RESEARCH ARTICLE Indian Journal of Agricultural Research, Volume 58 Special Issue: 979-986 (November 2024)

Best Linear Unbiased Prediction with Additive Main and Multiplicative Interaction for Stability Analysis of Barley Genotypes Evaluated in Coordinated Program

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10.18805/IJARe.A-5821

ABSTRACT

Background: Additive main and multiplicative interaction (AMMI) analysis had been exploited for multi environment trials for most of the crops. Usage of the best linear unbiased prediction (BLUP), along with AMMI tools, of the genotypes would improve the estimation of interaction effects.

Methods: AMMI based measures of adaptability have been enriched with the incorporation of BLUP of genotypes by new Superiority index that allowed variable weights for stability and yield of genotypes.

Result: Stability measure weighted average of absolute scores (WAASB) based on all significant interaction principal components ranked suitability of KB1754, RD3000, NDB1445 genotypes. Superiority index while weighting 0.65 and 0.35 for mean yield and stability arranged DWRB201, NDB1445, RD2552 as of stable high yield performance of barley genotypes. Corrected measure Modified AMMI Stability Value (MASV1) found RD2552, DWRB201, KB1762 and Modified AMMI Stability Value (MASV) ranked DWRB201, RD2552, KB1762. ASTAB measure achieved the desirable lower values for DWRB201 DWRB207, HUB268 genotypes. Biplot graphical analysis based on 60.7% of variation of the stability measures observed MASV1, ASTAB (AMMI based stability parameter), EV(Averages of the squared eigenvector values), SIPC (Sums of the absolute value of the IPC scores), Za (Absolute value of the relative contribution of IPCs to the interaction), W3, WAASB and MASV had been clubbed together. For the second year lower value of WAASB measure had observed for RD3016, KB1815 HUB273. Ranking of genotypes as per Superiority index found RD3017, RD2907, HUB274 as of stable high yield performance. Genotypes RD3017, RD2907 and NDB1173 pointed out by MASV1 while RD3017, RD2907, NDB1173 identified by MASV as the genotypes of choice. RD3017 NDB1173, RD2907 genotypes were selected as per values of ASTAB measure. Total of 71.8% of variation of the considered measures in biplot analysis expressed larger cluster comprised of AMMI based measures and a separate cluster of Superiority indexes as per mean, Geometric Adaptability Index (GAI) and HMGV also observed.

Key words: AMMI, ASTAB, MASV, SSI, WAASB.

INTRODUCTION

G×E interaction has been assessed by the differential expression of genotypes over the environments (Ajay *et al.,* 2020). AMMI model explains more information as comprises of additive main effects of genotype and environment and the multiplicative effect of G×E interaction (Gauch, 2013). Research studies observed the better performance of AMMI model than linear regression models and other multivariate procedures (Bocianowski *et al.,* 2019). Several of AMMI based stability measures are available in literature (Zali *et al.,* 2012; Agahi *et al.,* 2020). Researchers have introduced different selection criteria for simultaneous selection of yield and stability (Rao and Prabhakaran 2005; Farshadfar, 2008; Farshadfar *et al.,* 2011). BLUP and AMMI, two distinct approaches, utilized to distinguish the pattern from the random error components in G×E interactions (Piepho *et al.,* 2008). The benefits of two important techniques AMMI and BLUP nested into a Superiority Index measure for stability and adaptability of genotypes (Olivoto *et al.,* 2019).

MATERIALS AND METHODS

Sixteen advanced genotypes at seven locations and eighteen genotypes at five 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 Table 1 and 2 for ready reference.

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How to cite this article: Verma, A., Verma, R.P.S., Singh, J., Kumar, L., Singh, G.P. (2024). Best Linear Unbiased Prediction with Additive Main and Multiplicative Interaction for Stability Analysis of Barley Genotypes Evaluated in Coordinated Program. Indian Journal of Agricultural Research. 58 (Special Issue): 979-986. doi: 10.18805/IJARe.A-5821.

Submitted: 12-05-2021 **Accepted:** 01-11-2021 **Online:** 09-12-2021

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:

$WAASB_i$= Weighted average of absolute scores of the ith genotype (or environment).

