1757 and DWRB206 were most stable and KB1757 and DWRB206 would be stable by MASV measure respectively [12]. Measure W1 favoured DWRB188 and NDB943 while as per W2, genotypes identified were DWRB188 and NDB943, while W3 favoured DWRB204 and DWRB188 whereas values of measure W4 settled for DWRB204 and KB1750. Genotypes DWRB204 and K1149 had pointed out by W5 and W6 measures. Finally lower values of WAASB associated with stable nature of DWRB204 and K1149 genotypes as for considered locations of the zone at the same time maximum deviation from the average performance across environments obtained by KB1757 (Olivoto et al. 2019), [7].

3.2.2 Second year of study 2019-20

Least value of absolute IPCA1 expressed by UPB1086, Karan16, DWRB217 and higher value achieved by PL891 (Table 8). Stable behaviour of the genotypes DWRB217 followed by DWRB204, Karan16 as per low values of EV and maximum value possessed by PL891 genotype. SIPC ranked DWRB216, followed by Karan16, KB1848 as of stable nature, whereas PL891, would be of least stable type. Za measure revealed the preferences for DWRB217, DWRB204, and Karan16 as genotypes with descending order of stability, whereas PL891 genotype with the least stability. ASTAB values ranked DWRB216, Karan16 and KB1848 as stable genotypes and PL891 was least stable in this study. MASV1 and MASV measures showed the desirability for genotypes, DWRB216, Karan16 and KB1848. W1 favoured PL891, KB1843 and K1149 while as per W2, identified genotypes were PL891, K1149 and KB1843, while W3 favoured PL891, NDB943 and K1149 whereas values of measure W4 settled for PL891, NDB943 and KB1843. Genotypes PL891, KB1843 and NDB943 had pointed out by W5 and W6 measures. Finally values of WAASB selected PL891, KB1843 and NDB943 genotypes as for considered locations of the zone at the same time maximum deviation from the average performance across environments obtained by DWRB216.

3.3 Superiority Indexes as per AMMI and BLUP: Barley Genotypes

3.3.1 First year of study 2018-19

Mean vield of genotypes based on BLUP values favoured DWRB204 and NDB943 where DWRB204 and NDB943 selected by Geometric adaptability index while Harmonic mean of genotypic values pointed for DWRB204 and NDB943 as suitable genotypes as far as considered locations are concerned (Table 5). Stability alone is not a desirable selection criterion as stable genotypes may not be a high yielders, simultaneous use of yield and stability in single measure is essential [14,15]. а Simultaneous Selection Index also referred to as genotype stability index (GSI) or yield stability index (YSI) [16] was computed by adding the ranks of stability measure and mean yield of genotypes. Least ranks for IPCA1 measure exhibited by DWRB204 and DWRB188 were considered as stable with high yield, whereas high values suggested as least stable yield for DWRB206 genotype (Table 9). EV measure identified DWRB204 and KB1750 whereas SPIC favoured NDB943 and DWRB206 genotypes. Genotypes NDB943 and Karan 16 possessed lower value of Za measure. ASTAB measure achieved the desirable lower values for Karan16 Composite measure MASV1 and NDB943. found NDB943 and KB1750 and as per MASV ranks NDB943 and KB1750 genotypes would be of choice for these locations of the zone.

Superiority index assigned 0.65 and 0.35 weights for average yield and stability found DWRB204 and Karan16 as of stable performance with high yield. Least magnitude of SIgm ranked DWRB204 and Karan16 as desirable genotypes while values of SIhm measure favoured DWRB204 and Karan16 barley genotypes.

3.3.2 Second year of study 2019-20

Average yield as per BLUP values of genotypes favoured UPB1086 and Karan16 where Geometric adaptability index pointed for UPB1086 and Karan16 selected by while Harmonic mean of genotypic values pointed for UPB1086 and Karan16 as suitable genotypes as far as considered locations. Least ranks for Simultaneous Selection Index for IPCA1 measure exhibited by UPB1086 and Karan16 were considered as stable with high yield, whereas high values suggested as least stable yield for PL891 and DWRB206 genotype (Table 7). EV measure identified Karan16 and DWRB216 whereas SPIC favoured UPB1086 and Karan16. Genotypes Karan16 and UPB1086 possessed lower value of Za measure. Desirable lower values ASTAB measure achieved by Karan16 and DWRB216. Ranks of composite measure MASV1 and MASV found Karan16, DWRB216 genotypes would be of choice for these locations.

