



RESEARCH PAPER

AMMI confounded with BLUP of feed barley genotypes for superiority measures under NEPZ trials

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Abstract : AMMI analysis of feed barley genotypes evaluated for North Eastern Plains Zone of the country observed highly significant effects of environments (E), GxE interaction and genotypes (G). GxE Interaction effects accounted for 45.9% and 29.2% and environment effects explained 27.5% and 37.1%, during cropping seasons of 2018-19 and 2019-20, respectively. ASTAB measure achieved the desirable lower values for HUB113, DWRB137. Ranks of MASV1 and MASV measures considered HUB113, K508 genotypes would be of choice this zone. Superiority index assigned 0.65 and 0.35 weights for average yield and stability found HUB113, DWRB137 as of stable performance with high yield. Biplot graphical analysis as per 84.7 % of variation of the measures exhibited largest cluster comprised of MASV1 with ASTAB, EV, SIPC, Za, W2, WAASB and MASV measures. For the second-year Desirable lower values of ASTAB measure achieved by HUB69, Lakhan, RD3020. Ranks of composite measure MASV1 and MASV found Lakhan, HUB69, KB1830 genotypes would be of choice for these locations. Superiority index with assigned weights for yield and stability found Lakhan, DWRB213, KB1830 as of stable performance with high yield. About 79.3 % of variation of the measures under biplot analysis observed AMMI based measures were grouped together and mean yield joined hands with superiority measures of genotypes. The reliability of multi-locations trials would be increased with superiority Indexes as major features of AMMI and BLUP had been confounded. Option of assigning variable weights to the yield and stable performance help the researches to set their crop improvement targets.

Key Words : AMMI, ASV, ASV1, HMGV, GAI, HMPRVG, Biplots

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INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of 31 *Hordeum* species, belonging to the tribe *Triticeae*, of the grass family *Poaceae* also known *Gramineae*

(Kendel *et al.*, 2019). The main use of barley in feed industry is attributed to the adaptability of the crop for large variations in Agro-climatic conditions (Karkee *et al.*, 2020). Approximately 75–80% of global barley production is used as animal feed, 20–25% as malting,

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2–5% for human food, and the remaining part in biofuel industry to produce bioethanol (Badr *et al.*, 2000). There is no specific quality restriction to use barley grain in animal feed industry. Often, malting barley is destined to feed industry because there has been damage during agricultural phase or it has not met the quality level required by malting and brewing industries or due to market or price variations (Newton *et al.*, 2011).

AMMI (additive main-effects and multiplicative interaction) analysis had been advocated to retrieve the maximum information from multi-environment trials (MET) (Bocianowski *et al.*, 2019). The random nature of genotypes may be of more use in the comparison to fixed effects (Piepho *et al.*, 2008). Best Linear Unbiased Prediction (BLUP) is commonly preferred to predict the outcome of random variables (Agahi *et al.*, 2020). The advantages of AMMI and BLUP has been confounded in Superiority Index to put forward by weighted average of yield and stability of genotypes in crop improvement programme (Olivoto *et al.*, 2019).

MATERIAL AND METHODS

This zone has been identified to increase the total cereal production to ensure food security of the country. The states Bihar, eastern Uttar Pradesh, Jharkhand, Assam and plains of West Bengal together categorized as the North Eastern Plains Zone of India. Six feed

barley genotypes at five locations and fifteen 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 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 as weighted average of absolute scores calculated as:

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

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:

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

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 qY and qS were the weights for

Zobel <i>et al.</i> (1988)	Averages of the squared eigenvector values	$EV = \sum_{n=1}^N \lambda_{in}^2 / n$
Sneller <i>et al.</i> (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 <i>et al.</i> (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 <i>et al.</i> (2012)	Absolute value of the relative contribution of IPCs to the interaction	$Z_a = \sum_{n=1}^N \lambda_n \gamma_{in} $
Ajay <i>et al.</i> ,	MASV1	$MASV1 = \sqrt{\sum_{n=1}^{N-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}} PC_n \right)^2 + (PC_{n+1})^2}$
Olivato (2018 and 2019)	Superiority Index	$SI = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(\theta_Y + \theta_S)}$