$IPCA_{ik}$= Score of the ith genotype (or environment) in the kth.

IPCA and EP_k = Amount of the variance explained by the kth IPCA.

Superiority index allowed weighting between yield and stability measures (WAASB) to select genotypes that combined high performance and stability as:

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

Where:

rG_i and rW_i= Rescaled values for yield and WAASB, respectively, for the ith genotype.

G_i and W_i= Yield and the WAASB values for i^{th} genotype.

SI= Superiority index for the ith genotype that weights between yield and stability.

θ_Y and θ_S= Weights for yield and stability assumed to be of order 65 and 35 respectively in this study.

Zobel 1994	Averages of the squared eigenvector values	$EV = \sum_{n=1}^{n} \lambda_{in}^2 / n$
Sneller *et al.*, 1997	Sums of the absolute value of the IPC scores	$SIPC = \sum_{n=1}^{n} \lambda_n^{0.5} \gamma_{in}$
Rao and Prabhakaran, 2005	AMMI based stability parameter	$ASTAB = \sum_{n=1}^{n} \lambda_n \gamma_{ni}^2$
Zali *et al.*, 2012	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.*, 2012	Absolute value of the relative contribution of IPCs to the interaction	$Z_a = \sum_{n=1}^{N} \lvert \lambda_n \gamma_{in} \rvert$
Ajay *et al.*, 2020		$MASV1 = \sqrt{\sum_{n=1}^{n-1} \frac{SSIPC_n}{SSIPC_{n+1}} (PC_n)^2 + (PC_{n+1})^2}$
Resende and Durate, 2007	Relative performance of genotypic values across environments	$PRVG_{ij} = VG_{ij} / VG_i$
Resende and Durate, 2007	Harmonic mean of Relative performance of genotypic values $MHPRVG_i$ = Number of environments / $\sum_{j=1}^{k} \frac{1}{PRVGij}$	
Olivato *et al.*, 2019	Superiority Index	$SI = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{\theta_Y + \theta_S}$

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

First year of study 2018-19

Highly significant effects of environment (E), G×E interaction and genotypes (G) had been observed by AMMI analysis. Environment explained about 31.8% of the total sum of squares due to treatments significantly indicated diverse environments caused most of the variations in genotypes yield (Table 3). Significant proportion of G×E interaction deserved the stability estimation of genotypes over environments (Ajay *et al.,* 2020). Genotypes explained only 9.3% of total sum of squares, whereas G×E interaction accounted for 38.4% 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 wheat yield. Partitioning of G×E interaction revealed that the first five multiplicative terms (IPCA1, IPCA2, IPCA3, IPCA4 and IPCA5) of AMMI were significant and explained 35.4%, 29.6%, 25.7%, 5.7% and 2.8% of interaction sum of squares, respectively. Total of significant components were 99.2% and remaining 0.8% was the residual or noise that discarded (Oyekunle *et al.,* 2017).

Second year of study 2019-20

Highly significant effects of environment (E), G×E interaction and genotypes (G) had been observed by AMMI analysis. Environment explained about significantly 42.5% of the total sum of squares due to treatments indicating that diverse environments caused most of the variations in genotypes yield (Table 4). G×E interaction accounted for 30.3% whereas Genotypes contributed only 8.4% of total treatment variations in yield. Further analysis of G×E interaction observed three multiplicative terms (IPCA1, IPCA2 and IPCA3) explained 49.2%, 24.3% and 19.7% of interaction sum of squares, respectively. Total of these components were to the tune of 93.2% and remaining was noise that was discarded.

