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Research Article

Wheat genotypes as assessed by Additive main & multiplicative interactions (AMMI) and Best linear unbiased prediction (BLUP) for stability analysis under rainfed timely sown trials in Northern Hills Zone of India

Ajay Verma*
ICAR-Indian Institute of Wheat & Barley Research, Karnal-132001 (Haryana), India
G. P. Singh
ICAR-Indian Institute of Wheat & Barley Research, Karnal-132001 (Haryana), India

*Corresponding author. Email: verma.dwr@gmail.com

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Abstract

Stability analysis of wheat genotypes under rainfed timely sown trials in Northern Hills Zone of India by Additive main & multiplicative interactions (AMMI) analysis observed highly significant effects of the environment, GxE interaction and genotypes during 2018-19 and 2019-20. The ranking of genotypes had altered with utilization of more number of IPCA's in AMMI and WAASB measures. Environments contributed about 53%, GxE interaction accounted for 30.5% and Genotypes explained only 5.4% of the total sum of squares due to treatments in the first year. Wheat genotypes HS668, VL2035, VL2036 , HS562 had been selected by Analytic measures of adaptability and Superiority indexes. Different quadrants comprised of a cluster of arithmetic, geometric, harmonic means along with corresponding adaptability measures. Superiority Indexes considering averages grouped separately. This group maintained the right angles with a group of MASV & MASV1 measures. Clustering of Adaptability measures as per arithmetic, geometric and harmonic means placed in a quadrant. Second-year reflected VL2041, HS675, HS676 & HS562, HPW471 genotypes selected by adaptability and superiority indexes. About 68% of the total variation with 38.4% and 30.2% contributions by PC1 & PC2. Adaptability measures maintained the right angle with other stability measures, with the exception of Superiority indexes. There is an additional advantage with these measures to assign variable weights to the yield and stability as per the goal of breeding trials. These indexes have the potential to provide reliable estimates of genotypes in future studies as they are considered more number of significant IPCA's in biplots.

Keywords: AMMI model, Biplot analysis, MASV, SI, WAASB

INTRODUCTION

Large number of stability analysis measures have been developed to model GxE interactions efficiently (Mohammadi *et al*., 2015; Bocianowski *et al*., 2019; Agahi *et al*., 2020). AMMI based stability measures evaluate the stability of genotypes after reduction of the noise from the GxE interaction effects (Gauch 2013; Oyekunle *et al*., 2017; Ajay *et al*., 2020). Researchers have introduced various selection criteria for the simultaneous utilization of yield and stability of evaluated genotypes as stable varieties are generally not highly productive ((Kang, 1993; Rao and Prabhakaran 2005; Farshadfar, 2008; Farshadfar *et al*., 2011). BLUP and AMMI approach utilized to distinguish the useful pattern from the residual noise in interactions analysis procedures (Piepho *et al*., 2008; Mendas *et al*., 2012). The benefits of two important techniques AMMI and BLUP amalgamated into a Superiority Index measure for stability and adaptability of genotypes (Olivoto *et al*., 2019). The present study had assessed the stability and adaptability behaviour of wheat genotypes as per AMMI and BLUP of genotypes evaluated under rainfed timely sown trials in the Northern Hills Zone of India during 2018-19 and 2019-20.

MATERIALS AND METHODS

Northern hills zone comprised of J&K (except Jammu and Kathua distt.), Himachal Pradesh (except Una and

Paonta Valley), Uttarakhand (except Tarai area), Sikkim, hills of West Bengal and North-Eastern states. Sixteen advanced wheat genotypes at eight locations and sixteen genotypes at nine locations were evaluated under field trials at the northern hills zone during 2018-19 and 2019-20 cropping seasons. Field trials were conducted at research centers of All India Coordinated Wheat & Barley Improvement Program (AICWBP) in randomized complete block designs with three replications. Recommended agronomic practices were followed to harvest good yield. Details of locations along with parentage of evaluated wheat genotypes are mentioned in Tables 1 and 2 for ready reference.

Stability measure as a Weighted Average of Absolute Scores calculated as

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

$WAASB_i$ 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 weights to yield and stability measure (WAASB) to select genotypes that combine high performance and stability as

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

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 the WAASB values for *i*th genotype. SI superiority index for the *i*th genotype that weighted between yield and stability, and θY and θS were the weights for yield and stability assumed to be of order 65 and 35 respectively in this study, AMMISOFT version 1.0, available at https://scs.cals.cornell.edu/people/ hugh-gauch/ utilized for AMMI analysis of wheat genotypes evaluated under multi-location trials in the Peninsular Zone and further analysis was carried out by SAS software version 9.3. Stability measures had been compared with recent analytic measures of adaptability calculated as the relative performance of genetic values (PRVG) and harmonic mean based measure of the relative performance of the genotypic values (MHPRVG) for the simultaneous analysis of stability, adaptability, and yield (Mendes *et al.*, 2012).

