Ilmu Pertanian (Agricultural Science)
http://journal.ugm.ac.id/jip
Vol. 8 No. 2 August, 2023: 80–89| DOI: doi.org/10.22146/ipas.77761

Performance assessment of wheat genotypes based on the superiority index using additive main and multiplicative interaction effects and BLUP analysis

Ajay Verma* and Gyanendra Pratap Singh

ICAR-Indian Institute of Wheat and Barley Research
Gahoon Vihar, Karnal, Haryana 132001, India
*Corresponding author: verma.dwr@gmail.com

Article Info

Received : 15th September 2022
Revised : 5th June 2023
Accepted: 7th August 2023

Keywords:
AMMI model, BLUP values, superiority index, weighted average of absolute scores

Abstract

The simultaneous use of additive main and multiplicative interaction effects (AMMI) and best linear unbiased predictors (BLUP) has been reflected in the multi-location evaluation of trials for number of crops. The additional advantages of both these approaches would be combined in superiority index (SI) to have an edge over the commonly used approaches. The promising wheat genotypes had been considered under multi location trails in Peninsular zone of India during the cropping seasons of 2018–2019 and 2019–2020. The highly significant environmental effects contributed 44.1% and 35.3% of total sum of squares in the AMMI analysis, 20.6% and 26.2% were augmented by G × E interaction, while 10.8% and 7.5% were contributed by the genotypes. Wheat genotypes of UAS3001, MACS6222, GW322, and DDW48 expressed their superiority in BLUP values. Superiority indexes and adaptability measures had identified WHD964 and DDW48 genotypes for the second year of study. More than 75% variations among the considered measures were due to the first two interaction principal components (IPCA's) under Biplot analysis. Number of superiority index measures were clustered with adaptability measures in the same quadrant. Superiority index, the weighted measure of yield and consistent performance of genotypes would be more appropriate for stability and adaptabilities studies.

INTRODUCTION

Identification of promising genotypes was performed through multi location trials to determine the genetic potential as genotypes and environment interaction effects might hide the true potential of genotypes (Agahi et al., 2020). Significant genotype-environment interaction (GxE) and biased estimates of gene effects (Bocianowski et al., 2019) hid the degree of the relationship between the phenotypic and genotypic expression of traits. Over time, a good variety of statistical analytic techniques based on single trait and multiple traits to evaluate the adaptability or stable performance of genotypes have been developed (Ahakpaz et al., 2023). An appropriate estimation of significant GxE interactions in multi locations trials has been carried out by using additive main effects and multiplicative interaction (AMMI) analysis (Tekdal and Kendal, 2018). According to the goals of the breeding program, AMMI uses the largest fraction of the GxE interactions sum of squares and helps to appropriately partition the individual and interaction effects study field trial data (Esan et al., 2023). In the AMMI analysis, individual effects are tested for significance using ANOVA, and interaction effects are tested using principal component analysis (Oyekunle et al., 2017). The fixed character of main effects and interaction effects considered under AMMI analysis had raised the issues as it has traditionally been assumed that multi-location trials should not be analyzed with fixed effects (Ashwini et al., 2021).

How to cite: Verma, A., and Singh, G.P. (2023). Performance assessment of wheat genotypes based on the superiority index using additive main and multiplicative interaction effects and BLUP analysis. *Ilmu Pertanian (Agricultural Science)*, 8(2), pp. 80–89.

ISSN 0126-4214 (print) ISSN 2527-7162 (online)

The mean yield of genotypes under number of environments would be assessed by predicted performance as compared to the estimation (Al-Sayaydeh et al., 2023). Random environment also suggests the random effects of genotype x environment interaction. The prediction of the random effects would be provided by the Best Linear Unbiased Prediction (BLUP). Resende and Duarte (2007) put forward the good number of adaptability measures based on BLUP of genotypes with the stability / adaptability by harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV), and harmonic mean of relative performance of genotypic values (HMRPGV). The present study aimed to combine the salient features of both recent analytic tools to a superiority index measure (Olivoto et al., 2019) for the wheat genotypes studied under the irrigated timely sown conditions. This index would be useful for the breeders to consider the yield potential and the stable performance of the considered genotypes simultaneously.

MATERIALS AND METHODS

The major locations Niphad, Pune, Parbhani, Savalivihir, Dharwad, Bailahongal, Nippani, Bagalkot were considered in the Peninsular zone of the India to evaluate the promising wheat genotypes in 2018–2019 and 2019–2020 suitable seasons. Eleven wheat genotypes and eight genotypes of wheat were evaluated at major locations in research fields with four replications. The parentage details of the considered genotypes are described in Table 1 for quick reference.