Ranking of barley genotypes as per AMMI based stability measures

First year of study 2018-19

Least value of absolute IPCA1 expressed by HUB268, DWRB201, RD2999 and higher value achieved by RD3002 (Table 5). Low values of (EV) associated with stable behaviour, the genotypes HUB267 followed by RD2999, NDB1173 expressed lower values and maximum value by KB1754 genotype. Measure SIPC identified HUB267 followed by RD2999, DWRB201 as of stable nature,

whereas KB1754 would be of least stable type. Za measure considered absolute value of the relative contribution of IPCs to the interaction revealed DWRB201, HUB267 and RD2999 as genotypes with descending order of stability, whereas KB1754 genotype with the least stability. ASTAB measure observed genotypes HUB267 and DWRB201 as stable and KB1754 was least stable in this study (Rao and Prabhakaran 2005). All significant IPCAs had been considered by MASV and MASV1 measures. Values of MASV1 showed that the genotypes, RD2552, DWRB201 and RD2999 were most stable and DWRB201, HUB267 and RD2999 would be stable by MASV measure respectively (Ajay *et al.,* 2020). Measure W1 favoured RD3002 RD2552, RD3002 while as per W2, genotypes identified were RD3000, RD2552, RD3002 while W3 favoured RD3000, KB1754, RD3002 whereas W4 settled for KB1754, RD3000, NDB1445. Finally lower values of WAASB associated with stable nature of KB1754, RD3000, NDB1445 genotypes as for considered locations of the zone at the same time maximum deviation from the average performance across environments obtained by DWRB201.

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

Code	Genotype	Parentage	Code	Location	Latitude	Longitude
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
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
G7	DWRB201	DWRUB52/BONMRA-73//Prestige/PL426	E7	Vallabhnagar	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
G1	KB1845	PETUNIA1/5/POST/COPAL//GLORIA-BAR/COME/3/SIND89A-148/4/CARD/6/GLORIA-BAR/COPAL//BLLU/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
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
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/RM 1508/4/Arizona5908/Aths//Avt/Attiki/3/Ager *(4thGSBSN2016-17-52)*				
G17	RD3015	RD 2715/RD 2552				
G18	RD2552	RD2035/DL472				

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 contributionof factors	G×E interaction sum of squares (%)	Cumulative sum of squares (%) by IPCA's
Treatments	111	237.21	.0000000***	79.49		
Genotype (G)	15	205.41	.0000000***	9.30		
Environment (E)	6	1753.76	.0000000***	31.77		
G×E interactions	90	141.40	.0000000***	38.42		
IPC1	20	225.05	.0000000***		35.37	35.37
IPC2	18	209.27	.0000000***		29.60	64.97
IPC3	16	204.18	.0000000***		25.67	90.64
IPC4	14	51.54	.0038716**		5.67	96.31
IPC5	12	30.26	0.2688757		2.85	99.16
Residual	10	10.69	0.8241293			
Error	336	20.22				
Total	447	74.10				

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	G×E interaction sum of squares (%)	Cumulative sum of squares(%) by IPCA's
Treatments	89	160.59	.0000000 ***	81.17		
Genotype (G)	17	87.44	.0000000 ***	8.44		
Environment (E)	4	1868.68	.0000000 ***	42.45		
G×E interactions	68	78.40	.0000000 ***	30.28		
IPC1	20	131.18	.0000000 ***		49.21	49.21
IPC2	18	71.82	.0000000 ***		24.25	73.46
IPC3	16	65.62	.0000721 ***		19.69	93.16
Residual	14	26.06	0.150117			
Error	180	18.42				
Total	269	65.46				

Table 5: AMMI based measures and Weighted average of absolute scores for barley genotypes 2018-19.