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	RD 2552	RD2035/DL472	E1	Varanasi	25° 19' N	82° 59' E	81
G2	K1055		E2	Faizabad	26° 46' N	82° 9' E	97
G3	HUB113	KARAN280/C138	E3	Kanpur	26° 26' N	80° 19' E	126
G4	RD2969	RD2552/RD2503//RD 2715	E4	Ranchi	23°20'N	85°18'E	651
G5	DWRB137	DWR28/DWRUB64	E5	Sabour	25°23' N	87°04' E	46
G6	K508	K394/K141					

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	NDB1748	CEV96060/MSEL//CANELA ACBSSO	E1	Kanpur	26° 26' N	80° 19' E	126
G2	KB1830	RD 2784/Jyoti	E2	Saini	28°12' N	75°40' E	
G3	RD3020	RD 2035/ RD 2624//RD 2715	E3	Varanasi	25° 19' N	82° 59' E	81
G4	DWRB213	CONCHITA/DWRUB64	E4	Faizabad	26° 46' N	82° 9' E	97
G5	Lakhan	K12/IB226	E5	Chianki	23°45' N	85°30'E	215
G6	RD3022	RD 2607 / RD 2651	E6	Ranchi	23°20' N	85°18' E	651
G7	HUB269	31st INBON-04 / RD 2552	E7	Pusa	28°38' N	77°09' E	52
G8	PL925	VJM315/BH919	E8	Sabour	25°23' N	87°04' E	46
G9	HUB270	RD-2618 /RD-2660					
G10	KB1815	Ghinneri(smooth_awns)/6/JLB70-01/5/DeirAlla106//DL70/Pyo/3/RM1508 /4/Arizona5908/Aths//Avt/Attiki/3/Ager					
G11	RD3019	RD 2715 / RD 2552					
G12	K 603	K257/C138					
G13	PL918	VMorales/6/LEGACY//PENCO/CHEVRON-BAR/7/LIGNEE527 GERBEL/3 / BOYB* 2/ SURB//CI12225.2D/4/GLORIA-BAR/COME					
G14	KB1832	K 603 x RD 2715					
G15	RD3021	DWR 64 / RD 2503					

yield and stability would be of order 65 and 35, respectively for present study, 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

The results obtained from the present investigation as well as relevant discussion have been summarized under following heads :

AMMI analysis of barley genotypes :

First year of study 2018-19 :

Highly significant effects of environment (E), GxE interaction and genotypes (G) had been observed by AMMI analysis of feed barley genotypes evaluated for

North Eastern Plains Zone of the country. Environment explained 27.5% of the total sum of squares due to treatments indicating that diverse environments caused most of the variations in yield of evaluated genotypes (Table 1). GxE interaction accounted for 45.9% of treatment variations in yield and this significant proportion of GxE interaction demands the stability assessment of genotypes over environments (Agahi *et al.*, 2020). Genotypes explained only 13.5% of total sum of squares, whereas. More contributions of GxE interaction as compared to genotypes towards total sum of squares indicated the presence of complex interaction for the yield of genotypes (Gauch, 2013). First three multiplicative terms of GxE interaction explained significantly (IPCA1, IPCA2 and IPCA3) 56.5%, 24.5% and 17.5%, of interaction sum of squares with a total of 98.4 % and 1.6% was the discarded residual (Oyekunle *et al.*, 2017).

Second year of study 2019-20 :

Highly significant effects of environment (E), GxE interaction and genotypes (G) had contributed 37.1%, 29.2% and 10.5%, respectively of the total sum of squares due to treatments in yield of evaluated genotypes (Table 5). Three out of six multiplicative terms had expressed significant contribution towards GxE interaction. Percentage share of components were 54.7%, 15.7%, 13.7%, 10%, 8.4%, 3.6% and 2.6 % of interaction sum of squares. Total 98.7 % of components and discarded residual was only 1.3%.

Ranking of barley genotypes as per AMMI based stability measures:*First year of study 2018-19 :*

Least value of absolute IPCA1 expressed by

RD2969, K508 and higher value achieved by K1055 (Table 2). Low values of (EV) associated with stable behaviour, the genotypes RD 2552 followed by HUB113 expressed lower values and maximum value possessed by DWRB137 genotype. Measure SIPC identified RD 2552 followed by HUB113 as of stable nature, whereas DWRB137 would be of least stable type. Za measure considered absolute value of the relative contribution of IPCs to the interaction revealed RD 2552 and HUB113 as genotypes with descending order of stability. ASTAB measure observed genotypes HUB113 and RD 2552 as stable and K1055 was least stable in this study (Rao and Prabhakaran, 2005). All significant IPCAs had been considered by MASV1 and MASV measures. Values of MASV1 showed that the genotypes, HUB113 and K508 were most stable whereas genotypes HUB113,