The Weighted Average of Absolute Scores (WAASB) measure was calculated using the interaction principal components as follows:

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

where, WAASB$_i$ denotes the weighted average of absolute scores of the *i*th genotype (or environment), Interaction Principal Component (IPCA)$_{ik}$ is the score of the *i*th genotype (or environment) in the *k*th IPCA, and estimated proportion (EP)$_k$ is the amount

Table 1. Parentage details of the evaluated wheat genotypes during 2018–2019 and 2019–2020 at major locations

Genotype (2018–2019)	Parentage	Genotype (2019–2020)	Parentage
PBW823	(T. boeoticum 4992/2*PDW274//2*PBW703)	WHD964	D86135/ACO89//PORRON_4/3/SNITAN/10/PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBAD/5/AVO/HUI/7/PLATA_13/8/THKNEE_11/9/CHEN/ALTAR84/3/HUI/POC//BUB/RUFO/4/FNFOOT/11/CANELO_8//SORA/2*PLATA_12/12/TADIZ/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/H)
UAS428	(GREEN-14/YAN-10/AUK/UAS402)	DDW48	(HI8498/PDW233//PDW291)
DDW49	(PDW314/PDW233)	MACS6222	(HD2189*2/MACS2496)
UAS3001	(UAS259/GW322//HI 977)	MACS3949	(STOT//ALTAR84/ALD/3/THB/CEP7780//2*MUSK_4)
MACS3949	(STOT//ALTAR84/ALD/3/THB/CEP7780//2*MUSK_4)	HI8818	(HI8682/WH896)
MACS6222	(HD2189*2/MACS2496)	UAS428	(GREEN-14/YAN-10/AUK/UAS402)
GW322	(PBW173/GW196)	DDW49	(PDW314/PDW233)
DDW48	(HI8498/PDW233//PDW291)	GW322	(PBW173/GW196)
MACS6478	(CS/TH.SC//3*VN/3/MIRLO/BUC/4/MILAN/5/TILHI)		
HD3343	(PJN/BOW//OPATA*2/3CROC_1/A.SQUARROSA(224)//OPATA)		
WHD963	(BCRIS/BICUM/LLARETA INIA/3/DUKEM_12/2*RASCON_21/5/SOMAT_3/GREEN_22/4/GODRIN/GUTROS/DUKEM/3/THKNEE_11)		

of the variance explained by the *k*th IPCA (Zali et al., 2012).

Superiority index combines the yield potential and stable performance as

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

where rG_i 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 *i*th genotype. SI is the superiority index for the *i*th genotype weighted between yield and stability, and θY and θS are the weights for yield and stability assumed to be of order 65 and 35, respectively. Other widely utilized adaptability and stability measures were also considered in this study for the completeness (Ajay et al., 2019). Software's AMMISOFT and SAS were used in the current study for the analysis and interpretations of results.

RESULTS AND DISCUSSION

Cropping season 2018–2019

Analysis of main and interaction effects

The effects of environment (E), genotypes (G), and G x E interaction were highly significant as observed by AMMI analysis. About 44.1% of the total sum of squares due to treatments was explained by environmental variations (Table 2). The genotypes explained 10.8% of a total sum of squares, whereas G × E interaction accounted for 20.6% of yield variation. Higher G × E interaction effects over the genotypes effects was reported in several studies (Ajay et al., 2020). Sum of squares explained by seven multiplicative terms were 50.8%, 15.4%, 13%, 8.4%, 5.9%, 3.6% and 1.7 % respectively. About 98.8 % of interaction effects were accounted by seven significant multiplicative interaction components, while the remaining 1.2% was due to the residuals (Oyekunle et al., 2017).

Order of genotypes based on number of IPCA's

The numerical values of the interaction principal components axes in the AMMI analysis assist to judge the stability or adaptability of genotypes. The genotypes showing the lower absolute IPCA1 scores would produce less GxE interaction effects, regarded as of stable performance. Wheat genotypes of MACS6478, WHD963, and MACS6222 were pointed by least absolute IPCA-1 scores. Meanwhile, based on minimum IPCA-2 values, DDW49, MACS6222, and MACS6478 genotypes would be of choice (Table 3). Wheat genotypes of DDW48, UAS3001,

Table 2. Analysis of individual and interaction effects of the evaluated genotypes for 2018–2019 and 2019–2020 cropping season