RESULTS AND DISCUSSION

First-year (2018-19)

The present study observed that Environment (E), GxE interaction, and genotypes (G) effects were highly significant (P>0.001) for wheat genotypes evaluated under multi-location trials as mentioned by the AMMI analysis. Analysis observed the greater contribution of environments, GxE interactions, and genotypes to the total sum of squares (SS) compared to the residual effects. Further SS attributable to GxE interactions was partitioned as attributed to GxE interactions Signal and GxE interactions Noise. AMMI analysis is appropriate for data sets where-in SS due to were of magnitude at least of due to additive genotype main effects (Gauch, 2013). The SS for GxE interactions Signal was higher than genotype main effects, indicating the appropriateness of AMMI analysis. The environment significantly explained about 53% , GxE interaction accounted for

Mohamadi and Amri (2008)	Geometric Adaptability Index	$GAI = \sqrt[n]{\prod_{k=1}^{n} \bar{X}_k}$ …… Eq.1
Zali *et al*., (2012)	Modified AMMI stability Value	$MASV = \sqrt{\sum_{n=1}^{N-1} \frac{SSIPC_n}{SSIPC_{n+1}} (PC_n)^2 + (PC_{n+1})^2}$ …….Eq.2
Ajay *et al*. (2019)	MASV1	$MASV1 = \sqrt{\sum_{n=1}^{N-1} (\frac{SSIPC_n}{SSIPC_{n+1}} PC_n)^2 + (PC_{n+1})^2}$ ….Eq.3
Resende and Durate (2007)	Relative performance of genotypic values across environments	$PRVG_{ij} = VG_{ij} / VG_i$ …….Eq.4
Resende and Durate (2007)	Harmonic mean of Relative performance of genotypic values	$MHPRVG_{i.}$ = Number of environments / $\sum_{j=1}^{k} \frac{1}{PRVG_{ij}}$ …..Eq.5
Oliveto *et al*. (2019)	Superiority Index	$SI = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(\theta_Y + \theta_S)}$ ….Eq.6

Table 1. Details of locations and parentage of evaluated wheat genotypes 2018-19.

Code	Genotype	Parentage	Locations	Latitude	Longitude	Mean sea level
G 1	HPW 462	(VL804/PBW498)	Dhaulakuan	28°59 N	77°16 E	468
G 2	HPW 466	(PASTOR/HXL7573/2*BAU/3/SOKOLL/WBLL1)	Shimla	31°10' N	77°17'E	2276
G 3	VL 2038	(CHINA84-400022/PBW599)	Malan	32°08' N	76°35'E	846
G 4	VL 2037	(HS485/RAJ4174//HS485-5)	Bajaura	31°50'N	77°9'E	1103.85
G 5	HS 507	(KAUZ/MYNA/VUL//BUC/FLK/4/MILAN)	Wadura	21° 18' N	77° 41' E	508
G 6	UP 3038	(AKAW4510/AVOCET)	Khudwani	33° 70' N	75°10' E	1590
G 7	VL 2035	(PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07/4/BERKUT//PBW343*2/KUKUNA	Almora	29° 35' N	79° 39'E	1610
G 8	HS 667	(HPW251/FLW3//HS431)	Ranichauri	28° 43' N	81°02' E	2200
G 9	HS 668	(VL906/FLW13)				
G 10	HS 669	(VL907/VL876)				
G 11	UP 3039	(HUW640/LBPY06-15(SERI/DUCULA/PBW343)				
G 12	HS 562	(OASIS/SKUAZ//4*BCN/3/2*PASTOR)				
G 13	VL 2036	(SW89.5277/BORL95//SKAUZ/3/PRL/2*PASTOR/4/HEILO/5/WHEAR/SOKOLL)				
G 14	HPW 464	(Raj 3765/WR 251//HW 2045/PBW 493)				
G 15	HPW 463	(HPW155/HW4024 (P6)				
G 16	HD 3340	(DPW621-50/DW1293//DW1285)				

30.5% and Genotypes explained only 5.4% of the total sum of squares (Table 3). First six significant multiplicative terms explained 98.7 % and the remaining 1.3% residual was discarded (Oyekunle *et al*., 2017).

Ranking of genotypes vis-à-vis number of IPCA's

The stability or adaptability of genotypes over environments had been assessed by their IPCA scores in the AMMI analysis. More the IPCA scores reflected the specific adaptation of genotype to certain locations. Lower the IPCA scores converged to zero, indicating the more stable or adapted genotypes to all the locations. The ranking of genotypes as per the absolute value of IPCA-1 measure were VL2038, HD3340, HPW463, HPW 462 (Table 4). While for IPCA-2, genotypes HPW462, UP3039, VL2036 would be of choice. Values of IPCA-3 favoured HD 3340, HS 562, VL 2038 wheat genotypes. As per IPCA-4, VL 2036, VL 2035, VL 2038 genotypes would be of stable performance. General adaptation of HS507, UP3039, HS667, and specific adaptation of VL2037, VL2038 genotypes pointed by IPCA-5 measure. Genotypes HPW464, HS562, HS667 for the general along with HS669, HS668 for specific locations as identified by absolute values of IPCA-6. Analytic measures of adaptability MASV and MASV1 considered all significant six IPCAs of the analysis. Values of MASV pointed towards genotypes VL2037, HPW466, and HPW463 express stable yield whereas genotypes HPW463, HPW466 & VL2037 be of stable performance MASV1 measure respectively (Ajay *et al* 2019).