Source of variation	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	29	201.84	***	86.80		
Genotype (G)	5	181.74	***	13.48		
Environment (E)	4	462.74	***	27.45		
GxE interaction	20	154.68	***	45.88		
IPC1	8	218.29	***		56.448	56.448
IPC2	6	126.16	***		24.468	80.916
IPC3	4	135.42	***		17.510	98.426
Residual	2	24.35				
Error	90	9.89				
Total	119	56.67				

Genotype	IPCA1	MASV1	MASV	Za	EV	SIPC	ASTAB	W1	W2	WAASB
RD 2552	1.529	3.926	2.794	16.353	0.031	2.629	20.420	1.5288	1.2664	0.9865
K1055	3.511	8.370	5.666	33.628	0.119	5.207	88.369	3.5113	2.3561	2.0527
HUB113	1.176	3.282	2.483	18.841	0.036	3.109	18.345	1.1758	1.0308	1.0633
RD2969	0.132	4.144	3.769	19.738	0.086	3.676	35.234	0.1316	1.2075	1.0158
DWRB137	1.865	5.894	4.659	33.470	0.122	5.649	59.548	1.8655	2.0017	1.8751
K508	1.161	3.912	3.292	26.756	0.105	4.460	41.453	1.1612	1.0055	1.4427

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	Mean	Rk	Siam	Rk	GM	Rk	Sigm	Rk	HM	Rk	Sihm	Rk
RD 2552	9	6	6	6	7	8	7	35.59	5	47.18	5	35.30	5	51.78	5	34.99	5	54.43	4
K1055	12	11	11	12	12	12	12	34.21	6	0.00	6	33.12	6	0.00	6	32.21	6	0.00	6
HUB113	5	4	4	4	3	3	3	40.27	2	85.83	1	39.71	2	83.28	1	39.20	2	81.36	1
RD2969	5	7	7	7	7	8	8	36.59	4	54.99	4	35.89	4	55.35	4	35.12	4	54.41	5
DWRB137	6	7	7	6	6	6	6	41.60	1	70.83	2	41.55	1	70.83	2	41.51	1	70.83	2
K508	5	7	7	7	7	5	6	39.15	3	63.52	3	38.83	3	64.04	3	38.50	3	64.01	3

SI am, SI g, SI hm = Superiority index as per arithmetic, Geometric, Harmonic mean; Rk = Rank of genotypes

RD2552 identified by MASV measure (Ajay *et al.*, 2020). Measure W1 favoured K1055, DWRB137 while as per W2, identified genotypes were K1055, DWRB137. Lower values of WAASB anticipated the stable nature of K1055, DWRB137 genotypes as for considered locations of the zone at the same time maximum deviation

Table 4 : Loadings of measures as per two Principal Components 2018-19

Measure	PC1	PC2
IPCA1	0.2433	-0.0162
MASV1	0.2739	0.0212
MASV	0.2589	0.0889
Za	0.2220	0.2634
EV	0.1870	0.2480
SIPC	0.1983	0.3046
ASTAB	0.2655	0.0909
WAASB	0.2431	0.2081
W1	0.2433	-0.0162
W2	0.2576	0.0836
Varanasi	0.0211	0.4350
Faizabad	-0.1747	0.2525
Kanpur	0.0737	-0.1485
Ranchi	-0.2371	0.1620
Sabour	0.0692	0.3084
Mean	-0.1201	0.3965
Siam	-0.2293	0.2329
Sigm	-0.2354	0.2250
Sihm	-0.2374	0.2222
84.70	62.83	21.86

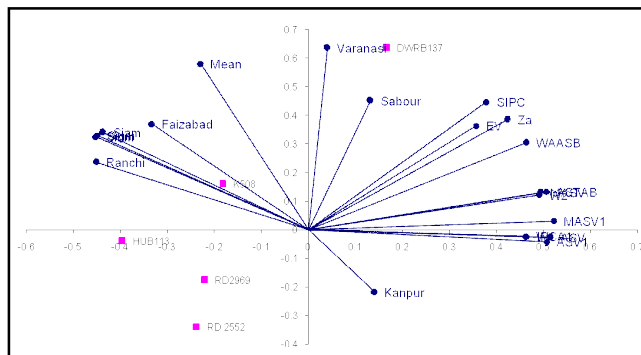


Fig. 1: Biplot analysis of superiority index and other measures of barley genotypes 2018-19

from the average performance across environments obtained by RD 2552 (Olivoto *et al.*, 2019).