Source	Sum of squares (2018–2019)	Mean sum of squares	Probability	Sum of squares (2019–2020)	Mean sum of squares	Probability
Genotypes (G)	4,440.94	444.09	. ***	985.05	140.72	. ***
Environments (E)	18,202.58	1,820.26	. ***	4,619.61	513.29	. ***
Interactions G × E	8,492.80	84.93	. ***	3,427.93	54.41	. ***
IPC1	4,317.94	227.26	. ***	1,793.38	119.56	. ***
IPC2	1,307.90	76.94	. ***	791.13	60.86	. ***
IPC3	1,105.01	73.67	**	406.02	36.91	
IPC4	714.65	54.97		215.55	23.95	
IPC5	500.45	45.50		169.23	24.18	
IPC6	305.32	33.92		48.65	9.73	
IPC7	142.63	20.38				
Residual	98.90	10.99		3.97	1.32	
Error	10,155.11	27.98		4,047.35	16.86	
G × EInteractions - Signal		(67.06%)			(69.01%)	
G × EInteractions - Noise		(32.94%)			(30.99%)	
Total	41,291.42	85.49		13,079.95	41.00	

and MACS6478 were favored by lower values of IPCA-3, while IPCA-4 values selected MACS6222, GW322, and UAS428 genotypes. IPCA-5 measure pointed out GW322, UAS428, and DDW48 genotypes. Genotypes of UAS3001, PBW823, and UAS428 were pointed by IPCA-6, while DDW49, MACS6222, and WHD963 would be desirable genotypes based on IPCA-7 measure. Adaptability measures modified AMMI stability value (MASV) and corrected modified AMMI stability value (MASV1) used the total variations accounted by significant IPCAs to identify MACS6478, MACS6222, UAS3001 and MACS6478, GW322, MACS6222 using MASV1 and MASV, respectively (Mohammadi et al., 2015).

Situations with the low proportion of the variance accounted by IPCA1 might lead to an inappropriate interpretation towards the stable performance of the genotypes. As an effective alternative to these situations, a new stability index called WAASB, based on the weighted average of absolute scores was proposed. The genotypes of MACS6478, WHD963, MACS6222, and WH1239 were preferred by W1, while W2 values settled for MACS6478, MACS6222, WHD963 and MACS6478. Meanwhile, MACS6222 and WHD963 genotypes were pointed by W3 measure (Table 3). Values of W4 settled for MACS6478, MACS6222, and WHD96, while W5 favored genotypes of MACS6478, MACS6222, and WHD963. The genotypes of MACS6478, MACS6222, and WHD963 were ranked on higher side based on W6 measure. WAASB measure would be more realistic since it has been computed from all the interaction principal components axes as reported by Olivoto et al. (2019). The stable yield performance of MACS6478, MACS6222, and WHD963 genotypes were justified by WAASB measure.

Performance of genotypes by simultaneous use of AMMI and BLUP

Modelling the genotypic performance under MET trials as of random nature might be preferable over the fixed effects implied in traditional analytic tools. Wheat genotypes of MACS6222, UAS3001, and DDW48 had higher mean yield based on their BLUP values. The larger values of the geometric mean (GM) measure had been expressed by UAS3001, MACS6222, and GW322 genotypes (Table 4). The higher values of harmonic mean of genotypic values (HMGV) were expressed by UAS3001, MACS6222, and GW322 genotypes. Values of HMRPGV measure top ranked UAS3001, MACS6222, and GW322 genotypes. Meanwhile, the values of RPGV settled for UAS3001, MACS6222, and DDW48 (Resende and Duarte, 2007).

The superiority index based on yield and stability measures in the ratios of 65:35 pointed out for MACS6222, UAS3001, and GW322 genotypes. Meanwhile, the values of SI measure based on GM and WAASB, selected MACS6222, UAS3001, and GW322 genotypes. The values of SI measure using HM and WAASM selected MACS6222, UAS3001, and GW322 genotypes. The RPGV and HMRPGV pointed out MACS6222, UAS3001, GW322, and DDW48 as adaptable genotypes.

Table 3. The adaptability and stability measures of the evaluated genotypes (2018–2019)

Genotype	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	IPCA6	IPCA7	MASV1	MASV	W1	W2	W3	W4	W5	W6	WAASB
PBW 823	-4.201	-0.786	0.675	0.427	-0.504	-0.211	-0.348	14.043	7.883	4.201	3.337	2.818	2.514	2.323	2.183	2.113
UAS 428	2.126	1.288	-1.526	0.360	0.170	0.255	-0.529	7.892	5.035	2.126	1.914	1.839	1.651	1.510	1.427	1.392
DDW 49	1.590	0.113	2.728	1.424	0.738	1.067	0.020	8.206	6.104	1.590	1.217	1.511	1.500	1.428	1.404	1.351
UAS 3001	-0.751	1.246	0.428	-1.956	0.678	-0.014	-1.413	5.081	4.268	0.751	0.876	0.789	0.937	0.912	0.853	0.874
MACS 3949	1.084	-2.563	-0.627	1.097	0.557	-1.040	-0.936	6.454	5.220	1.084	1.459	1.296	1.271	1.203	1.192	1.183
MACS 6222	0.638	-0.160	-1.555	0.080	-1.393	1.027	-0.116	5.077	4.002	0.638	0.517	0.719	0.638	0.710	0.731	0.708
GW 322	-1.079	-1.266	-0.919	-0.314	0.031	1.298	0.802	5.454	3.958	1.079	1.126	1.086	0.988	0.897	0.923	0.919
DDW 48	1.399	-0.758	0.262	-1.401	0.329	-1.423	1.083	6.465	4.526	1.399	1.237	1.047	1.092	1.019	1.046	1.048
MACS 6478	0.291	-0.286	0.614	-1.428	0.351	0.610	0.505	3.372	2.848	0.291	0.289	0.353	0.489	0.476	0.485	0.486
HD 3343	-1.599	2.007	-1.067	1.318	1.385	-0.637	0.763	7.523	5.592	1.599	1.702	1.578	1.545	1.530	1.471	1.444
WHD 963	0.501	1.165	0.988	0.394	-2.344	-0.930	0.169	5.906	4.888	0.501	0.669	0.731	0.688	0.845	0.851	0.825