Change in the ranking of genotypes with the utilization of numbers of significant IPCA's in the WAASB estimation had been also assessed. The genotypes were ranked based on 1, 2,...,*6* IPCA in the WAASB estimation. The genotype with the smallest value of WAASB was ranked with first-order. Genotypes preferences varied as VL2036, UP3039, HS668, VL2037 based on W1 values whereas VL2036, UP3039, VL2035, HS668 as per W2 values while UP 3039, VL2035, VL2037, HS668 by values of W3 (Table 5). Genotypes UP3039, VL2035, VL2036, VL2037 pointed by W4; W5 favoured UP3039, VL2035, VL2036, HS668, and lastly by W6 the genotypes of choice would be UP3039, VL2035, VL2036, HS668. Stability measure WAASB based on all six significant IPCA's settled for UP3039, VL2035, VL2036, HS668 genotypes for considered locations of the zone for stable high yield. The genotypes ranking had been altered by the number of significant IPCAs included in the WAASB calculations. This reinforced the benefits of using the WAASB index since it captured all the variations of IPCAs to compute the stability performance (Olivoto *et al*., 2019).

Productive and broadly adapted genotypes by AMMI + BLUP tools

An average yield of genotypes as per BLUP values selected HS668, HS669, HS562, VL2036 wheat geno-

Table 2. Details of locations and parentage of evaluated wheat genotypes 2019-20.

Code	Genotype	Parentage	Locations	Latitude	Longitude	Mean sea level
G 1	HS507	(KAUZ/MYNA/VUL//BUC/FLK/4/MILAN)	Dhaulakuan	28°59 N	77°16 E	468
G 2	SKW356	(SEL-VL968)	Shimla	31°10 ' N	77°17'E	2276
G 3	VL2042	(TX71A983.4/TX69D4812//PYN/3/VPM/MOS83.11.4-8//PEW/HSB3177 (Yr15+Yr24)/6*Avocet//2*BAXTER/FLW13	Malan	32°08 ' N	76°35'E	846
G 4	HPW471	(HPW236/VL900)	Bajaura	31°50'N	77°9'E	1103.85
G 5	HS675	(HS240*2FLW20//HS240*2/FLW13)	Wadura	21° 18' N	77° 41' E	508
G 6	HPW472	(HPW155/HD29)	Khudwani	33° 70' N	75°10' E	1590
G 7	VL2039	(RL6043/4*NAC//PASTOR/3/BABAX/VL892)	Almora	29° 35 ' N	79° 39 'E	1610
G 8	HS677	(ID8900994W/VEE/3/CHEN/AES/HD2932)	Ranichauri	28° 43 ' N	81°02 ' E	2200
G 9	HS676	(VL907/DL460)	Umiam	25°53' N	91°27' E	
G 10	UP3064	(RAJ3765/HD3121)				
G 11	HS678	(VL907/HD2997)				
G 12	HS562	(OASIS/SKUAZ//4*BCN/3/2*PASTOR)				
G 13	HPW470	(NAC/TH.AC//3*MIRLO/BUC/4PASTOR)				
G 14	HPW469	(HPW89/VL867)				
G 15	VL2041	(NESSER/SAULSKU32/MACS6240//HS507)				
G 16	VL2040	(17thDSBWYT99(SERI.1B//KAUZ/HEVO/3/AMAD/4/PYN/BAU//MILAN/5/ OPATA/ RAYON//KAUZ)				

Table 3. AMMI analysis of wheat genotypes evaluated under rainfed timely sown trials during 2018-19 & 2019-20.

Source	Degree of Freedom 18-19	Degree of Freedom 19-20	Mean Sum of Squares 18-19	Mean Sum of Squares 19-20	Level of Significance 18-19	Level of Significance 19-20
Treatments	127	143	242.41	218.91	.0000000 ***	.0000000 ***
Genotypes (G)	15	15	124.66	185.53	.0000000 ***	.0000000 ***
Environments (E)	7	8	2623.83	2167.13	.0000000 ***	.0000000 ***
Interactions GxE	105	120	100.47	93.21	.0000000 ***	.0000000 ***
IPC1	21	22	192.74	169.69	.0000000 ***	.0000000 ***
IPC2	19	20	125.04	164.26	.0000000 ***	.0000000 ***
IPC3	17	18	108.06	104.59	.0000000 ***	.0000000 ***
IPC4	15	16	69.20	77.15	.0000000 ***	.0000000 ***
IPC5	13	14	51.74	33.00	.0000000 ***	.0000050 ***
IPC6	11	12	40.62	27.24	.0000422 ***	.0022316 **
		10		23.61		0.1065
Residual	9	8	14.67	3.00	0.1609	0.9657
Error	384	432	10.05	10.01		
Total	511	575	67.80	61.96		

types is given in Table 6. This measure was simple but not exploited the full information contained in the dataset. Geometric mean was suggested to evaluate the adaptability of genotypes. Geometric mean observed HS668, VL2036, HS562, VL2035 were of top-ranked genotypes. As Resende (2007) proposed, a method to rank genotypes considering the yield and stability, simultaneously is the harmonic mean of genetic values (HMGV). In the context of mixed models, the Harmonic Mean of Genotypic Values were calculated as genotypes with greater values would be recommended. Harmonic Mean of yield expressed higher values for

Table 4. Modified AMMI stability values as per significant IPCA's 2018-19.