Second year of study 2019-20 :

Minimum value of absolute IPCA1 expressed by KB1815, DWRB213, RD3021 and higher value achieved by K603, PL918 (Table 8). Stable behaviour of the genotypes HUB69 followed by NDB1748, KB1815 as per low values of EV and maximum value possessed by K603, PL918 genotype. SIPC ranked KB1815, followed by KB1830, HUB69 as of stable nature, whereas K 603, PL918 would be of least stable type. Za measure revealed the preferences for KB1815, KB1830 and HUB69 as genotypes with descending order of stability, whereas K603, PL918 genotype with the least stability. ASTAB values ranked HUB69, KB1815 and RD3019 as stable genotypes and K603, PL918 was least stable in this study. MASV1 showed the desirability for

Table 5: AMMI analysis and percentage contribution of significant interaction principal components (2019-20)

Source of variation	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	119	204.15	***	76.874		
Genotype (G)	14	237.83	***	10.536		
Environment (E)	7	1675.30	***	37.109		
GxE interaction	98	94.26	***	29.229		
IPC1	20	252.63	***		54.70	54.70
IPC2	18	80.55	***		15.70	70.39
IPC3	16	79.05	*		13.69	84.09
IPC4	14	55.16			8.36	92.45
IPC5	12	27.75			3.60	96.05
IPC6	10	24.29			2.63	98.68
Residual	8	15.21				
Error	240	30.45				
Total	359	88.03				

genotypes, Lakhan, KB1815 and HUB69 while MASV selected HUB69, RD3020, KB1815 genotypes. Ranks of W1 favoured K603, PL918, PL925 while as per W2, identified genotypes were PL925, PL918, K603, while W3 chose K603, PL918, PL925 whereas values of measure W4 settled for K603, PL918, PL925. Genotypes K603, PL918, PL925 had pointed out by W5 measure. As per ranks of WAASB measure, selected genotypes were K603, PL918, PL925 as for considered locations of the zone at the same time maximum deviation from

the average performance across environments obtained by KB1815, KB1830.

Superiority indexes as per AMMI and BLUP : Barley genotypes:

First year of study 2018-19 :

Mean yield of genotypes based on BLUP values favoured DWRB137, HUB113 whereas DWRB137, HUB113 selected by Geometric adaptability index while Harmonic mean of genotypic values pointed for

Table 6 : Modified 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	W5	WAASB
NDB1748	1.457	6.297	4.062	14.866	0.019	4.353	37.126	1.4573	0.6254	1.2216	1.1761	1.1108	1.0747
KB1830	0.423	4.380	3.585	10.365	0.022	4.104	30.891	0.4229	1.3223	0.6383	0.7010	0.6721	0.6586
RD3020	1.026	4.519	3.237	12.880	0.025	4.533	29.299	1.0259	1.2861	1.0023	0.9168	0.8709	0.8868
DWRB213	0.309	5.292	4.364	13.963	0.043	6.443	42.600	0.3090	0.8439	0.7394	0.7947	0.8055	0.8189
Lakhan	0.431	4.037	3.526	11.404	0.023	4.423	33.588	0.4312	1.4325	0.8037	0.7759	0.7341	0.7287
RD3022	1.626	6.629	4.313	16.954	0.037	5.988	43.236	1.6259	0.9616	1.2798	1.1754	1.1902	1.1841
HUB69	0.680	4.272	3.064	10.499	0.018	4.175	18.268	0.6805	0.5132	0.6209	0.6826	0.6932	0.6806
PL925	2.291	8.830	5.508	22.357	0.040	6.809	77.632	2.2913	2.1240	1.8763	1.7295	1.6560	1.6273
HUB270	1.438	6.975	5.047	19.418	0.040	6.685	60.390	1.4377	1.4429	1.5452	1.3902	1.3747	1.3322
KB1815	0.138	4.095	3.485	8.147	0.022	3.628	26.834	0.1377	0.2132	0.5099	0.4703	0.4912	0.4803
RD3019	0.863	4.915	3.770	10.840	0.037	4.525	27.907	0.8634	0.3277	0.6550	0.6482	0.7218	0.7089
K 603	3.408	12.871	7.537	30.230	0.056	8.603	132.953	3.4079	1.6862	2.5664	2.4071	2.3074	2.2402
PL918	3.236	12.258	7.093	26.599	0.044	6.872	115.454	3.2357	2.0538	2.3045	2.2336	2.1139	2.0236
KB1832	1.997	8.298	5.188	20.923	0.041	6.700	62.491	1.9970	1.3153	1.6049	1.5820	1.4953	1.4856
RD3021	0.378	5.334	4.010	11.261	0.029	4.950	30.545	0.3780	0.8065	0.5342	0.6901	0.6822	0.6788