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	W1	W2	W3	W4	WAASB
RD2794	0.9777	0.0353	5.7968	16.88	51.42	7.94	4.89	0.9777	1.1743	1.2685	1.2833	1.2503
HUB267	0.2403	0.0115	2.8172	7.55	13.64	5.26	2.83	0.2403	0.2850	0.5448	0.5365	0.5439
RD2999	0.2141	0.0183	3.3412	10.59	36.33	3.67	3.22	0.2141	1.1035	0.8731	0.8142	0.8052
NDB1708	1.0327	0.0513	6.0237	15.71	57.97	6.06	4.76	1.0327	1.3415	1.0835	1.1605	1.1398
DWRB207	0.4052	0.0339	4.7014	11.57	34.39	7.72	4.49	0.4052	0.4110	0.7527	0.8079	0.8121
KB1762	1.3091	0.0311	5.4706	15.47	42.41	5.46	3.73	1.3091	1.2953	1.1760	1.1567	1.1519
DWRB201	0.1872	0.0461	3.6856	6.87	22.99	3.72	2.70	0.1872	0.2484	0.3624	0.3788	0.4468
KB1754	0.8507	0.0516	6.5966	22.71	110.33	15.30	8.11	0.8507	1.2800	1.9059	1.7874	1.7311
HUB268	0.1596	0.0227	3.7002	10.65	32.07	8.37	4.60	0.1596	0.3261	0.7637	0.8002	0.7703
KB1706	0.9500	0.0213	4.5730	13.71	35.44	4.48	3.29	0.9500	1.2648	1.0868	1.0457	1.0343
NDB1173	1.9334	0.0206	4.4705	15.88	50.38	7.07	4.11	1.9334	1.3540	1.3733	1.2914	1.2420
RD3000	2.3994	0.0336	5.6970	20.38	83.85	6.15	4.51	2.3994	2.1688	1.7903	1.6629	1.6059
RD2552	2.5236	0.0276	4.5816	15.23	64.40	3.62	3.32	2.5236	1.8587	1.3130	1.2250	1.1999
RD3002	2.5512	0.0278	5.0773	16.85	65.53	5.24	3.72	2.5512	1.6984	1.4293	1.3496	1.3150
NDB1445	0.3770	0.0371	5.3830	17.45	75.97	7.13	5.17	0.3770	1.5283	1.4060	1.3732	1.3209
RD2907	2.3109	0.0303	5.0677	16.56	65.33	7.87	4.57	2.3109	1.2986	1.3873	1.3052	1.2791

Second year of study 2019-20

Least absolute values of IPCA1 expressed by RD2907, HUB274, KB1845 and higher value achieved by KB1815 (Table 6). Minimum values of EV associated with stable behaviour of RD3015, NDB1173, RD2907 genotypes and maximum value had by RD3016 genotype. SIPC measure identified RD2907, NDB1173 followed by RD3015 for the lower value, whereas RD3016 would be of least stable behaviour. Za measure revealed RD2907, NDB1173 and RD3015 genotypes in descending order of stability, whereas RD3016 genotype with the least stability. ASTAB measure observed genotypes NDB1173, RD2907 and RD3015 as most stable and genotype RD3016 was least stable in this study (Rao and Prabhakaran 2005). RD2907, NDB1173, RD3015 genotypes were of choice by of MASV1 and MASV measure observed RD2907, NDB1173, RD3015 as the stable genotypes while KB1815 would be unstable (Ajay *et al.,* 2019). W1 measure selected KB1815, BH1032, RD2794 while measure W2 favoured KB1815, RD3016, HUB273 barley genotypes. Lower value of WAASB measure had observed for RD3016, KB1815, HUB273 and large value by RD2907.

Table 6: AMMI based measures and Weighted average of absolute scores of barley genotypes 2019-20.

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	W1	W2	WAASB
KB1845	0.2330	0.061	3.648	16.48	35.36	3.03	2.92	0.2330	0.6405	0.9801
DWRB214	0.5716	0.021	2.128	10.81	14.45	2.53	2.27	0.5716	0.8698	0.6919
RD3017	0.5655	0.008	1.368	7.43	5.92	1.68	1.41	0.5655	0.6405	0.4902
HUB274	0.1808	0.017	1.986	9.18	10.81	2.01	1.89	0.1808	0.5346	0.5565
BH1033	0.4907	0.012	1.941	9.73	8.53	1.87	1.65	0.4907	0.6512	0.6157
RD2794	1.9216	0.034	3.300	19.13	32.01	4.09	2.99	1.9216	1.4597	1.2894
RD3018	1.4636	0.044	3.498	18.78	32.04	3.46	2.73	1.4636	1.0737	1.2201
RD2907	0.0184	0.006	0.850	3.71	3.42	0.78	0.78	0.0184	0.0331	0.2136
NDB1730	0.6049	0.026	2.791	13.68	16.62	2.33	2.10	0.6049	0.7463	0.8526
KB1822	1.4944	0.031	2.854	16.25	26.66	3.70	2.92	1.4944	1.4378	1.0926
NDB1742	0.3350	0.038	2.806	13.01	21.70	2.20	2.11	0.3350	0.4612	0.7832
BH1032	2.1386	0.043	3.428	20.33	41.47	4.74	3.54	2.1386	1.8079	1.3872
RD3016	1.6569	0.092	5.518	28.25	64.81	5.16	4.41	1.6569	1.8678	1.8045
NDB1173	0.3316	0.004	0.905	4.81	2.59	1.10	0.95	0.3316	0.4082	0.3146
HUB273	1.8888	0.061	4.623	24.91	49.09	4.81	3.85	1.8888	1.8272	1.6300
KB1815	2.8812	0.059	3.842	23.83	62.47	5.90	4.18	2.8812	1.9649	1.6484
RD3015	0.7494	0.004	0.952	6.01	4.16	1.54	1.09	0.7494	0.5327	0.4187
RD2552	0.4384	0.017	2.120	10.30	10.51	1.68	1.53	0.4384	0.4761	0.6375

