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Research Article

AMMI with BLUP analysis for stability assessment of wheat genotypes under multi locations timely sown trials in Central Zone of India

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Abstract

AMMI analysis explained the highly significant effects of the environment, GxE interaction, and genotypes for wheat genotypes evaluated under restricted irriation timely sown multi-location trials in the Central zone of the country during 2018-19 and 2019-20. About 77.1%, 12.2% & 2.3% had been contributed by environments, interactions and genotypes of the total sum of squares due to treatments respectively in the first year. The utilization of more number of IPCA's in AMMI and WAASB stability measures had altered the ranking of genotypes. Analytic measures of adaptability and Superiority indexes as per BLUP of genotypes identified DBW110, MP3288. Adaptability measures as per arithmetic, geometric and harmonic means and their corresponding values expressed deviation as observed in a seperate quadrant of Biplot graphical analysis. However, this group maintained the right angle with MASV, MASV1, and stability measures. The cluster of Superiority indexes as per averages yield of wheat genotypes placed in the adjacent quadrant. Superiority indexes favored HI8823, MP3288, DBW110 wheat genotypes for high yield and stable performance for the second year. Adaptability measures as per arithmetic, geometric and harmonic means along with the corresponding values of RPGV & MHRPGV expressed bondage and placed in a different quadrant. Cluster of Superiority indexes as per averages of the yield of wheat genotypes seen in the same quadrant as more than 73.5% variation accounted for by the first two principal components.

Introduction

AMMI analysis had been employed mostly to have an efficient estimation of GxE interactions crop breeding trials even large number of other statistical procedures for the stability analyses has been validated in literature [1]. Recently the effects of genotypes, environments, or both to be advocated as of random nature [2]. BLUP have proved its potential to improve the predictive accuracy of random effects under mixed model approach [3]. Both BLUP and AMMI, approaches, seperated the pattern from the random error components in GxE interactions analysis [4]. Integration of stability of performance with yield, is necessary for selecting high yielding, stable genotypes [5]. Both yield and stability of performance should be considered simulaneously, to reduce the effect of G x E interaction and make selection more precise and reliable [6]. These two approaches have been used separately in the field evaluation of genotypes under multi location trials [7]. Benefits of these two important techniques, AMMI and BLUP, utilized to define Superiority Index measure for the stability and adaptability of genotypes [5]. The current study dealt with the analysis of G x E interaction and yield stability through AMMI with BLUP techniques for evaluated wheat genotypes.

Materials and methods

States of India comprised by Madhya Pradesh, Chhattisgarh, Gujarat, Rajasthan (Kota and Udaipur divisions) and Jhansi division of Uttar Pradesh is known as Central Zone. This zone is well established for the quality products of wheat especially chapatti in the country and abroad. Six promising wheat genotypes in advanced trials evaluated at twelve major locations of the zone and eight genotypes at thirteen locations during 2018-19 and 2019-20 cropping seasons respectively. Field trials were conducted at research centers in randomized

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complete block designs with three replications. Recommended agronomic practices were followed to harvest good yield. Details of genotype parentage along with environmental conditions were reflected in Tables 1,2 for ready reference.

Stability measure as Weighted Average of Absolute Scores has been calculated as

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

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 weights to yield and stability measure (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 the WAASB values for *i*th genotype. SI Superiority index for the *i*th genotype that weighted between yield and stability, θY and θS were the weights for yield and stability assumed to be of order 65 and 35 respectively in this study,

Mohamadi & Amri 2008 [8]	Geometric Adaptability Index	$GAI = \sqrt[n]{\prod_{k=1}^{n} \bar{X}_k}$
Zali et al 2012 [9]	Modified AMMI stability Value	$MASV = \sqrt{\sum_{n=1}^{N-1} \frac{SSIPC_n}{SSIPC_{n+1}} (PC_n)^2 + (PC_{n+1})^2}$
Ajay et al 2019 [2]	MASV1	$MASV1 = \sqrt{\sum_{n=1}^{N-1} (\frac{SSIPC_n}{SSIPC_{n+1}} PC_n)^2 + (PC_{n+1})^2}$
Resende & Durate 2007 [10]	Relative performance of genotypic values across environments	$PRVG_{ij} = VG_{ij} / VG_i$
Resende & Durate 2007 [10]	Harmonic mean of Relative performance of genotypic values	$MHPRVG_{i.} = \text{Number of environments} / \sum_{j=1}^{k} \frac{1}{PRVG_{ij}}$
Oliveto et al 2019 [5]	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. 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 [11].