Genotype	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	IPCA6	MASV1	MASV	R_{IPCA1}	R_{MASV}	R_{MASV1}
HPW 462	-2.027	0.249	1.608	-0.684	-1.015	0.401	5.281	4.271	4	7	5
HPW 466	-1.355	-1.601	-1.116	-1.940	0.477	-0.302	5.558	4.763	6	2	2
VL 2038	2.506	0.744	0.332	-0.261	-1.566	0.645	5.368	4.360	1	6	4
VL 2037	0.385	1.165	0.460	-0.918	2.521	1.083	5.450	4.815	13	1	3
HS 507	1.249	-2.793	0.435	0.522	0.035	0.711	5.253	4.720	8	4	6
UP 3038	0.910	-1.310	1.888	-1.084	-0.662	-0.685	5.252	4.446	11	5	7
VL 2035	0.478	-0.612	0.622	-0.184	0.703	-0.790	2.370	2.066	12	16	16
HS 667	1.657	2.070	0.550	-0.430	-0.140	0.281	4.630	3.992	5	9	11
HS 668	-0.333	0.979	0.960	0.720	0.931	-1.338	3.614	3.197	14	13	14
HS 669	1.091	0.649	-1.798	0.360	-0.312	-1.829	4.695	3.983	10	11	9
UP 3039	0.049	-0.278	-0.855	0.888	-0.070	0.940	2.607	2.260	15	15	15
HS 562	1.142	-0.625	-0.303	1.648	0.525	-0.125	3.913	3.314	9	12	13
VL 2036	-0.033	-0.299	-2.438	-0.040	-0.194	0.834	5.062	4.179	16	8	8
HPW 464	-1.293	1.697	-1.009	-0.947	-0.740	0.069	4.646	3.991	7	10	10
HPW 463	-2.197	0.632	0.910	2.038	-0.259	0.446	5.742	4.729	3	3	1
HD 3340	-2.229	-0.667	-0.248	0.313	-0.234	-0.341	4.060	3.187	2	14	12

Table 5. Weighted average of absolute scores and ranks of wheat genotypes 2018-19.

Genotype	W1	W2	W3	W4	W5	W6	WAASB	R_{W1}	R_{W2}	R_{W3}	R_{W4}	R_{W5}	R_{W6}	R_{WAASB}
HPW 462	2.03	1.33	1.40	1.30	1.27	1.21	1.21	13	9	12	12	13	13	13
HPW 466	1.35	1.45	1.37	1.45	1.35	1.28	1.28	11	10	11	15	15	15	15
VL 2038	2.51	1.81	1.44	1.27	1.30	1.26	1.26	16	14	14	10	14	14	14
VL 2037	0.38	0.69	0.63	0.67	0.85	0.86	0.86	4	5	3	4	5	6	6
HS 507	1.25	1.86	1.50	1.36	1.23	1.20	1.20	9	16	15	14	12	12	12
UP 3038	0.91	1.07	1.28	1.25	1.19	1.16	1.16	6	8	9	9	9	10	10
VL 2035	0.48	0.53	0.55	0.50	0.52	0.54	0.54	5	3	2	2	2	2	2
HS 667	1.66	1.82	1.50	1.35	1.23	1.17	1.17	12	15	16	13	11	11	11
HS 668	0.33	0.59	0.68	0.69	0.71	0.75	0.75	3	4	4	5	4	4	4
HS 669	1.09	0.92	1.14	1.03	0.96	1.02	1.02	7	6	7	7	7	8	8
UP 3039	0.05	0.14	0.32	0.40	0.37	0.41	0.41	2	2	1	1	1	1	1
HS 562	1.14	0.94	0.78	0.90	0.86	0.81	0.81	8	7	6	6	6	5	5
VL 2036	0.03	0.14	0.72	0.63	0.59	0.60	0.60	1	1	5	3	3	3	3
HPW 464	1.29	1.45	1.34	1.28	1.23	1.15	1.15	10	11	10	11	10	9	9
HPW 463	2.20	1.58	1.41	1.50	1.38	1.32	1.32	14	12	13	16	16	16	16
HD 3340	2.23	1.61	1.27	1.13	1.05	1.00	1.00	15	13	8	8	8	7	7

R_{W1}, R_{W2}, R_{W3}, R_{W4}, R_{W5}, R_{W6}, R_{WAASB} = Rank of genotypes as per number of IPCA's in WAASB values

HS668, HS562, HS 669, VL2035 genotypes.