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
RD2794	24	27	29	28	24	29	29	31.60	15	29.57	14	31.21	15	30.51	14	30.81	14	31.78	13
HUB267	13	10	10	11	10	15	11	33.83	9	65.05	6	33.40	8	66.89	6	32.96	7	69.31	5
RD2999	14	13	13	14	17	13	14	32.68	11	49.56	8	32.11	12	49.66	8	31.50	11	49.82	9
NDB1708	20	25	25	19	20	18	23	33.31	10	45.03	10	32.60	9	44.34	10	31.89	10	44.03	10
DWRB207	11	16	13	10	9	17	14	35.70	5	71.35	4	35.23	5	73.82	3	34.73	4	77.07	2
KB1762	15	13	16	12	11	11	11	36.51	4	68.01	5	35.53	4	66.94	5	34.46	5	65.51	6
DWRB201	5	17	6	4	5	6	4	36.80	3	89.32	1	36.22	3	91.48	1	35.54	2	93.92	1
KB1754	21	30	30	30	30	30	30	32.55	14	23.37	15	31.36	14	18.55	15	30.17	15	13.29	15
HUB268	8	12	11	11	10	22	19	34.04	7	60.38	7	33.60	6	62.27	7	33.12	6	64.52	7
KB1706	20	16	18	18	17	16	16	32.65	12	43.11	11	31.81	13	41.11	11	30.96	12	38.95	12
NDB1173	18	9	11	16	14	16	14	34.16	6	48.46	9	33.56	7	49.12	9	32.92	8	49.98	8
RD3000	22	18	21	23	23	17	18	33.88	8	36.47	12	32.46	10	30.55	13	30.87	13	22.65	14
RD2552	17	8	9	9	13	3	7	37.59	2	74.58	3	36.40	2	72.40	4	35.18	3	70.28	4
RD3002	32	23	26	28	29	21	22	29.35	16	11.34	16	28.98	16	11.34	16	28.61	16	11.34	16
NDB1445	6	14	12	15	15	12	16	38.26	1	76.18	2	37.31	1	76.18	2	36.26	1	76.18	3
RD2907	26	21	22	24	25	26	24	32.56	13	35.77	13	32.29	11	38.13	12	32.00	9	41.16	11

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.

Superiority indexes as per AMMI and BLUP: Barley genotypes

First year of study 2018-19

Stability alone is not a desirable selection criterion as stable genotypes may not be a high yielder, simultaneous use of yield and stability in a single measure is essential (Kang 1993; Farshadar *et al.,* 2008). Simultaneous Selection Index also referred to as genotype stability index (GSI) or yield stability index (YSI) (Farshadar *et al.,* 2011) was computed by adding the ranks of stability measure and mean yield of genotypes. Least ranks for IPCA1 measure exhibited by DWRB201, NDB1445 and HUB268 were considered as stable with high yield, whereas high values suggested as least stable yield for RD3002 genotype (Table 7). EV measure identified RD2552, NDB1173 andHUB267 whereas SPIC favoured DWRB201, RD2552 and HUB267genotypes. Genotypes DWRB201, RD2552 and DWRB207 possessed lower value of Za measure. ASTAB measure achieved the desirable lower values for DWRB201, DWRB207, HUB268. Composite measure MASV1 found RD2552, DWRB201, KB1762 and as per MASV ranks DWRB201, RD2552, KB1762 genotypes would be of choice for these locations of the zone.