Table 4. Superiority index as per the BLUP and BLUE of the evaluated genotypes (2018–2019)

Genotype	AMu	SI au	GMu	SI gu	HMu	SI hu	RPGVu	MHRPGVu	AMe	SI ae	GMe	SI ge	HMe	SI he	RPGVe	MHRPGVe
PBW 823	40.12	0.00	39.91	0.00	39.69	0.00	0.8637	0.8444	38.32	0.00	37.98	0.00	37.65	0.00	0.8243	0.8022
UAS 428	47.58	71.70	46.93	69.22	46.38	66.86	1.0071	1.0029	47.16	66.66	46.33	63.41	45.60	60.64	0.9965	0.9879
DDW 49	48.20	77.20	47.46	74.12	46.83	71.27	1.0186	1.0138	48.40	74.76	47.55	71.27	46.80	68.38	1.0226	1.0137
UAS 3001	48.69	91.14	48.41	91.64	48.15	91.64	1.0381	1.0351	49.55	91.64	49.31	91.64	49.09	91.64	1.0584	1.0534
MACS 3949	47.91	78.63	47.23	75.99	46.67	73.61	1.0134	1.0093	48.28	77.67	47.56	74.99	46.96	72.88	1.0220	1.0149
MACS 6222	48.75	95.23	48.28	94.25	47.85	92.91	1.0347	1.0330	48.99	92.00	48.45	90.28	47.94	88.66	1.0392	1.0356
GW 322	48.31	87.37	47.99	87.51	47.69	87.16	1.0289	1.0265	48.88	86.80	48.55	86.30	48.23	85.81	1.0416	1.0374
DDW 48	48.62	86.93	47.99	84.73	47.45	82.55	1.0294	1.0260	49.15	85.59	48.53	83.43	47.99	81.67	1.0414	1.0369
MACS 6478	46.59	83.74	46.22	83.29	45.89	82.65	0.9904	0.9892	46.29	81.17	45.88	80.33	45.51	79.66	0.9835	0.9815
HD 3343	46.78	64.54	46.53	65.02	46.29	65.06	0.9989	0.9937	47.29	66.34	47.03	66.28	46.76	66.16	1.0113	1.0025
WHD 963	46.07	72.50	45.57	71.01	45.12	69.39	0.9769	0.9748	45.33	68.27	44.65	65.96	44.01	63.81	0.9592	0.9529

Remarks: Arithmetic, geometric and harmonic mean of BLUP values are expressed by AMu, GMu, HMu, while AMe, GMe, HMe are considered the BLUE values.

Performance of genotypes by simultaneous use of AMMI and BLUE

The wheat genotypes of UAS3001, DDW48, and MACS6222 were identified by more average yield (Table 4). GM measure observed the larger values of UAS3001, GW322, and DDW48 genotypes. The Harmonic mean of genotypes (HM) settled for UAS3001, GW322, and DDW48 (Resende and Duarte, 2007). Genotypes of UAS3001, GW322, and DDW48 were settled by relative performance of genotypic values measure. The superiority index measure by assigning 65:35 weights to yield and stability pointed out MACS6222, UAS3001, and GW322 genotypes. Additionally, UAS3001, MACS6222, and GW322 genotypes were taken into account for SI values with GM and stability. Values of SI considering the HM measure and WAASB pointed the same genotypes. RPGV and MHRPGV measures also identified UAS3001, GW322, and DDW48 genotypes as having more adaptable performance.

Association analysis among measures

Random effects of genotypes

A graphical analytic biplot displays a two-way classification of treatments by locations factors, such that relationships among the treatments, among the locations, and the underlying interactions between the treatments and locations visualized simultaneously. About 75.3% of the total variation among the superiority indexes, stability, and adaptability measures in the current study were explained by the first two significant Principal Components (Table 5) with 64.9% and 10.4% of their contributions (Mohammadi et al., 2015). The stability measures while using several interaction principal components grouped with MASV and MASV1 measures (Figure 1). Adaptability measures, RPGV and MHRPGV expressed tight association, and the cluster of these measures was placed in another quadrant. Next group of the superiority indexes was also placed in the same quadrant.