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

Code	Genotype	Parentage	Locations	Latitude	Longitude	Mean sea level
G1	HI 8627	(HD4672/PDW233)	Vijapur	23°33' N	72°45' E	129.4
G2	DBW 110	(KIRITATI/4/2*SERI1B*2/3/KAUZ*2/BOW//KAUZ)	Dhandhuka	22° 22' N	71° 59' E	24
G3	UAS 466	(AMRUTH//BIJAGA YELLOW/AKDW299-16)	Sanosara	21° 72' N	71° 76' E	89
G4	MP 3288	(DOVE/BUC/DL788-2)	Anand	22° 33' N	72° 56' E	39
G5	DBW 277	(NI 5439/ MACS 2496)	Indore	22° 43' N	75° 51' E	550
G6	DDW 47	(PBW34/RAJ1555//PDW314)	Jabalpur	23° 10' N	79° 55' E	403
			Bhopal	23° 15' N	77° 24' E	496
			Powarkheda	22° 70' N	77° 73' E	308
			Gwalior	26° 13' N	78° 10' E	213
			Pratapgarh	24° 03' N	74° 77' E	491
			Udaipur	24° 34' N	73° 41' E	585
			Bilaspur	22° 4' N	82° 9' E	264

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

Code	Genotype	Parentage	Environments	Latitude	Longitude	Mean sea level
G1	MPO1357	(PDW02/TERTER//GW1133)	Vijapur	23°33' N	72°45' E	129.4
G2	HI8627	(HD4672/PDW233)	Dhandhuka	22° 22' N	71° 59' E	24
G3	UAS466	(AMRUTH//BIJAGA YELLOW/AKDW299-16)	Amreli	21° 36' N	71° 13' E	126
G4	UAS472	(BIJAGAYELLOW/(YAZI_1/AKAKI_4//SOMAT_3/3/AUK/GUIL//GREEN/5)	Sanosara	21° 72' N	71° 76' E	89
G5	DBW110	(KIRITATI/4/2*SERI1B*2/3/KAUZ*2/BOW//KAUZ)	Indore	22° 43' N	75° 51' E	550
G6	MP3288	(DOVE/BUC/DL788-2)	Jabalpur	23° 10' N	79° 55' E	403
G7	HI8823	(HI8709/HD4676)	Bhopal	23° 15' N	77° 24' E	496
G8	DDW47	(PBW34/RAJ1555//PDW314)	Powarkheda	22° 70' N	77° 73' E	308
			Gwalior	26° 13' N	78° 10' E	213
			Pratapgarh	24° 03' N	74° 77' E	491
			Udaipur	24° 34' N	73° 41' E	585
			Bilaspur	22° 4' N	82° 9' E	264
			Ambikapur	23° 6' N	83° 11' E	623

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Results and discussion

First-year 2018-19

Environment (E), Genotypes (G), and GxE interaction effects were highly significant as mentioned by the AMMI analysis (Table 3). Analysis observed the greater contribution of environments, GxE interactions, and genotypes to the total sum of squares (SS) as 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 was appropriate for data sets where-in SS due to were of magnitude at least of due to additive genotype main effects [12]. The SS for GxE interactions Signal was higher compared to genotype main effects, indicated appropriateness of AMMI analysis. The environment significantly explained about 77.1% of the total sum of squares due to treatments indicating that diverse environments caused most of the variations in genotypes yield [13]. Genotypes explained only 2.3% of the total sum of squares, whereas GxE interaction accounted for 12.2% of treatment variations in yield. First four significant multiplicative terms explained 94.7 % of interactions sum of squares and the remaining 5.3% was the discarded residual [14].

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

The IPCA scores of genotypes in the AMMI analysis were an indication of stability or adaptability over environments. The greater the IPCA scores, the more specific adapteded genotype to certain locations. The more the IPCA scores approximate to zero, the more stable or adapted the genotypes is overall the locations. The ranking of genotype as per absolute IPCA-1 scores were DDW47, MP3288 (Table 4). While for IPCA-2, genotypes DBW277, DDW47 would be of choice. Values of IPCA-3 favored DBW277, DBW110 wheat genotypes. As per IPCA-4, DDW47, DBW110 genotypes would be of stable performance. Analytic measures of adaptability MASV and MASV1 consider all significant IPCAs of the analysis. Genotypes DDW47, DBW277 had been identified by MASV & MASV1 measures (Ajay et al., 2019). To identify how the ranks of evaluated wheat genotype altered with utilizing numbers of IPCA in the WAASB estimation, the genotype's ranks were obtained while considering 1, 2,..., *p* IPCA's in the WAASB calculations. WAASB = |IPCA1| for using only first IPCA. The genotype with the smallest WAASB value had been ranked with the first-order. Preferences of wheat genotypes as per W1, W2 & W3 measures were the same as DDW47, MP3288 identified as two promising genotypes through the higher-order varied from these measures. Stability measure WAASB based on all significant IPCA's settled for DDW47, MP3288 genotypes for considered locations of the zone for stable high yield. The genotypes ranking was altered by the extent to which IPCAs were included in the WAASB estimation. This reinforces the benefits of using the WAASB index since it captures the variations of all IPCAs to compute the stability [5].