Table 7 : Superiority index measures and corresponding ranking of genotypes 2019-20

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	Mean	Rk	Slam	Rk	GM	Rk	Slgm	Rk	HM	Rk	Slhm	Rk
NDB1748	19	11	13	18	17	18	17	28.53	9	54.21	7	27.78	8	58.01	7	27.02	9	62.19	7
KB1830	8	8	6	6	10	8	9	32.91	4	91.10	3	31.62	5	87.17	4	30.40	5	85.37	4
RD3020	13	11	12	12	9	10	7	32.31	5	82.66	5	31.27	6	80.72	5	30.30	6	80.39	5
DWRB213	4	15	12	10	11	9	12	33.69	2	93.00	2	33.14	2	92.28	2	32.68	2	92.24	2
Lakhan	6	6	6	7	8	2	5	33.73	1	95.06	1	33.32	1	95.06	1	32.92	1	95.06	1
RD3022	19	17	17	18	18	18	17	28.65	8	52.81	9	27.11	10	52.14	9	25.55	10	53.53	9
HUB69	12	7	9	9	7	9	7	32.29	6	86.62	4	31.70	4	87.20	3	31.18	3	88.36	3
PL925	28	26	28	28	28	28	28	23.78	15	12.19	15	22.52	13	18.36	14	21.23	11	25.68	14
HUB270	19	20	21	21	21	21	21	28.27	10	47.41	10	27.72	9	52.56	8	27.18	8	57.78	8
KB1815	12	14	12	12	13	13	14	26.65	11	53.73	8	23.25	12	45.16	10	19.12	13	39.21	12
RD3019	19	20	18	16	15	18	18	25.95	12	44.63	11	23.61	11	42.57	11	20.69	12	41.60	11
K 603	22	22	22	22	22	22	22	29.20	7	35.41	13	28.44	7	38.41	12	27.71	7	42.08	10
PL918	28	28	28	28	28	28	28	25.06	14	12.68	14	21.39	15	4.31	15	18.16	15	4.31	15
KB1832	15	15	15	15	15	15	15	33.30	3	77.20	6	32.08	3	73.24	6	30.98	4	71.49	6
RD3021	16	20	21	18	18	21	20	25.13	13	39.88	12	22.05	14	34.63	13	19.10	14	35.17	13

DWRB137, HUB113 as suitable genotypes as far as considered locations are concerned (Table 3). Higher yield may not be a desirable selection criterion as high yielders may not be stable genotypes, that is why simultaneous use of yield and stability in a single measure had been recommended (Kang 1993 and Farshadfar *et al.*, 2008). Simultaneous Selection Index or genotype stability index (GSI) or yield stability index (YSI) (Farshadfar *et al.*, 2011) was considered the ranks of stability along with mean yield of genotypes. Least ranks for IPCA1 measure exhibited by HUB113, RD2969 were considered as stable with high yield, whereas high values suggested as least stable yield for K1055 genotype (Table 7). EV measure identified HUB113 and RD2552 whereas SPIC favoured HUB113 and RD2552 genotypes. Genotypes HUB113 and DWRB137 possessed lower value of Za measure. ASTAB measure achieved the desirable lower values for HUB113, DWRB137. Lower ranks MASV1 and MASV found HUB113, K508 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 HUB113, DWRB137 as of stable performance with high yield. Least ranked of Sigm and SIhm measures pointed for HUB113, DWRB137 as desirable barley genotypes.