Superiority index with assigned weights for yield and stability found Karan16 and UPB1086 as of stable performance with high yield. Least magnitude of SIgm ranked Karan16 and UPB1086 as desirable genotypes while values of SIhm measure favoured Karan16 and DWRB204 barley genotypes.

3.4 Biplot Graphical Analysis

3.4.1 First year of study 2018-19

Biplot graphical analysis considered two significant PCAs as for 40.4 % of variation of the measures had been accounted [17]. Loadings of studied measures as per first two significant principal components were reflected in Table 9. Stability measures of barley genotypes grouped into three major clusters. MASV1 clubbed with ASTAB. EV. SIPC. Za. W6. WAASB and MASV measures. Measure IPCA1 clubbed with SI corresponding to yield based measures. W2, W3 and W4 measures observed in different group. Angles among the measures depict the degree of association as acute angles depict strong relationships for W2, W3 and W4. Right angles between group of AMMI based and Superiority index measures show no relationship.

3.4.2 Second year of study 2019-20

Loadings of stability, adaptability measures as per first two significant principal components were reflected in Table 10. Biplot graphical analysis based two significant PCAs accounted for 78.1% of variation of the studied measures observed three clusters of stability measures of barley genotypes. MASV1 grouped with ASTAB, EV, SIPC and MASV measures. Za measure joined with W2, W3, W4, W5, W6 and WAASB. Average yield clustered with superiority indexes as per GAI and HMGV. Measures W1 and IPCA1 observed as outliers. Angles among the measures depict the degree of association as acute angles depict strong relationships for W2, W3, W4, W5 and Za measures. Right angles between group of AMMI based and Superiority index measures show no relationship.

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	DWRB188	PENCO/CHEVRON-BAR/3/LEGACY//PENCO/CHEVRON-BAR	E1	Gwalior	26° 13' N	78° 10' E	213
G2	DWRB206	ZIGZIG/4/TOCTE//HIGO/LINO/3/PETUNIA1	E2	Hisar	29 ° 10' N	75°46'E	229
G3	DWRB204	ALELI/4/EGYPT4/TERAN78//P.STO/3/QUINA	E3	Durgapura	26 °51'N	75°47'E	390
G4	K1149	K12/K572-10//EB410	E4	Faizabad	26° 46' N	82° 9' E	97
G5	KB1750	Sel. INBYT-HI-11 (2016-17)	E5	Varanasi	25° 19' N	82° 59' E	81
G6	KB1757	CHAMICO/TOCTE//CONGONA/3/PETUNIA2/4/PENCO/CHEVRON-BAR	E6	Morena	26° 30' N	78° 00' E	177
G7	NDB943	K 1178/Karan 748	E7	Udaipur	24° 34' N	73° 41' E	585
G8	PL891	IBON 343/12th HSBN-176	E8	Vijapur	23°33' N	72°45' E	129.4
G9	Karan 16	AZAM (DWARF)1/EB7576	E9	Pantnagar	29°02'N	79 [°] 48'E	243.8
			E10	Ludhiana	30 [°] 54' N	75°48'E	247
			E11	Kanpur	26° 26' N	80° 19' E	126
			E12	Sabour	25°23' N	87°04' E	46
			E13	Karnal	29° 43' N	70°58'E	245

Table 1. Parentage details of barley genotypes and locations of the country 2018-19

Table 2. Parentage details of barley genotypes and locations of the country 2019-20