Table 3: AMMI analysis of wheat genotypes evaluated under Multi location 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	83	103	426.13	298.41	.0000000 ***	.0000000 ***
Genotype (G)	5	7	178.26	69.83	.0000000 ***	.0001087 ***
Environment (E)	11	12	2288.70	2,098.36	.0000000 ***	.0000000 ***
GxE interaction	55	84	72.68	60.33	.0000000 ***	.0000000 ***
IPC1	17	18	162.35	154.95	.0000000 ***	.0000000 ***
IPC2	15	16	50.25	59.42	.0000000 ***	.0000046 ***
IPC3	13	14	45.34	37.48	.0000019 ***	.0046801 **
IPC4	11	12	33.75	38.27	.0008550 ***	0.0664857
IPC5		10		15.35		0.5967352
IPC6		8		17.20		0.6060953
Residual	9	6	27.75	8.73	.0251341	0.7687105
Error	252	312	12.83	15.83		
Total	335	415	115.23	85.96		

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

Genotype	IPCA1	IPCA2	IPCA3	IPCA4	MASV1	MASV	W1	W2	W3	WAASB	R_{IPCA1}	R_{MASV1}	R_{MASV}	R_{W1}	R_{W2}	R_{W3}	R_{WAASB}
HI 8627	-1.650	-1.994	-1.103	1.331	4.756	4.158	1.650	1.731	1.621	1.587	3	4	4	3	3	4	4
DBW 110	2.465	-1.137	-0.523	0.340	4.456	3.643	2.465	2.151	1.865	1.689	5	3	3	5	5	5	5
UAS 466	-3.357	0.745	-0.676	-1.433	5.719	4.671	3.357	2.740	2.377	2.268	6	6	5	6	6	6	6
MP 3288	0.833	2.796	-0.594	1.361	5.389	4.772	0.833	1.297	1.174	1.195	2	5	6	2	2	2	2
DBW 277	2.277	-0.194	-0.232	-1.932	4.120	3.480	2.277	1.784	1.511	1.560	4	2	2	4	4	3	3
DDW 47	-0.568	-0.216	3.128	0.332	3.304	3.358	0.568	0.485	0.949	0.878	1	1	1	1	1	1	1

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

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Stable and productive génotypes by AMMI & BLUP

An average yield of genotypes as per BLUP values of genotypes yield selected DBW110, DBW277 wheat genotypes (Table 5). This method is simple, but not fully exploiting all information contained in the dataset. A geometric mean is used to evaluate the adaptability of genotypes and genotypes with high GM will be desirable. Geometric mean top-ranked DBW110, MP3288 genotypes. As proposed by Resende [15], 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 expressed higher values for DBW110, MP3288 genotypes. Moreover, the Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) method proposed by Resende [15] that used Restricted Maximum Likelihood (REML) or Best Linear Unbiased Prediction (BLUP) as similar to the methods of Lin and Binns [16] and Annicchiarico [17]. In the HMRPGV method for stability analysis, the genotypes can be simultaneously sorted by genotypic values (yield) and stability using the harmonic means of the yield so that the smaller the standard deviation of genotypic performance among the locations. Values of HMRPGV ranked DBW110, MP3288 the performance of the genotypes among the locations. When considering the yield and adaptability simultaneously, the recommended approach is the relative performance of genetic values (RPGV) overcrop years. For adaptability analysis, the Relative Performance of Genotypic Values had been measured across environments and settled for DBW110, MP3288 wheat genotypes.

While assigning 65 and 35 weights to average yield (AM) and stability, the Superiority index pointed out DBW110, MP3288 genotypes would maintain high yield and stable performance. SI measure, considered GM and stability, selected DBW110, MP3288 genotypes. Values of SI, using HM and stability, favored the same set of wheat genotypes DBW110, MP3288. Analytic measures of adaptability RPGV and MHRPGV pointed out DBW110, MP3288 would be more adaptable genotypes.