Fixed effects of genotypes

Table 6 reflects nearly 75.2% of the total variation augmented by the first two significant principal components with respective contributions of 64% and 11.2 %. Adaptability measures MASV, MASV1 and stability measures constituted the first group (Ajay et al., 2020). Adaptability measures expressed their deviation from the adaptability measures as placed in a different quadrant (Figure 2) along with the cluster of superiority indexes.

Second-year 2019–2020

Analysis of main and interaction effects

Nearly 35.3% of the total sum of squares was accounted by environmental effects (Table 2). Effects of G × E interaction accounted for 26.2% of variation, while genotypes contributed only 7.5%. The significant six multiplicative terms of G × E interaction were able to explain 52.3%, 23.1%, 11.8%, 6.3%, 4.9% and 1.4 %. About 99.9 % of the total variation was accounted by significant components.

Table 5. Percentage share of BLUP based measures (2018–2019)

Measure	PC1	PC2
IPCA1	-0.1652	-0.2067
IPCA2	-0.0114	-0.0421
IPCA3	0.0419	0.1375
IPCA4	0.1086	-0.2599
IPCA5	0.0000	-0.4136
IPCA6	-0.0499	-0.0095
IPCA7	-0.0319	0.1042
MASV1	0.2462	-0.0912
MASV	0.2317	-0.1520
W1	0.2403	-0.1099
W2	0.2382	-0.1606
W3	0.2360	-0.2094
W4	0.2338	-0.2337
W5	0.2377	-0.2140
W6	0.2365	-0.2213
WAASB	0.2355	-0.2283
AMu	-0.2266	-0.2727
SI au	-0.2488	-0.1109
GMu	-0.2291	-0.2610
SI gu	-0.2497	-0.0999
HMu	-0.2302	-0.2512
SI hu	-0.2500	-0.0906
RPGVu	-0.2270	-0.2703
MHRPGVu	-0.2311	-0.2514
% variation explained	64.96	10.43

Table 6. Percentage share of BLUE based measures (2018–2019)

Measure	PC1	PC2
IPCA1	0.1597	0.1345
IPCA2	0.0095	0.0223
IPCA3	-0.0427	-0.1302
IPCA4	-0.1118	0.2145
IPCA5	0.0087	0.4452
IPCA6	0.0475	-0.0125
IPCA7	0.0332	-0.0861
MASV1	-0.2479	0.0932
MASV	-0.2328	0.1498
W1	-0.2416	0.1164
W2	-0.2383	0.1705
W3	-0.2373	0.2049
W4	-0.2340	0.2353
W5	-0.2383	0.2136
W6	-0.2370	0.2204
WAASB	-0.2356	0.2297
AMe	0.2260	0.2733
SI ae	0.2503	0.1101
GMe	0.2273	0.2686
SI ge	0.2509	0.1042
HMe	0.2274	0.2647
SI he	0.2508	0.1000
RPGVe	0.2249	0.2792
MHRPGVe	0.2296	0.2585
% variation explained	64.05	11.21

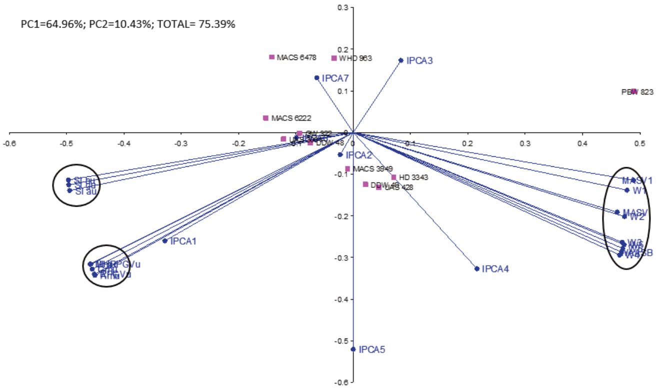

Figure 1. Association analysis among BLUP based measures (2018–2019)

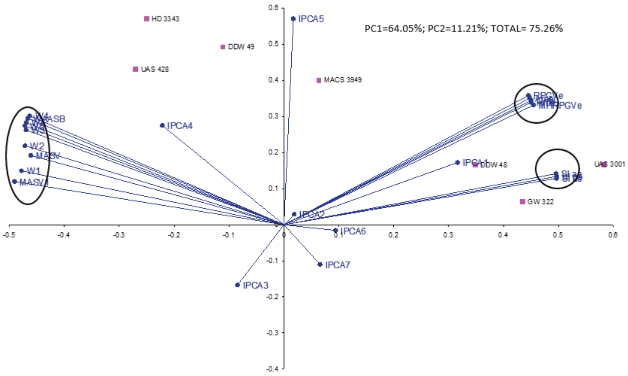

Figure 2. Association analysis among BLUE based measures (2018–2019)