Average yield of genotypes favoured NDB1445, RD2552, DWRB201 where Geometric adaptability index selected NDB1445, RD2552, DWRB201 while Harmonic mean of yield values pointed for NDB1445, DWRB201, RD2552 as suitable genotypes as far as considered locations are concerned. Superiority index while weighting 0.65 and 0.35 for average yield and stability found DWRB201, NDB1445 and RD2552 as of stable performance with high yield. Least magnitude of SIgm ranked DWRB201, NDB1445, DWRB207 as desirable genotypes while SIhm measure favoured DWRB201, DWRB207, NDB1445 barley genotypes.

Second year of study 2019-20

Ranks for IPCA1 measure favoured HUB274, RD2907, RD3017 as per the least values, whereas large values of KB1815 suggested unstable high yield (Table 8). EV measure settled for RD3017, NDB1173 and HUB274

Table 9: Loadings of measures as per two principal components 2018-19.

Measure	PC1	PC2
IPCA1	0.1984	-0.3679
MASV1	0.1784	0.3560
MASV	0.2193	0.3480
Za	0.3050	0.0561
EV	0.1151	0.2694
SIPC	0.2623	0.1239
ASTAB	0.2855	0.1199
W1	0.1984	-0.3679
W2	0.2424	-0.1927
W3	0.3035	0.0063
W4	0.3051	0.0231
WAASB	0.3059	0.0244
Hisar	-0.1241	-0.2077
Faizabad	-0.0608	0.2917
Khumer	-0.1450	0.0957
Dalipnagar	-0.0292	-0.0485
Banasthali	0.0693	-0.0162
Hisar	-0.0385	-0.3127
Vallabhnagar	-0.0047	0.2537
Siam	-0.2459	0.1196
Sigm	-0.2587	0.1085
Sihm	-0.2694	0.0974
60.72	45.72	14.50

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
KB1845	21	34	33	30	32	29	31	22.22	18	18.14	18	21.97	18	18.14	17	21.73	15	20.60	16
DWRB214	22	21	21	21	21	23	23	26.20	13	49.88	13	25.01	15	43.90	13	23.79	14	39.63	12
RD3017	11	7	7	7	7	8	7	29.31	3	74.15	1	28.58	3	71.13	1	27.72	3	68.21	2
HUB274	7	11	11	10	12	12	12	28.62	5	68.33	3	28.02	4	66.06	3	27.29	5	64.10	6
BH1033	21	19	19	20	19	20	20	26.13	14	51.15	11	25.49	12	48.65	11	24.93	12	48.32	11
RD2794	22	17	18	20	18	20	20	28.46	6	51.18	10	28.01	5	49.87	10	27.52	4	49.40	10
RD3018	20	22	22	21	21	20	19	28.00	8	49.76	14	26.66	9	42.82	14	25.03	11	35.60	13
RD2907	10	12	10	10	11	10	10	27.90	9	71.29	2	27.42	6	69.77	2	26.92	6	69.40	1
NDB1730	14	13	13	14	13	13	12	28.67	4	62.09	7	27.26	7	54.69	7	26.03	8	49.84	9
KB1822	15	12	13	13	13	15	14	30.08	2	65.82	4	29.68	2	64.88	6	29.30	2	64.67	5
NDB1742	12	19	17	16	17	15	16	28.40	7	61.91	8	25.46	13	44.76	12	21.48	16	23.44	15
BH1032	28	24	24	26	26	26	26	26.79	11	38.34	15	24.11	16	22.88	16	21.33	18	9.18	17
RD3016	15	19	19	19	19	18	19	32.40	1	65.00	6	32.15	1	65.00	5	31.90	1	65.00	4
NDB1173	14	11	12	12	11	12	12	27.35	10	65.51	5	27.10	8	65.54	4	26.88	7	66.90	3
HUB273	27	29	29	29	28	28	28	26.75	12	32.79	16	26.21	10	30.90	15	25.63	9	30.29	14
KB1815	35	32	33	33	34	35	34	25.69	17	25.63	17	23.60	17	13.84	18	21.41	17	3.97	18
RD3015	27	18	19	19	19	19	19	25.80	16	53.37	9	25.30	14	51.74	8	24.80	13	51.85	8
RD2552	21	22	22	22	21	19	20	26.11	15	50.54	12	25.88	11	50.63	9	25.62	10	52.09	7