Second year of study 2019-20 :

Higher average yield of genotypes as per BLUP values favoured Lakhan, DWRB213, KB1830 where Geometric adaptability index pointed for Lakhan, DWRB213, KB1832 while Harmonic mean of genotypic values pointed for Lakhan, DWRB213, HUB69 as suitable genotypes as far as considered locations. Least ranks for Simultaneous Selection Index for IPCA1 measure exhibited by DWRB213, Lakhan, KB1830 were considered as stable with high yield, whereas high values suggested as least stable yield for PL918, PL925 genotype (Table 7). EV measure identified Lakhan HUB69 and KB1830 whereas SPIC favoured KB1830, Lakhan and HUB69. Genotypes KB1830, Lakhan and HUB69 possessed lower value of Za measure. Desirable lower values of ASTAB measure achieved by HUB69, Lakhan, RD3020. Ranks of composite measure MASV1 and MASV found Lakhan HUB69, KB1830 genotypes would be of choice for these locations. Superiority index with assigned weights for yield and stability found Lakhan, DWRB213, KB1830 as of stable performance with high yield. Least ranks of Lakhan, DWRB213, HUB69

pointed as desirable genotypes by Sigm and SIhm measures more over largest rank of PL918 made unsuitable barley genotype.

Biplot graphical analysis :

First year of study 2018-19 :

Two significant PCAs accounted for 84.7 % of variation of the studied measures (Bocianowski *et al.*, 2019). Loadings of studied measures as per first two significant principal components were reflected in Table 4. Biplot graphical analysis observed largest cluster comprised of MASV1 with ASTAB, EV, SIPC, Za, W2, WAASB and MASV measures. Measure IPCA1 showed altogether behaviour and observed as an outlier. SI corresponding to yield based measures grouped. Angles among the measures depict the degree of association as acute angles depict strong relationships

Table 8 : Loadings of measures as per two Principal Components 2019-20

Measure	PC1	PC2
IPCA1	0.2522	0.0771
MASV1	0.2574	0.0627
MASV	0.2533	0.0678
Za	0.2524	0.1211
EV	0.2110	0.0620
SIPC	0.2252	0.1369
ASTAB	0.2500	0.0943
WAASB	0.2539	0.1116
W1	0.2522	0.0771
W2	0.2486	0.0954
W3	0.2512	0.1170
W4	0.2523	0.1143
W5	0.2547	0.1077
Kanpur	-0.0283	-0.1142
Saini	-0.0738	-0.2190
Varanasi	-0.0257	0.3371
Faizabad	-0.0771	0.2422
Chianki	-0.1686	0.2062
Ranchi	-0.1098	0.1790
Pusa	-0.0625	0.3551
Sabour	-0.0578	0.3560
Mean	-0.1392	0.3337
Siam	-0.2116	0.2322
Sigm	-0.2030	0.2623
SIhm	-0.1925	0.2805
79.30	57.18	22.12

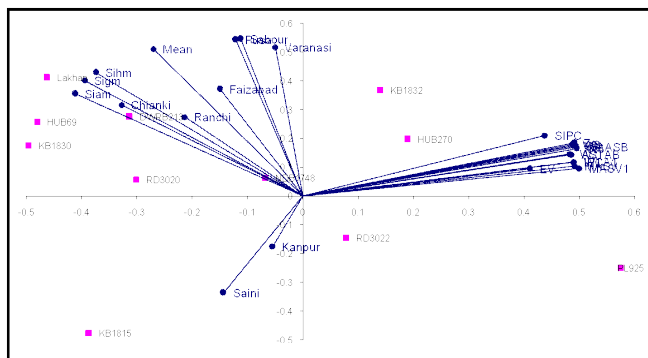


Fig. 2: Biplot analysis of stability and adaptability measures of barley genotypes 2019-20

of Mean with SI measures. Right angles between group of AMMI based and Superiority index measures showed no association regarding the performance of genotypes.

Second year of study 2019-20 :

Loadings of stability, adaptability measures as per first two significant principal components were reflected in Table 8. Biplot graphical analysis based two significant PCAs accounted for 79.3 % of variation of the measures. Two clusters of measures observed. AMMI based measures grouped together and yield joined hands with superiority indexes of genotypes. Acute angle of mean and SI measures depict the degree of strong association. Right angles between AMMI based and superiority indexes highlighted the difference of opinion regarding stable high yield of feed barley genotypes as far this zone is concerned.

Conclusion:

Simultaneous utilization of AMMI and BLUP of genotypes be more appropriate to recommend high-yielder stable barley genotypes. Superiority indexes would increase the reliability of multi-locations trials as major features of AMMI and BLUP had been combined. Option of assigning variable weights to the yield and stable performance would help the researches to set their crop improvement targets.

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