Order of genotypes based on number of IPCA's

Absolute IPCA-1 scores identified MACS3949, WHD964, and DDW48 genotypes. Meanwhile, IPCA-2, HI8818, and DDW48 would be genotypes of choice (Table 7). Values of IPCA-3 favored DDW49 and HI8818 genotypes. According to IPCA-4, GW322 and WHD964 genotypes would be of stable performance. MACS3949 and UAS428 genotypes were pointed by IPCA-5 measure. Genotypes of DDW48 and DDW49 identified by absolute values of IPCA-6. MASV1 identified WHD964 and MACS3949 genotypes, while genotypes of HI8818 and DDW49 were pointed by MASV measure (Mohammadi et al., 2015).

Values of W1 measure preferred MACS3949, WHD964, and DDW48, and W2 values selected DDW48, WHD964, and MACS3949. Meanwhile, DDW48, HI8818, and MACS3949 were pointed by W3 measure (Table 7). Genotypes of DDW48, WHD964, and MACS3949 were pointed by W4, while W5 favored DDW48, WHD964, and MACS3949 genotypes. According to WAASB, all significant IPCA's had settled for DDW48, WHD964, and MACS3949 genotypes.

Performance of genotypes by simultaneous use of AMMI and BLUP

Wheat genotypes of WHD964 and DDW48 expressed the more yield based on BLUP estimates (Table 8). WHD964 and DDW48 genotypes expressed the higher geometric mean. Meanwhile, WHD964 and DDW48 genotypes achieved higher values of harmonic mean. WHD964 and DDW48 genotypes were top ranked by HMRPGV measure. Wheat genotypes of WHD964 and DDW48 were pointed out by the relative performance of genotypic values. The superiority index selected WHD964 and DDW48 genotypes as having high yield and stable performance. Based on SI, GM and WAASB pointed towards WHD964 and DDW48 genotypes. The same genotypes had been favored by SI using HM and WAASB. Measures of RPGV and HMRPGV settled for WHD964 and DDW48 genotypes.

Performance of genotypes by simultaneous use of AMMI and BLUE

Wheat genotypes of WHD964 and DDW48 were identified having more average yield (Table 8). Higher values of geometric mean were expressed

Table 7. The adaptability and stability measures of the evaluated genotypes (2019–2020)

Genotype	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	IPCA6	MASV1	MASV	W1	W2	W3	W4	W5	WAASB
WHD964	0.548	-1.357	2.067	0.238	-0.241	-0.859	5.608	4.422	0.548	0.821	1.032	0.954	0.889	0.888
DDW48	0.665	-0.656	-1.171	-1.579	1.317	-0.269	6.317	4.443	0.665	0.662	0.748	0.831	0.875	0.854
MACS6222	-1.554	1.760	1.566	-0.525	0.650	0.823	6.735	4.987	1.554	1.624	1.614	1.506	1.428	1.406
MACS3949	-0.507	-2.353	-0.437	0.864	0.026	1.102	5.651	4.514	0.507	1.130	1.012	0.997	0.909	0.916
HI8818	-1.546	-0.357	-0.306	-1.078	-1.237	-0.359	6.044	3.960	1.546	1.145	1.002	1.010	1.030	1.007
UAS428	-2.142	1.079	-1.235	1.182	-0.156	-0.573	6.357	4.674	2.142	1.783	1.690	1.640	1.505	1.472
DDW49	1.770	0.735	-0.079	1.085	0.975	-0.333	5.863	3.970	1.770	1.421	1.193	1.182	1.163	1.134
GW322	2.766	1.150	-0.404	-0.186	-1.335	0.468	8.370	5.477	2.766	2.221	1.913	1.741	1.704	1.660

Table 8. Superiority index based on BLUP and BLUE of the evaluated genotypes (2019–2020)

Genotype	AMu	SI au	GMu	SI gu	HMu	SI hu	RPGVu	MHRPGVu	AMe	SI ae	GMe	SI ge	HMe	SI he	RPGVe	MHRPGVe
WHD964	44.97	98.53	44.75	98.53	44.55	98.53	1.057	1.053	46.02	98.53	45.82	98.53	45.64	98.53	1.083	1.079
DDW48	43.61	77.29	43.46	77.83	43.32	78.57	1.026	1.024	43.95	76.14	43.78	76.21	43.62	76.26	1.034	1.031
MACS6222	41.86	24.11	41.54	21.00	41.27	19.00	0.982	0.977	41.54	24.31	41.15	21.59	40.82	19.41	0.974	0.967
MACS3949	43.33	69.95	43.21	70.79	43.08	71.79	1.020	1.017	43.56	68.99	43.41	69.13	43.25	69.19	1.026	1.021
HI8818	41.08	28.36	40.96	28.36	40.84	28.97	0.967	0.964	40.39	28.36	40.25	28.36	40.11	28.36	0.951	0.947
UAS428	42.23	27.44	41.96	25.35	41.70	23.67	0.992	0.987	42.66	34.37	42.34	32.54	42.02	30.62	1.003	0.994
DDW49	41.77	34.40	41.48	31.79	41.22	29.97	0.980	0.977	41.02	30.19	40.65	27.50	40.30	25.07	0.961	0.956
GW322	41.58	8.41	41.19	3.99	40.81	0.00	0.975	0.967	41.29	10.47	40.78	6.22	40.26	1.74	0.968	0.954