Biplot analysis of measures

Table 6 reflected approximately 81.5% of the total variation with 45.1% & 36.4 % contributions of the first two significant PC's [18]. A group comprised of MASV, MASV1 & stability measures by utilizing the number of interaction principal components (Figure 1). Adaptability measures as per arithmetic, geometric and harmonic means along with the corresponding values of RPGV & MHRPGV expressed bondage and placed together in a different quadrant. However, this group maintained right angle with MASV, MASV1 & stability measures. The cluster of Superiority indexes as per averages of the yield of wheat genotypes seen in a different quadrant. Moreover, the performance of genotypes would be more or less the same by Superiority indexes and adaptability measures as acute angles observed in corresponding rays.

Second-year 2019-20

Environment (E), genotypes (G) and GxE interaction effects were highly significant as mentioned by the AMMI analysis (Table 3). The environment significantly explained about 70.1%, GxE interaction accounted for 14.2% and genotypes accounted for only 1.3% of the total sum of squares. Significant six multiplicative terms explained 98.7 % and the remaining 1.3% residual was discarded.

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

The preference order of genotypes as per IPCA-1 scores was DDW47, UAS466, HI8823 (Table 7). While the values of IPCA-2 selected MP3288, UAS466, DBW110 genotypes would be of choice. Values of IPCA-3 favored DBW110, MP3288, UAS472 wheat genotypes. As per IPCA-4, UAS472, DDW47, HI8627 genotypes would be of stable performance. DBW110, HI8627, MPO1357, genotypes pointed by IPCA-5 measure. Genotypes HI8823, MPO1357, DDW47 were identified by absolute values of IPCA-6. Analytic MASV and MASV1 measures of adaptability considered all significant IPCAs of the analysis simultaneously. MASV1 identified genotypes UAS466, HI8627, MP3288 would express stable yield whereas genotypes HI8627, UAS466, UAS472 be of stable performance by MASV measure respectively.

Genotype preferences varied from DDW47, UAS466, HI8823 based on W1 whereas UAS466, DDW47, HI8627 as per W2 values while UAS466, DDW47, HI8627 by values of W3 (Table 8). Genotypes UAS466, DDW47, HI8627 were pointed by W4; W5 favored UAS466, DDW47, HI8627. Stability measure WAASB based on all significant IPCA's settled for UAS466, DDW47, HI8627 genotypes for considered locations of the zone for stable high yield. The genotype ranking was altered by the extent to the number of IPCAs included in the WAASB estimation. This reinforced the benefits of using the WAASB

Table 5: 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	MHRPGVu	Rk	RPGVu	Rk
HI 8627	38.04	4	46.35	4	36.83	4	46.08	4	35.79	4	45.24	4	0.9806	4	0.9898	4
DBW 110	40.39	1	79.58	1	39.40	1	79.58	1	38.55	1	79.58	1	1.0470	1	1.0605	1
UAS 466	37.51	5	21.11	6	35.81	5	14.66	6	34.29	5	8.07	6	0.9489	5	0.9679	5
MP 3288	39.08	3	71.96	2	38.15	2	74.45	2	37.39	2	76.54	2	1.0162	2	1.0246	2
DBW 277	39.18	2	64.36	3	38.11	3	64.69	3	37.18	3	64.49	3	1.0140	3	1.0244	3
DDW 47	36.13	6	35.00	5	34.77	6	35.00	5	33.69	6	35.00	5	0.9272	6	0.9328	6

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

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Table 6: Loadings of measures as per first two significant Principal Components (2018-19).

Measure	PC1	PC2
IPCA1	-0.2764	-0.1720
IPCA2	-0.0125	-0.0116
IPCA3	0.1899	-0.2661
IPCA4	-0.0467	-0.1721
MASV1	-0.0493	0.2891
MASV	0.0089	0.2039
W1	-0.0367	0.3482
W2	-0.0800	0.3665
W3	-0.0109	0.3681
W4	-0.0153	0.3759
WAASB	-0.0153	0.3759
AMu	-0.3332	0.0805
SI au	-0.3252	-0.1155
GMu	-0.3397	0.0385
SI gu	-0.3169	-0.1408
HMu	-0.3415	0.0004
SI hu	-0.3085	-0.1617
RPGVu	-0.3373	0.0584
MHRPGVu	-0.3409	0.0218
81.52	45.11	36.41