genotypes. Minimum ranks of SPIC favoured RD3017, RD2907 and HUB274 genotypes. Lower value of Za measure possessed by RD3017, HUB274 and RD2907 genotypes for stable higher yield as compared to others genotypes. Barley genotypes RD3017, NDB1173, RD2907 were selected as per values of ASTAB measure accounted AMMI analysis with BLUP of genotypes yield values. Composite measure MASV1 selected RD3017, RD2907, NDB1173 while RD3017, RD2907, NDB1173 identified by MASV as genotypes of choice for these locations of the zone. Superiority index while weighting 0.65 and 0.35 for GAI and stability found RD3017, RD2907 and HUB274 as of stable performance with high yield. While considering Harmonic mean and stability identified RD2907, RD3017, NDB1173 barley genotypes.

Maximum yield expressed by RD3016 followed by KB1822 and RD3017 as good variation had been observed from 32.4 to 22.2 q/ha among genotypes. Genotypic adaptability index expressed the higher values by RD3016 KB1822, RD3017 whereas Harmonic mean of genotypic values ranked RD3016, KB1822, RD3017 barley genotypes. Superiority index had observed lower value expressed by RD3017, RD2907, HUB274 and large value by KB1815.

Biplot clustering pattern

First year of study 2018-19

Loadings of studied measures as per first two significant principal components were reflected in table 9. Biplot graphical analysis considered two PCAs accounted as

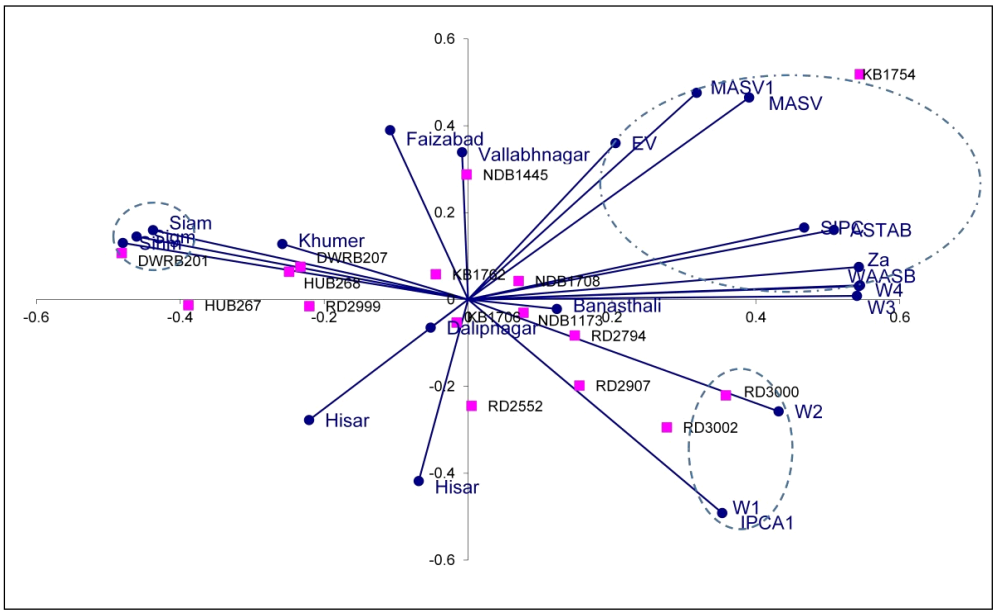

Fig 1: Biplot analysis of superiority index and other measures of barley genotypes 2018-19.