Moreover, the Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) proposed by Resende (2007) was similar to the methods of Lin and Binns (1988) and Annicchiarico (1992). The genotypes could be simultaneously sorted by yield and stability using the harmonic means of the yield and genotypic performance with smaller the standard deviation among the locations would be recommended/identified values of HMRPGV ranked HS668, HS669, HS562, VL2035 the performance of the genotypes among the locations. The relative performance of genetic values (RPGV) overcrop years was recommended while simultaneously considering the yield and adaptability. The relative performance of Genotypic Values had settled for HS668, HS669, HS562, VL2036 wheat genotypes.

While assigning 65 and 35 weights to yield and stability, the Superiority index pointed out that HS 668, HS669, HS562, VL2035 genotypes would maintain high yield and stable performance. SI considered GAI

Table 6. Superiority index and analytic adaptability measures based on BLUP's of genotypes 2018-19.

Genotype	AMu	Rk	SI au	Rk	GMu	Rk	SI gu	Rk	HMu	Rk	SI hu	Rk	RPGVu	Rk	MHRPGVu	Rk
HPW 462	29.82	14	18.91	14	29.09	14	19.82	14	28.35	13	22.29	13	0.940	14	0.914	14
HPW 466	31.34	10	32.87	11	30.14	11	27.50	11	28.89	11	24.22	12	0.975	11	0.946	11
VL 2038	33.21	5	54.45	8	31.88	7	45.71	8	30.50	9	39.13	9	1.031	7	1.004	7
VL 2037	33.17	6	69.11	7	32.39	6	65.82	7	31.68	5	64.33	6	1.041	5	1.025	6
HS 507	30.83	13	30.53	12	29.48	13	24.17	13	27.78	14	17.90	14	0.961	13	0.918	13
UP 3038	31.91	9	43.95	9	31.29	9	43.61	9	30.67	7	44.32	8	1.007	8	0.988	9
VL 2035	32.87	7	78.32	4	32.47	4	79.12	2	32.08	4	80.26	2	1.038	6	1.033	4
HS 667	31.09	11	34.56	10	29.96	12	30.10	10	28.75	12	27.37	11	0.970	12	0.940	12
HS 668	34.38	1	86.70	1	34.08	1	86.70	1	33.78	1	86.70	1	1.094	1	1.080	1
HS 669	34.07	2	72.85	6	33.20	2	67.67	6	32.28	3	63.39	7	1.065	2	1.052	2
UP 3039	32.34	8	77.57	5	31.49	8	74.46	5	30.60	8	72.59	4	1.007	9	1.001	8
HS 562	33.85	3	78.53	3	33.17	3	75.46	4	32.43	2	72.81	3	1.064	3	1.051	3
VL 2036	33.78	4	85.87	2	32.46	5	76.58	3	30.99	6	68.47	5	1.044	4	1.025	5
HPW 464	28.77	15	9.69	16	27.53	15	6.76	16	26.23	16	6.32	16	0.892	15	0.862	15
HPW 463	30.88	12	26.53	13	30.21	10	26.83	12	29.52	10	28.29	10	0.979	10	0.947	10
HD 3340	28.47	16	12.20	15	27.49	16	12.20	15	26.43	15	13.92	15	0.891	16	0.858	16

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 7. Loadings of measures as per two principal components 2018-19.

Measure	PC1	PC2
IPCA1	0.0972	-0.2907
IPCA2	0.0083	-0.0480
IPCA3	-0.0633	-0.1197
IPCA4	0.0783	0.0153
IPCA5	0.1381	0.0057
IPCA6	-0.0538	0.1050
MASV1	-0.1728	-0.3107
MASV	-0.1607	-0.3240
W1	-0.2212	-0.1059
W2	-0.2429	-0.1347
W3	-0.2524	-0.1737
W4	-0.2512	-0.1861
W5	-0.2488	-0.2209
W6	-0.2422	-0.2496
WAASB	-0.2422	-0.2496
AMu	0.2277	-0.2968
SI au	0.2653	-0.1191
GMu	0.2355	-0.2784
SI gu	0.2692	-0.0993
HMu	0.2367	-0.2542
SI hu	0.2696	-0.0769
RPGVu	0.2284	-0.3010
MHRPGVu	0.2403	-0.2603
% variance explained	57.83	14.33

and stability selected HS668, VL2035, VL2036, HS562 genotypes. The SI while using HM and stability favoured the same set of wheat genotypes HS668, VL2035, HS 562, UP 3039. Analytic adaptability measures RPGV and MHRPGV pointed out HS668, HS 669, HS562, VL2036, HS668, HS669, HS562, VL2035 genotypes would be more adaptable.