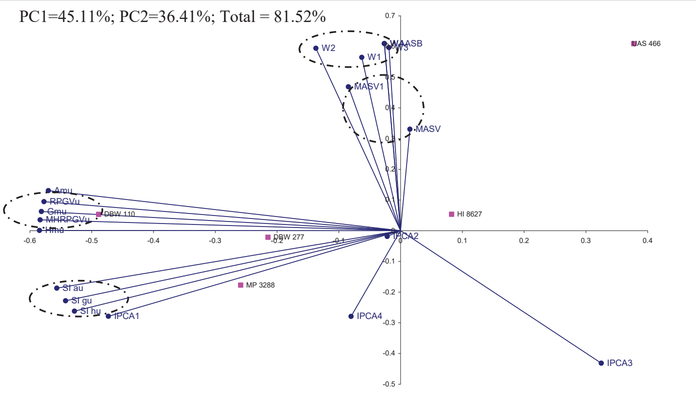

Figure 1: Biplot analysis of measures as per first two significant PCA's (2018-19).

index since it captures the variations of all IPCAs to compute the stability.

Stable and Productive genotypes by AMMI & BLUP

Average yield based on BLUP values of genotypes selected HI8823, MP3288, DBW110 wheat genotypes (Table 9). Geometric mean observed HI8823, MP3288, DBW110 were top-ranked genotypes. Harmonic Mean of yield expressed higher values for MP3288, HI8823, DBW110 genotypes. Values of HMRPGV ranked MP3288, HI8823, DBW110 the performance of the genotypes among the locations. Relative Performance of Genotypic Values had settled for HI8823, MP3288, DBW110 wheat genotypes.

While assigning 65 and 35 weights to average yield (AM) and stability, the Superiority index pointed out HI8823, MP3288, DBW110 genotypes would maintain high yield and stable performance. SI measure considered GM and stability, selected HI8823, MP3288, DBW110 genotypes. Values of SI, using HM and stability, favored the same set of wheat genotypes HI8823, MP3288, DDW47. Analytic measures of adaptability RPGV and MHRPGV pointed out HI8823, MP3288, DBW110 would be more adaptable genotypes.

Biplot analysis of measures

The first two significant PC's jointly has explained 73.5% of the total variation with 44.7% & 28.8% contributions by PC1 & PC2 (Table 10). The first group comprised of MASV, MASV1 while the second observed for stability measures by utilizing many interaction principal components (Figure 2). Adaptability measures as per arithmetic, geometric and harmonic means along with the corresponding values of RPGV & MHRPGV expressed bondage and placed in a different quadrant. However, this group maintained nearly the right angle with stability measures. The cluster of Superiority indexes as per averages of the yield of wheat genotypes seen in the same quadrant. The performance difference of genotypes would be very minimum by Superiority indexes as compared to adaptability measures.

Conclusions

GxE interaction in multi-location trials had been studied by AMMI model. Recent analytic measures advocated simultaneous use of stability & yield to recommend high-

Table 7: Modified AMMI stability values as per significant IPCA's 2019-20.

Genotype	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	IPCA6	MASV1	MASV	R_{IPCA1}	R_{MASV1}	R_{MASV}
MPO1357	-1.075	-1.706	2.285	0.751	-0.328	-0.512	7.534	5.489	4	6	6
HI8627	-1.147	1.129	-1.410	-0.307	-0.226	-0.690	5.128	3.725	5	2	1
UAS466	-0.451	0.250	0.796	-2.046	0.611	1.428	4.404	3.860	2	1	2
UAS472	-2.291	-0.361	-0.643	-0.101	1.276	-0.869	6.109	4.299	7	4	3
DBW110	3.782	0.328	0.378	-0.994	-0.034	-1.088	7.234	5.488	8	5	5
MP3288	1.866	-0.058	-0.514	2.028	1.082	0.864	5.877	4.617	6	3	4
HI8823	-0.824	2.537	0.646	0.852	-1.067	0.318	8.887	5.825	3	8	8
DDW47	0.139	-2.119	-1.540	-0.182	-1.313	0.549	8.422	5.625	1	7	7

Table 8: Weighted average of absolute scores and ranks of genotypes 2019-20.