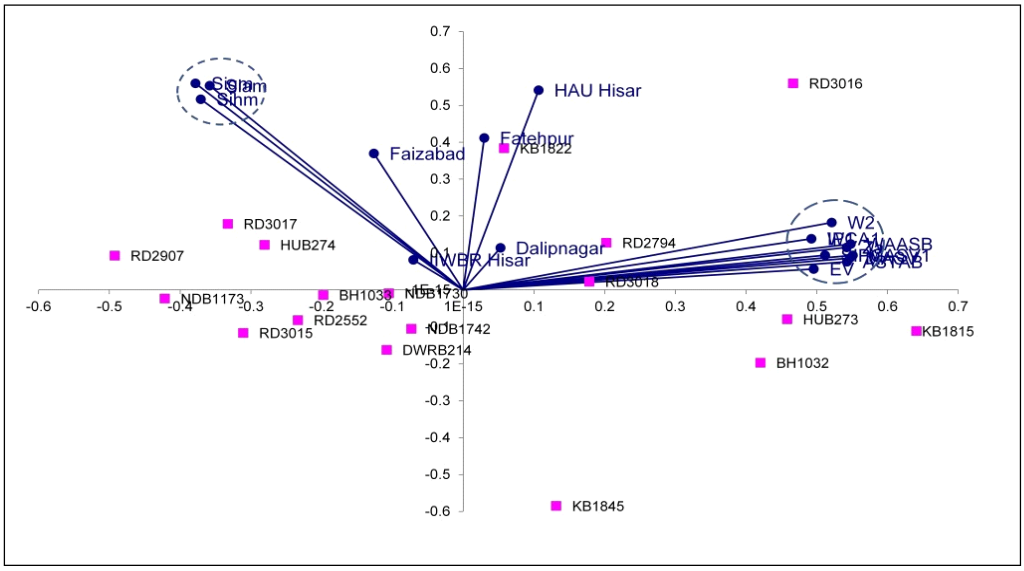

Fig 2: Biplot analysis of stability and adaptability measures of barley genotypes 2019-20.

Table 10: Loadings of measures as per two principal components 2019-20.

Measure	PC1	PC2
IPCA1	0.2752	0.1081
MASV1	0.3080	0.0731
MASV	0.3056	0.0671
Za	0.3031	0.0900
EV	0.2771	0.0441
SIPC	0.2861	0.0733
ASTAB	0.3034	0.0595
W1	0.2752	0.1081
W2	0.2913	0.1426
WAASB	0.3063	0.0970
Siam	-0.2002	0.4322
Sigm	-0.2115	0.4372
Sihm	-0.2073	0.4034
IIWBR Hisar	-0.0393	0.0636
HAU Hisar	0.0597	0.4226
Dalipnagar	0.0295	0.0889
Faizabad	-0.0705	0.2888
Fatehpur	0.0167	0.3215
71.76	56.87	14.89

60.7% of variation of the stability measures accounted by both (Bocianowski *et al.,* 2019). Studied measures grouped into three major clusters. MASV1 clubbed with ASTAB, EV, SIPC, Za, W3, WAASB and MASV measures (Fig 1). Yield based measures clubbed with corresponding SI measures. Measure IPCA1 and W2 maintained distance from measures and observed as outliers in different quadrant.

Second year of study 2019-20

Biplot graphical analysis based on first two significant principal component analysis (PCA) of the measures to explore the association if any among them (Fig 2). However, the loadings of the measures as per first two PCs were reflected in Table 10. Nearly 71.8% of variation of the stability measures accounted by two PCAs. Two major groups of measures depicted in Fig 2. Large number of AMMI based measures clubbed together and separate cluster of SI was also observed. Superiority indexes depicted very strong association ship irrespective of average, geometric or harmonic values of genotypes. AMMI based measures and stability measures as per absolute values of scores tend to be of strong correlated pattern.

CONCLUSION

Simultaneous use of stability and yield would be more appropriate to recommend high-yielding stable genotypes. Advantages of AMMI and BLUP had been combined in Superiority Indexes to increase the reliability of multi-locations trials analysis. The researchers may prioritize the productivity of a genotype rather than its stability (and vice-versa) as per the goal of crop breeding trials.

ACKNOWLEDGEMENT

The barley genotypes were evaluated at research fields at coordinated centers of AICW & BIP across the country. First author sincerely acknowledges the hard work of all the staff for field evaluation and data recording of genotypes.

Conflict of interest

All authors declare that they have no conflict of interest.

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