Biplot analysis of measures

The Principal components analysis was performed to study the relationships among the stability and adaptability measures based on BLUP of wheat genotypes. Loadings of the considered measures were tabulated as per the first two significant PC as explained 72.2% of the total variation in the original variables with respective contributions were 57.8 & 14.3 percent (Table 7). Four groups of measures were observed in graphical Biplot analysis. The smallest group comprised of MASV & MASV1 measures (Fig. 1). The nearby group clustered stability measures by utilizing the varying number of the interaction of principal components for calculation. Adaptability measures as per arithmetic, geometric and harmonic means and their corresponding values expressed bondage in a group placed in a different quadrant. However, this group maintained the right angle with stability measures. This quadrant also showed a cluster of Superiority indexes as per averages of the yield of wheat genotypes. Performance of genotypes would be different by Superiority indexes as compared to their behaviour as per values of MASV & MASV1 measures.

Second-year of study 2019-20

The AMMI analysis of variance of 16 wheat genotypes evaluated over nine locations revealed that 7.8 % of the total sum of squares (SS) was attributable to the genotypes (G), 48.6% to the environments (E), and 3.4% to GxE interaction effects (Table 3). Large SS due to E indicated that the locations were quite diverse induced

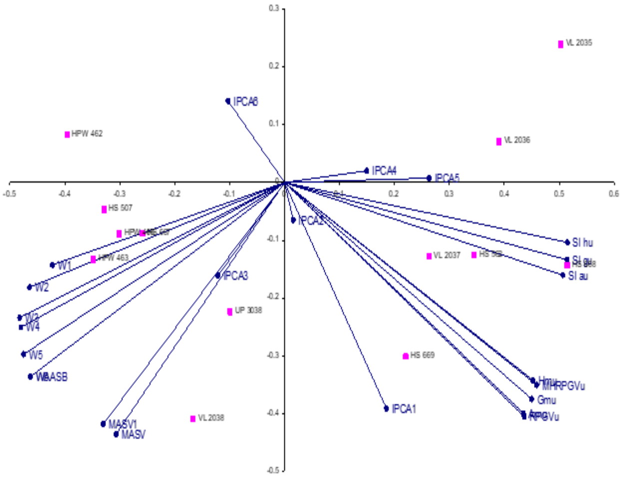

Fig. 1. *Biplot analysis of stability & adaptability measures of wheat genotypes 2018-19.*

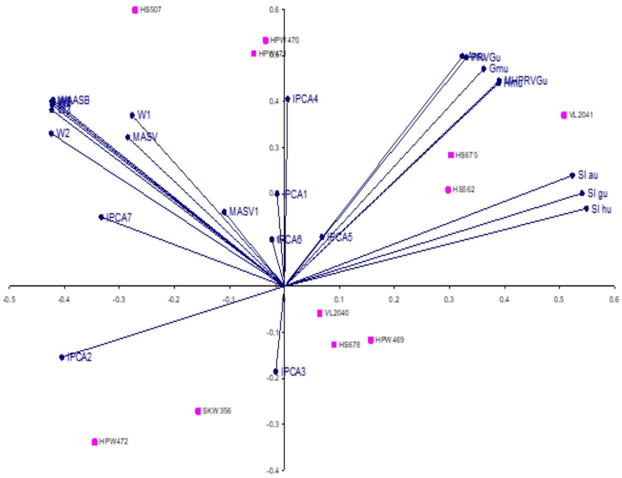

Fig. 2. *Biplot analysis of stability & adaptability measures of wheat genotypes 2019-20.*

Table 8. Modified AMMI stability values as per significant IPCA's 2019-20.

Genotype	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	IPCA6	IPCA7	MASV1	MASV	R $_{IPCA1}$	R $_{MASV1}$	R $_{MASV}$
HS507	-2.617	0.220	-1.903	2.230	-0.350	0.362	0.074	8.862	6.252	16	12	15
SKW356	-2.146	0.293	-0.027	-0.335	-1.198	0.327	1.019	5.506	3.761	13	3	3
VL2042	2.456	1.972	-0.708	0.150	-0.648	0.649	0.342	8.826	5.284	14	11	12
HPW471	2.549	-1.057	-0.752	-0.242	-0.279	0.330	0.899	6.321	4.307	15	5	6
HS675	0.897	1.471	-0.936	1.054	0.177	-0.042	-1.278	4.691	3.807	11	2	4
HPW472	0.496	2.214	-0.506	-0.407	1.209	0.278	0.105	5.607	4.299	4	4	5
VL2039	-0.849	2.483	1.391	-0.664	0.306	-0.880	0.621	10.770	5.830	10	13	14
HS677	-0.717	0.183	-0.327	-2.283	-0.316	-0.642	-0.357	7.664	4.334	6	8	7
HS676	-0.291	-0.459	0.113	0.464	-0.308	-0.856	-0.686	8.597	3.142	3	10	2
UP3064	0.078	-1.003	0.511	-0.371	-0.977	-0.204	-1.057	3.725	2.772	2	1	1
HS678	-0.795	0.327	2.574	0.414	0.097	0.349	-0.362	8.290	5.252	8	9	11
HS562	0.832	-1.061	1.520	0.298	0.193	1.130	-0.711	12.247	5.212	9	14	10
HPW470	1.394	-1.342	0.993	1.663	-0.160	-1.547	0.943	16.202	6.715	12	16	16
HPW469	0.062	-1.382	-1.634	-1.358	-0.478	-0.335	-0.259	6.730	4.573	1	6	8
VL2041	-0.629	-1.503	-0.831	-0.137	2.346	-0.393	0.101	6.746	4.877	5	7	9
VL2040	-0.720	-1.356	0.522	-0.476	0.385	1.474	0.606	14.943	5.598	7	15	13

differences among the yields of genotypes. The small proportion of SS due to G indicated that the differences among the genotypes were not very high. The magnitude of GxE SS was 4.38 times more than that for the SS due to G, thus, indicating that the differences in the response of the genotypes across environments were substantial and the genotypes need multi-locational testing. The first seven significant multiplicative terms explained 99.9 % of interactions sum of squares.