Table 9. Percentage share of BLUP based measures (2019–2020)

Measure	PC1	PC2
IPCA1	-0.0129	0.2042
IPCA2	-0.2245	0.0248
IPCA3	0.0602	0.2085
IPCA4	-0.0278	0.1403
IPCA5	0.1076	-0.0543
IPCA6	-0.0758	0.0908
MASV1	-0.1408	0.4478
MASV	-0.2572	0.0347
W1	-0.2530	0.1698
W2	-0.2334	0.2708
W3	-0.2399	0.2324
W4	-0.2512	0.1979
W5	-0.2496	0.2080
WAASB	0.2645	0.1169
AMu	0.2395	0.2654
SI au	0.2659	0.1004
GMu	0.2457	0.2364
SI gu	0.2670	0.0836
HMu	0.2362	0.2787
SI hu	0.2427	0.2506
RPGVu	62.33	13.04
MHRPGVu	-0.2311	-0.2514
% variation explained	62.33	13.04

Table 10. Percentage share of BLUE based measures (2019–2020)

Measure	PC1	PC2
IPCA1	0.0230	-0.1212
IPCA2	0.2277	-0.0425
IPCA3	-0.0591	-0.1628
IPCA4	0.0253	-0.1482
IPCA5	-0.1034	0.0842
IPCA6	0.0829	-0.0433
MASV1	0.1378	-0.4192
MASV	0.2599	-0.0588
W1	0.2548	-0.1781
W2	0.2317	-0.2811
W3	0.2381	-0.2504
W4	0.2511	-0.2124
W5	0.2494	-0.2218
WAASB	-0.2682	-0.1203
AMu	-0.2357	-0.2812
SI au	-0.2697	-0.1065
GMu	-0.2425	-0.2561
SI gu	-0.2709	-0.0927
HMu	-0.2309	-0.2968
SI hu	-0.2406	-0.2639
RPGVu	61.1	14.08
MHRPGVu	-0.2311	-0.2514
% variation explained	61.1	14.08

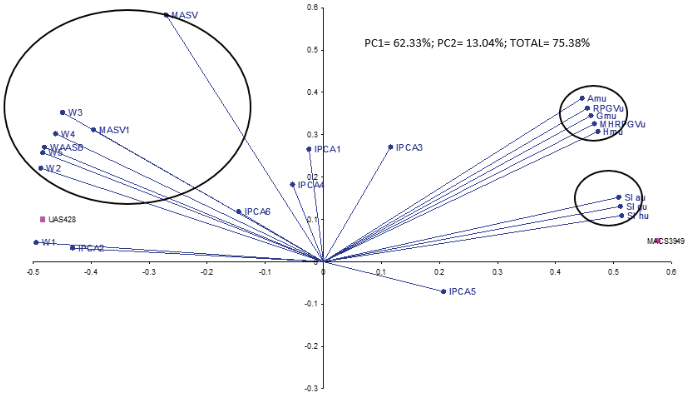

Figure 3. Association analysis among BLUP based measures (2019–2020)

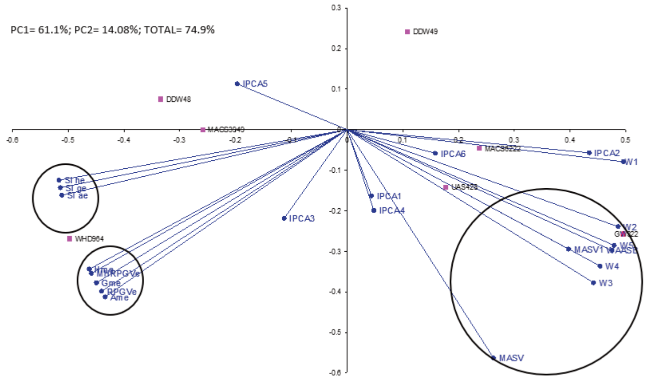

Figure 4. Association analysis among BLUE based measures (2019–2020)

by WHD964 and DDW48. Meanwhile, higher values of harmonic mean were shown by WHD964 and DDW48 wheat genotypes. WHD964 and DDW48 genotypes were selected by HMRPGV values. Genotypes of WHD964 and DDW48 would be of choice as per the relative performance of genotypic values. The superiority index measure pointed out for WHD964 and DDW48 genotypes. Moreover, SI values for GM and stability selected WHD964 and DDW48 genotypes. The same wheat genotypes were pointed out by values of SI based on HM and WAASB. The same genotypes of WHD964 and DDW48 were also identified by RPGV and HMRPGV measures.