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	UPB1086	MSEL//LIMON/BICHY2000	E1	Durgapura	26 °51'N	75° 47'E	390
G2	DWRB204	ALELI/4/EGYPT4/TERAN78//P.STO/3/QUINA	E2	Faizabad	26° 46' N	82° 9' E	97
G3	KB1843	LACEY/9/MOLA/BERMEJO//NISPERO/5/CM67-B/RYE//CAM-B/3/ROW906.73/4/	E3	Gwalior	26° 13' N	78° 10' E	213
		GLORIA-BAR /COME/6/LINO/7/PINON/8/ PETUNIA 1					
G4	PL891	IBON 343/12th HSBN-176	E4	HAU Hisar	29° 10' N	75°46'E	229
G5	Karan16	AZAM (DWARF)1/EB7576	E5	Jhansi			
G6	DWRB216	BLLU/5/PETUNIA1/6/LEGACY//PENCO/CHEVRON-BAR	E6	Kanpur	26° 26' N	80° 19' E	126
G7	K1149	K12/K572-10//EB410	E7	Karnal	29° 43' N	70 [°] 58'E	245
G8	KB1848	ICNB93-369/IRAN(Kordistan)	E8	Ludhiana	30 [°] 54' N	75 [°] 48 'E	247
G9	NDB943	K 1178/Karan 748	E9	Modipuram	29° 05' N	77 [°] 70'E	226
G10	DWRB217	PETUNIA2/M112	E10	Pantnagar	29°02'N	79 [°] 48'E	243.8
			E11	Tikamgarh	24° 45' N	78° 50' E	349
			E12	Udaipur	24° 34' N	73° 41' E	585
			E13	Varanasi	25° 19' N	82° 59' E	81
			E14	Vijapur	23°33' N	72°45' E	129.4

Source	Degree of freedom	Mean Sum of Squares	Level of significance	Proportional contribution	GxE interaction	Cumulative Sum of Squares
				of factors	Sum of Squares (%)	(%) by IPCA's
Treatments	116	438.02	***	89.74		
Genotype (G)	8	199.97	***	2.83		
Environment (E)	12	3298.26	***	69.90		
GxE interactions	96	100.33	***	17.01		
IPC1	19	142.89	***		28.19	28.19
IPC2	17	135.86	***		23.98	52.17
IPC3	15	112.65	***		17.54	69.71
IPC4	13	82.73	***		11.17	80.88
IPC5	11	74.13	***		8.47	89.34
IPC6	9	63.18	***		5.90	95.24
IPC7	7	52.91	**		3.85	99.09
Residual	5	17.54				
Error	351	16.55				
Total	467	121.24				

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

Table 4. AMMI measures and Weighted average of absolute scores for barley genotypes 2018-19

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	W1	W2	W3	W4	W5	W6	WAASB
DWRB188	0.760	0.059	8.209	20.601	101.292	6.657	6.001	0.7600	1.9953	1.6201	1.3682	1.3036	1.3222	1.2896
DWRB206	2.593	0.056	7.552	18.024	82.194	4.860	4.481	2.5934	1.3770	1.0799	1.1352	1.1701	1.0625	1.1051
DWRB204	1.920	0.059	9.179	23.499	104.163	6.683	5.940	1.9200	1.7125	1.9018	1.8915	1.7055	1.6358	1.5059
K1149	0.840	0.062	9.094	22.391	94.253	6.756	6.034	0.8401	1.4715	1.5252	1.4429	1.5750	1.4656	1.3863
KB1750	2.316	0.056	8.704	21.291	87.446	5.727	5.121	2.3157	1.4473	1.5215	1.5174	1.3334	1.3470	1.3217
KB1757	1.627	0.027	5.318	13.679	52.546	4.680	4.091	1.6265	0.8621	1.2339	1.0381	0.9847	0.9330	0.8778
NDB943	2.336	0.061	7.978	19.455	84.788	5.877	5.229	2.3359	1.7709	1.3400	1.1297	1.1449	1.2641	1.2045
PL891	0.176	0.057	7.656	18.195	72.197	5.426	4.956	0.1764	1.1456	1.1511	1.2186	1.0728	1.0238	1.0914
Karan 16	0.928	0.062	8.457	19.311	78.177	6.123	5.507	0.9281	0.5316	0.8437	1.0970	1.1989	1.1360	1.1302

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	MEAN	Rk	Slam	Rk	GM	Rk	Slgm	Rk	НМ	Rk	Slhm	Rk
DWRB188	7	11	10	11	13	12	13	36.01	5	35.83	5	34.34	5	30.90	6	32.74	5	25.59	7
DWRB206	16	9	9	9	11	9	9	34.33	7	24.47	8	33.24	7	26.34	8	32.22	7	28.67	6
DWRB204	7	6	10	10	10	9	8	39.19	1	65.00	1	37.77	1	65.00	1	36.46	1	65.00	1
K1149	11	17	16	16	15	17	17	34.21	8	7.28	9	32.94	9	6.66	9	31.76	9	6.66	9
KB1750	11	7	11	11	10	8	8	36.20	4	36.54	4	34.34	4	29.11	7	32.40	6	19.04	8
KB1757	14	10	10	10	10	10	10	34.17	9	35.00	6	33.03	8	36.13	4	32.02	8	38.58	5
NDB943	10	9	6	7	7	7	7	36.71	2	49.71	3	35.43	2	50.22	3	34.05	2	48.48	3
PL891	7	10	9	9	8	9	9	34.73	6	30.37	7	33.78	6	34.32	5	32.89	4	38.78	4
Karan 16	7	11	9	7	6	9	9	36.43	3	50.14	2	35.14	3	50.56	2	34.02	3	52.17	2