Ranking of genotypes vis-à-vis number of IPCA's

Wheat genotypes HPW469, UP3064, HS676, HPW472 were ranked as per absolute IPCA-1 scores for general adaptation (Table 8). In contrast, IPCA-2 selected, HS677, HS507, SKW356 genotypes as of choice for considered locations of the zone. Values of IPCA-3 favoured SKW356, HS676, HS677 wheat genotypes. As per IPCA-4, VL2041, VL2042, HPW471 genotypes would be of stable performance. HS678, HPW470, HS675 genotypes pointed by IPCA-5 measure for general and VL2041, HPW472 for specific locations. Genotypes for general adaptation were HS675, UP3064, HPW472 identified by absolute values of IPCA-6 and HPW469, VL2040 for specific locations. Lastly, IPCA-7

Table 9. Weighted average of absolute scores and ranks of genotypes 2019-20.

Genotype	W1	W2	W3	W4	W5	W6	WAASB	R_{W1}	R_{W2}	R_{W3}	R_{W4}	R_{W5}	R_{W6}	R_{WAASB}
HS507	2.617	1.438	1.549	1.651	1.573	1.515	1.459	16	13	13	16	16	16	16
SKW356	2.146	1.235	0.947	0.855	0.876	0.850	0.856	13	10	6	5	5	5	6
VL2042	2.456	2.218	1.858	1.602	1.545	1.503	1.457	14	16	16	15	15	15	15
HPW471	2.549	1.815	1.561	1.364	1.299	1.253	1.239	15	15	14	13	13	12	12
HS675	0.897	1.179	1.121	1.111	1.055	1.007	1.018	11	9	10	11	11	11	11
HPW472	0.496	1.341	1.142	1.032	1.043	1.007	0.971	4	11	11	10	10	10	10
VL2039	0.849	1.653	1.591	1.452	1.383	1.359	1.330	10	14	15	14	14	14	14
HS677	0.717	0.455	0.424	0.702	0.679	0.677	0.665	6	2	2	3	3	3	3
HS676	0.291	0.374	0.312	0.334	0.333	0.358	0.370	3	1	1	1	1	1	1
UP3064	0.078	0.533	0.528	0.504	0.533	0.517	0.539	2	3	3	2	2	2	2
HS678	0.795	0.565	1.044	0.950	0.898	0.872	0.852	8	4	8	7	6	6	5
HS562	0.832	0.945	1.082	0.965	0.918	0.928	0.920	9	6	9	8	7	7	9
HPW470	1.394	1.369	1.279	1.336	1.266	1.279	1.266	12	12	12	12	12	13	13
HPW469	0.062	0.711	0.931	0.995	0.964	0.934	0.908	1	5	5	9	9	8	8
VL2041	0.629	1.059	1.005	0.875	0.963	0.936	0.904	5	8	7	6	8	9	7
VL2040	0.720	1.033	0.911	0.846	0.818	0.849	0.840	7	7	4	4	4	4	4

settled for HS507, VL2041, HPW472 genotypes for the studied locations of the zone. MASV and MASV1consider all significant IPCAs of the analysis. Values of analytic measures of adaptability MASV1 identified genotypes UP3064, HS675, SKW356, HPW472 would express stable yield whereas genotypes UP3064, HS676, SKW356, and HS675 be of stable performance by MASV measure respectively.

Values of W1 measure prefered HPW469, UP3064, HS676, HPW472 genotypes whereas W2 measure settled for HS676, HS677, UP3064, HS678 while genotypes HS676, HS677, UP3064, VL2040 by W3 values (Table 9). Wheat genotypes HS676 UP3064, HS677, VL2040 were pointed by W4; values of W5 measure favoured HS676, UP3064, HS677, VL2040, and lastly by W6 values genotypes of choice would be HS676, UP3064, HS677, VL2040. WAASB stability measure utilized all significant IPCA's settled for HS676, UP3064, HS677, VL2040 genotypes for considered locations of the zone for stable high yield. The genotype ranking was altered by the number of IPCAs included in the WAASB measure.

Productive and broadly adapted genotypes by AMMI + BLUP tools

The average of BLUP's values ranked VL2041, HS675, HS507 & HPW471 genotypes as the order of choice (Table 10). Superiority index selected VL2041, HS675, HS562 & HS676 genotypes. Higher values of GM associated with VL2041, HS675, HPW470, HPW471 genotypes. Moreover, the superiority index values found the suitability of VL2041, HS675, HS676 & HS562.