Genotype	W1	W2	W3	W4	W5	WAASB	R_{W1}	R_{W2}	R_{W3}	R_{W4}	R_{W5}	R_{WAASB}
MPO1357	1.075	1.249	1.404	1.318	1.268	1.228	4	4	6	5	5	5
HI8627	1.147	1.142	1.182	1.067	1.024	1.007	5	3	3	3	3	3
UAS466	0.451	0.395	0.455	0.665	0.662	0.703	2	1	1	1	1	1
UAS472	2.291	1.756	1.590	1.394	1.388	1.360	7	7	7	7	7	7
DBW110	3.782	2.825	2.461	2.267	2.155	2.098	8	8	8	8	8	8
MP3288	1.866	1.365	1.238	1.343	1.329	1.305	6	6	5	6	6	6
HI8823	0.824	1.299	1.202	1.155	1.151	1.107	3	5	4	4	4	4
DDW47	0.139	0.688	0.815	0.731	0.761	0.749	1	2	2	2	2	2

Table 9: Superiority index and analytic adaptability measures based on BLUP's of genotypes 2019-20.

Genotype	AMu	Rk	SI au	Rk	GMu	Rk	SI gu	Rk	HMu	Rk	SI hu	Rk	MHRPGVu	Rk
MPO1357	39.52	8	21.84	8	38.70	8	21.84	8	37.90	8	0.959	8	0.964	8
HI8627	40.55	5	52.10	6	39.71	6	51.13	5	38.92	6	0.985	6	0.989	6
UAS466	39.88	7	43.57	7	38.96	7	41.07	7	38.12	7	0.967	7	0.970	7
UAS472	41.07	4	55.74	3	40.21	4	53.92	4	39.35	4	0.995	4	1.003	4
DBW110	41.69	3	52.12	5	40.71	3	47.17	6	39.74	3	1.004	3	1.020	3
MP3288	42.06	2	81.02	2	41.47	2	84.84	2	40.87	1	1.028	1	1.033	2
HI8823	42.23	1	89.88	1	41.47	1	89.88	1	40.75	2	1.028	2	1.033	1
DDW47	40.41	6	55.14	4	39.74	5	58.17	3	39.08	5	0.986	5	0.989	5

Table 10: Loadings of measures as per first two significant Principal Components (2019-20).

Measure	PC1	PC2
IPCA1	-0.1810	-0.0878
IPCA2	-0.1362	0.1359
IPCA3	0.0331	-0.1559
IPCA4	-0.1341	0.1405
IPCA5	-0.0338	-0.0742
IPCA6	0.1102	0.2696
MASV1	-0.1064	0.0415
MASV	-0.1174	-0.0118
W1	-0.2294	-0.2371
W2	-0.2495	-0.2282
W3	-0.2297	-0.2557
W4	-0.2392	-0.2479
W5	-0.2453	-0.2390
W6	-0.2424	-0.2430
WAASB	-0.2424	-0.2430
AMu	-0.2868	0.1444
SI au	-0.2022	0.2910
GMu	-0.2788	0.1721
SI gu	-0.1880	0.3090
HMu	-0.2667	0.1992
SI hu	-0.1636	0.3296
RPGVu	-0.2880	0.1459
MHRPGVu	-0.2677	0.1977
73.56	44.73	28.83

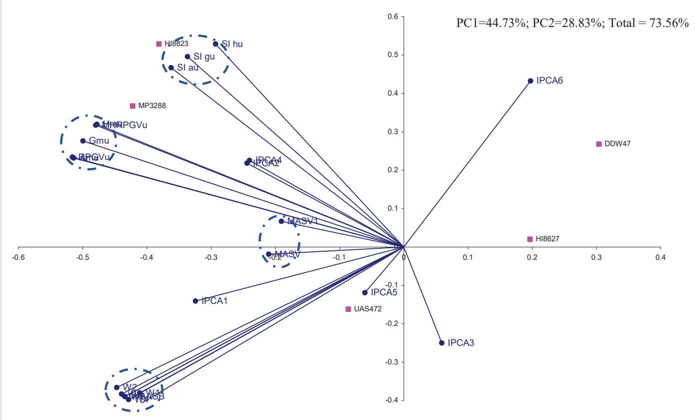

Figure 2: Biplot analysis of measures as per first two significant PCA's (2019-20)

yielding stable wheat genotypes. Infact both BLUP and AMMI have their efficacy increased depending on factors intrinsic to analysis. In the present study, the main advantages of AMMI and BLUP had been combined to increase the reliability of multi-locations trials analysis. The more interesting advantage provided by Superority Indexes that different weights may be assigned to the yield performance and stability. As per the goal of a breeding program or a cultivar recommendation trial, the researcher 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 a biplots while considering more of IPCA's.

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