Table 5. Superiority index measures and corresponding ranking of genotypes 2018-19

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; Rk = Rank of genotypes

Table 6. Loadings of measures as per two Principal Components 2018-19

Measure	PC1	PC2
IPCA1	0.0135	-0.2131
MASV1	0.2464	0.1348
MASV	0.2444	0.1481
Za	0.2685	0.1124
EV	0.1924	0.1378
SIPC	0.2485	0.1344
ASTAB	0.2558	0.0762
W1	0.0135	-0.2131
W2	0.1677	0.0067
W3	0.2061	-0.0105
W4	0.2406	-0.0014
W5	0.2483	0.1091
W6	0.2709	0.0538
WAASB	0.2723	0.0850
Gwalior	0.0942	-0.2925
Hisar	0.0003	-0.1948
Durgapura	0.0897	-0.0604

Faizabad	-0 0261	-0.0565	
Varanasi	-0.201	-0.0518	
Morena	0.2000	-0.0010	
	0.2220	-0.2407	
Vijapur	0.0000	0.1573	
Njapu Doptogor	0.2000	-0.1575	
Fallilaya	0.1492	0.0404	
Luoniana	0.0381	-0.0532	
Kanpur	0.0641	-0.1738	
Sabour	0.1236	0.0422	
Karnal	0.1829	0.1841	
Mean	0.2248	-0.2574	
Siam	0.1157	-0.3811	
Sigm	0.0907	-0.3809	
Siĥm	0.0546	-0.3563	
56.99	40.43	16.57	

 Table 7. AMMI analysis and percentage contribution of significant interaction principal components (2019-20)

Source	Degree of	Mean Sum of Squares	Level of significance	Proportional contribution of	GxE interaction	Cumulative Sum of Squares
	freedom			factors	Sum of Squares (%)	(%) by IPCA's
Treatments	139	569.56	***	94.42		
Genotype (G)	9	1284.74	***	13.79		
Environment (E)	13	3847.56	***	59.65		
GxE interactions	117	150.33	***	20.98		
IPC1	21	279.92	***		33.42	33.42
IPC2	19	224.55	***		24.26	57.68
IPC3	17	130.33	***		12.60	70.28
IPC4	15	117.60	***		10.03	80.31
IPC5	13	112.55	***		8.32	88.62
IPC6	11	93.82	***		5.87	94.49
IPC7	9	60.72	***		3.11	97.60
Residual	12	35.21	***			
Error	420	11.14				
Total	559	150.00				

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	W1	W2	W3	W4	W5	W6	WAASB
UPB1086	0.122	0.052	7.922	17.415	149.665	9.402	7.473	0.1216	1.8309	1.5562	1.3462	1.2818	1.3085	1.2739
DWRB204	0.590	0.062	9.592	18.170	117.906	6.987	6.393	0.5898	0.6000	0.9979	1.1789	1.3229	1.2603	1.2285
KB1843	2.219	0.049	9.292	20.618	119.200	6.894	5.953	2.2191	1.8963	1.5366	1.6361	1.6444	1.6067	1.5290
PL891	4.974	0.063	9.519	25.413	260.899	8.460	7.115	4.9745	3.6011	2.9546	2.5303	2.3825	2.2011	2.0724
Karan16	0.497	0.040	7.253	13.607	65.927	5.042	4.600	0.4972	0.6659	0.8227	1.0291	0.9053	0.8907	0.9254
DWRB216	0.653	0.026	6.595	13.089	47.994	4.658	4.034	0.6532	0.8812	0.8779	0.9912	0.8960	0.9114	0.9164
K1149	1.640	0.047	7.998	17.668	98.423	6.360	5.266	1.6405	2.0075	1.7047	1.5139	1.3824	1.2799	1.3250
KB1848	1.607	0.043	8.252	16.631	73.887	5.471	4.725	1.6068	1.2450	1.1114	1.0300	1.1307	1.1510	1.1732
NDB943	1.446	0.058	9.680	20.317	132.201	7.446	6.586	1.4459	1.3790	1.7773	1.6765	1.5517	1.5476	1.4709
DWRB217	0.515	0.061	9.407	17.209	96.921	7.217	6.202	0.5151	0.5202	0.7166	0.8518	1.0092	1.1389	1.1253