The harmonic mean of yield settled for VL2041, HS675, HPW470 & HPW471 genotypes. While superiority index while assigning 65 and 35 percent weight to yield and stability found VL2041, HS676, HS675 & HS562 as recommended genotypes. Measures of adaptability RPGV and MHRPGV measures selected VL2041, HS675, HPW470 & HPW471 along with the least stable yield of VL2039.

Biplot analysis of measures

The loadings of the measures were reflected in Table 11 as per the first two significant Principal Components as these PCs accounted for 68.8% of the total variation in the original variables. Most of the measures had clustered in five major groups by Biplot analysis (Fig 2). The cluster of MASV1 with IPCA1 & IPCA6 was observed near to origin. Group of stability measures as per a different number of interaction principal components observed near to cluster of MASV & W1 measure. The cluster of arithmetic, geometric, harmonic means along with corresponding adaptability measures was seen in a different quadrant. Group of Superiority Indexes considering averages were also found in the same quadrant. Clusters of this quadrant maintained right angles with clusters of other quadrants. This group maintained the right angles with a group of MASV & MASV1 measures. Moreover, different behaviour of genotypes would be expected as adaptability measures in comparison to the performance by stability measures.

Conclusion

GxE interaction study in multi-environment trials was carried out by a well-established AMMI model. The simultaneous consideration of stability measures and yield

Table 10. Superiority index and adaptability measures of genotypes 2019-20.

Genotype	AMu	Rk	SI au	Rk	GMu	Rk	SI gu	Rk	HMu	Rk	SI hu	Rk	RPGVu	Rk	MHRPGVu	Rk
HS507	29.88	3	57.21	10	28.47	6	51.72	11	26.87	6	45.59	12	1.075	5	1.028	6
SKW356	26.64	13	50.60	13	25.16	13	46.68	13	23.42	14	41.26	13	0.943	13	0.911	14
VL2042	27.01	10	34.26	14	25.85	12	32.45	15	24.71	12	30.79	15	0.974	12	0.930	12
HPW471	29.77	4	63.38	6	28.86	4	61.69	6	27.97	4	60.24	7	1.075	4	1.054	4
HS675	29.92	2	71.71	2	29.38	2	72.61	2	28.81	2	73.13	3	1.094	2	1.072	2
HPW472	24.98	15	33.56	15	24.09	15	35.08	14	23.22	15	36.20	14	0.901	15	0.874	15
VL2039	22.75	16	4.13	16	21.47	16	4.13	16	20.24	16	4.13	16	0.812	16	0.771	16
HS677	25.92	14	51.02	12	25.00	14	51.64	12	24.05	13	51.78	11	0.929	14	0.915	13
HS676	26.98	12	68.93	4	26.47	10	71.97	3	25.92	8	74.09	2	0.977	10	0.975	8
UP3064	26.98	11	63.56	5	26.34	11	65.61	5	25.65	10	66.85	5	0.974	11	0.968	11
HS678	27.45	9	57.20	11	26.62	8	57.56	9	25.83	9	57.97	8	0.992	8	0.971	10
HS562	29.41	6	70.82	3	28.71	5	70.81	4	27.94	5	70.32	4	1.068	6	1.049	5
HPW470	29.65	5	61.59	7	28.97	3	61.60	7	28.30	3	61.61	6	1.078	3	1.058	3
HPW469	27.75	7	57.83	9	26.89	7	57.79	8	25.98	7	57.22	9	0.998	7	0.986	7
VL2041	30.85	1	82.85	1	30.26	1	82.85	1	29.69	1	82.85	1	1.125	1	1.107	1
VL2040	27.55	8	58.46	8	26.52	9	57.27	10	25.45	11	55.79	10	0.985	9	0.971	9

Table 11. Loadings of measures as per two principal components 2019-20

Measure	PC1	PC2
IPCA1	-0.0077	0.1216
IPCA2	-0.2322	-0.0939
IPCA3	-0.0091	-0.1125
IPCA4	0.0033	0.2469
IPCA5	0.0390	0.0646
IPCA6	-0.0134	0.0616
IPCA7	-0.1912	0.0912
MASV1	-0.0629	0.0976
MASV	-0.1633	0.1964
W1	-0.1591	0.2254
W2	-0.2433	0.2015
W3	-0.2428	0.2324
W4	-0.2426	0.2395
W5	-0.2413	0.2421
W6	-0.2428	0.2436
WAASB	-0.2416	0.2458
AMu	0.1854	0.3034
SI au	0.3002	0.1463
GMu	0.2077	0.2866
SI gu	0.3104	0.1225
HMu	0.2234	0.2680
SI hu	0.3150	0.1025
RPGVu	0.1895	0.3015
MHRPGVu	0.2239	0.2709
% variance explained	38.36	30.42

would be more appropriate to recommend high-yielding stable wheat genotypes. In the present study, the main advantages of AMMI and BLUP were combined to increase the reliability of multi-locations 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.

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Conflict of interest

The authors declare that they have no conflict of interest.

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