Association among measures

Random effects of genotypes

The first two significant PC has explained about 75.4% of the total variation (Table 9) with respective 62.3% and 13% contributions. MASV, MASV1 and other measures considered two or more of interaction principal components grouped together (Figure 3). Adaptability measures had expressed bondage with RPGV and MHRPGV values and placed in other quadrant along with the cluster of the Superiority indexes.

Fixed effects of genotypes

About 74.9% of the total variation was explained by two significant PCs, with their respective contributions being 65.1% and 14% (Table 10). MASV, MASV1, and measures that used two or more interaction principal components were grouped. Adaptability measures values maintained the expressed deviation from the measures and observed in a different quadrant (Figure 4).

CONCLUSIONS

Wheat genotypes of UAS3001, MACS6222, GW322, and DDW48 expressed their superiority based on values of best linear unbiased predictors, while for the second year of study, WHD964, DDW48 were identified by superiority index and adaptability measures. More than 75% variations among the considered measures were accounted by first two interaction principal components (IPCA's) under Biplot analysis. The number of superiority indexes measures were clustered with adaptability measures in the same quadrant in the present study. The stability measures considering the stability and yield performance simultaneously would be more appropriate to recommend high-yielding stable wheat genotypes.

ACKNOWLEDGMENTS

The authors would like to thank all the staff members under All India Coordinated Wheat and Barley Improvement Program (AICW&BIP) working at centers under Peninsular Zone of the country for their dedication to complete the field evaluation.

REFERENCES

Agahi, K., Ahmadi J., Oghan, H. A., Fotokian, M. H., and Orang, S.F. (2020). Analysis of genotype × environment interaction for seed yield in spring oilseed rape using the AMMI model. *Crop Breeding and Applied Biotechnology*, 20(1), e26502012.

Ajay, B. C., Aravind, J., Fiyaz, R. A., Kumar, N., Lal, C., Kona, P., Dagla, M. C., and Bera, S. K. (2019). Rectification of modified AMMI stability value (MASV). *Indian J Genet,* 79(4), pp. 726–731.

Ajay, B.C., Bera, S.K., Singh, A.L., Kumar, N., Gangadhar, K., and Kona, P. (2020). Evaluation of Genotype × Environment interaction and yield stability analysis in peanut under phosphorus stress condition using stability Pprameters of AMMI model. *Agric Res*, 9, pp. 477–486.

Ashwini, K.V.R., Ramesh, S., and Sunitha, N.C. (2021). Comparative BLUP, YREM-based performance and AMMI model-based stability of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] genotypes differing in growth habit. *Genet Resour Crop Evol.*,68, pp. 457–467.

Bocianowski, J., Niemann, J., and Nowosad, K. (2019). Genotype-by environment interaction for seed quality traits in interspecific cross-derived Brassica lines using additive main effects and multiplicative interaction model. *Euphytica*, 215(7), pp. 1–13.

Mohammadi, M., Sharifi, P., Karimizadeh, R., Jafarby J.A., Khanzadeh, H., Hosseinpour, T., Poursiabidi, M.M., Roustaii, M., Hassanpour, H.M., and Mohammadi, P. (2015). Stability of grain yield of durum wheat genotypes by AMMI model. *Agric For*, 61(3), pp. 181–193.

Olivoto, T., Lucio A.Dal'Col, Gonzalez, Silva, J.A., and da, Marchioro, V.S .(2019). Mean performance and stability in multi-environment trials I: Combining features of AMMI and BLUP techniques. *Agron J*, 111, pp.1–12

Oyekunle, M., Menkir, A., Mani, H., Olaoye, G., Usman, I.S., Ado, S. (2017). Stability analysis of maize cultivars adapted to tropical environments using AMMI analysis. *Cereal Res Commun*, 45, pp. 336–345.

Resende, M.D.V, and Duarte, J.B. (2007). Precision and quality control in variety trials. *Pesquisa Agropecuaria Tropical*, 37, pp. 182–194.

Tekdal, S., and Kendal, E. (2018). AMMI Model to assess durum wheat genotypes in multi-environment trials. *J Agr Sci Tech,* 20, pp. 153–166.

Zali, H., Farshadfa,r E., Sabaghpour, S.H., and Karimizadeh, R.(2012). Evaluation of genotype × environment interaction in chickpea using measures of stability from AMMI model. *Ann* B*iol Res*, 3, pp. 3126–3136.