Table 8. AMMI measures and Weighted average of absolute scores of barley genotypes 2019-20

 Table 9. Superiority index measures and corresponding ranking of genotypes 2019-20

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	Mean	R _k	GM	R _k	НМ	R _k	Slam	R _k	Slgm	R _k	SIhm	R _k
UPB1086	2	7	4	6	10	11	11	40.18	1	38.34	1	36.63	3	89.18	2	89.18	2	89.11	3
DWRB204	7	12	12	10	9	9	10	38.60	3	37.64	3	36.65	1	83.29	3	87.55	3	90.55	2
KB1843	18	14	15	18	16	14	14	28.78	9	27.00	9	25.49	9	29.02	9	33.38	9	39.75	9
PL891	20	20	18	20	20	19	19	26.05	10	23.01	10	19.26	10	0.00	10	0.00	10	0.00	10
Karan16	4	4	4	4	4	4	4	39.55	2	38.09	2	36.64	2	96.86	1	98.66	1	99.66	1
DWRB216	11	7	7	7	7	7	7	34.06	6	32.88	5	31.65	5	71.85	5	76.84	4	81.29	4
K1149	16	12	12	14	13	12	12	32.06	8	30.45	8	29.00	7	50.29	8	54.18	8	59.02	8
KB1848	14	10	12	10	10	10	10	33.10	7	30.89	7	28.61	8	59.65	6	60.65	6	62.18	6
NDB943	11	12	15	13	13	13	13	34.78	5	32.84	6	30.96	6	58.40	7	59.90	7	61.94	7
DWRB217	7	12	11	8	8	11	10	35.75	4	34.01	4	32.32	4	73.29	4	75.31	5	77.47	5

Measure	PC1	PC2	
IPCA1	-0.2227	-0.0624	
MASV1	-0.1119	0.3109	
MASV	-0.1118	0.3293	
Za	-0.2176	0.1261	
EV	-0.1087	0.2747	
SIPC	-0.1299	0.1858	
ASTAB	-0.1950	0.1906	
W1	-0.2227	-0.0624	
W2	-0.2106	0.0160	
W3	-0.2134	0.0694	
W4	-0.2171	0.0655	
W5	-0.2241	0.0869	
W6	-0.2245	0.1058	
WAASB	-0.2264	0.0931	
Durgapura	0.1705	0.2032	
Faizabad	0.1204	-0.1791	
Gwalior	0.0395	-0.2371	
HAU	0.2214	0.0883	
Jhansi	0.1366	0.2019	
Kanpur	0.1021	0.2553	
Karnal	0.0350	0.2484	
Ludhiana	-0.0053	0.2438	
Modipuram	0.1023	0.2233	
Pantnagar	0.1729	0.1039	
Tikamgarh	0.1683	0.0179	
Udaipur	0.1353	0.2606	
Varanasi	0.1576	0.1651	
Vijapur	0.1973	-0.1196	
Mean	0.2047	0.1795	
Siam	0.2258	0.0965	
Sigm	0.2280	0.0837	
Sihm	0.2296	0.0681	
78.09	57.05	21.04	

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



Fig. 1. Biplot analysis of superiority index & other measures of barley genotypes 2018-19



Fig. 2. Biplot analysis of stability & adaptability measures of barley genotypes 2019-20

4. CONCLUSION

G×E interaction study in multi-environment trials had been carried out by a well-established AMMI model. The simultaneous consideration of stability measures and yield would be more appropriate to recommend high-yielding stable genotypes. In the present study, the main advantages of AMMI and BLUP had been combined to increase the reliability of multilocations trials analysis. An additional advantage was provided by Superiority Indexes to assign variable weights to the yield and stability performance. Depending upon the goal of crop breeding trials, the researchers may prioritize the productivity of a genotype rather than its stability (and vice-versa). The stability index of genotype performance has the potential to provide reliable estimates of stability in future studies along with a joint interpretation of performance and stability in biplots while considering the number of significant IPCA's.

DISCLAIMER

The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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