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BLUP & AMMI model for stability analysis of wheat genotypes evaluated under irrigated timely sown trials in North Eastern Plains Zone of India

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Environments explained 49.4%, G×E interaction 28.1%, and genotypes only 5.6% of the total sum of squares due to treatments for the first year of studied period 2018-2019 and 2019-2020. More than 95% of variations had been accounted for by the first seven interaction principal components. Superiority indexes had identified WH1239, DBW187, HD3249 genotypes as per the BLUE estimates. Same genotypes were highlighted by superiority and other measures based on BLUP of genotypes. Adaptability measures as per BLUEs expressed deviation from other measures and maintained the right angle with MASV1 and stability measures in Biplot analysis. Superiority indexes were clustered in the same quadrant. Similar clustering patterns had been displayed by measures based on BLUPs. Wheat genotypes HD3249, K1006 selected by superiority indexes and adaptability measures for the second year. Biplot analysis utilized 80% variability accounted by two PCs. Adaptability measures were placed in a different quadrant. However, measures maintained nearly the right angle with other stability measures with exception of superiority indexes. A similar pattern of clustering had been observed for adaptability as well as superiority indexes as per BLUP of genotypes.

Key words: AMMI model, MASV, WAASB, SI, SSI, Biplot analysis.

INTRODUCTION

A large number of statistical analytics has been developed to estimate G×E interactions under multi location trials (Agahi et al., 2020). Widely utilized AMMI analysis considered the fixed-effect of genotypes under linear model (Mohammadi et al., 2015). Recently, it may be reasonable to consider genotypes, environments, or both to be random effects in a mixed model approach (Piepho et al., 2008; Mendes et al., 2012). BLUP proved the potential to improve the predictive accuracy of

random effects (Ajay et al., 2020). BLUP and AMMI, two distinct approaches, utilized to distinguish the pattern from the random error components in G×E interactions. AMMI analysis retained most of the G×E pattern in the first interaction principal component axis (IPCA), while most of the random error had been explained by the last IPCAs (Gauch, 2013). BLUP, on the other hand, first estimated the effects of the ANOVA model and then attributes weights to these effects and could thus be

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considered a shrinkage estimator (Piepho, 1994). Frequently, these two models have been used separately in the field evaluation of genotypes under multi location trials (Sa'diyah and Hadi, 2016; Ashwini et al., 2021). Taking into account the importance of AMMI and BLUP, the benefits of these two important techniques were incorporated into a measure superiority index for stability and adaptability of genotypes (Olivoto et al., 2019). Further, the behavior of stability and adaptability measures had been compared as per BLUP and BLUE of wheat genotypes evaluated under multi-location trials under irrigated timely sown trials in the North Eastern Plains Zone of the country.

MATERIALS AND METHODS

The zone has immense potential to increase the wheat production of the country as highly productive states Bihar, eastern Uttar Pradesh, Jharkhand, Assam and plains of West Bengal comprise the North Eastern Plains Zone of the India. Still scope to increase the cereal production of the country has untapped and additional production to the potential of crops to ensure food security of the country. Eleven promising wheat genotypes at advanced stages

tested at fifteen major locations and six genotypes at seventeen yield. Details of locations and parentage of evaluated genotypes are shown in Tables 1 and 2 for ready reference.

Stability measure Weighted Average of Absolute Scores (WAASB) was calculated as:

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

Where WAASBi 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 *θ_Y* and *θ_S* were the weights for yield and stability assumed to be of order 65 and 35, respectively in this study.

Mohamadi and Amri (2008) Geometric Adaptability Index

$$GAI = \sqrt[n]{\prod_{k=1}^n \bar{X}_k}$$

Zali et al. (2012) Modified AMMI stability Value

$$MASV = \sqrt{\sum_{n=1}^{N-1} \frac{SSIPC_n}{SSIPC_{n+1}} (PC_n)^2 + (PC_{n+1})^2}$$

Ajay et al. (2019) **MASV1**

$$MASV1 = \sqrt{\sum_{n=1}^{N-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}} PC_n \right)^2 + (PC_{n+1})^2}$$

Resende and Durate (2007) Relative performance of genotypic values across environments

$$PRVG_{ij} = VG_{ij} / VG_i$$

Resende and Durate (2007) Harmonic mean of Relative performance of genotypic values

$$MHPRVG_i = \text{Number of environments} / \sum_{j=1}^k \frac{1}{PRVG_{ij}}$$

Oliveto et al. (2019) Superiority Index

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

AMMI analysis was performed using AMMISOFT version 1.0, available at <https://scs.cals.cornell.edu/people/hugh-gauch/> and SAS software version 9.3. Stability measures compared 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 AMMI analysis

AMMI analysis gave highly significant effects of environment (E), genotypes (G), and Gx E interaction.

Table 1. Details of location and parentage of evaluated wheat genotypes (2018-2019).

Code	Genotype	Parentage	Location	Latitude	Longitude	Mean sea level
G 1	HD 3249	(PBW343*2/KUKUNA//SRTU/3/PBW343*2/KHVAKI)	Kanpur	26° 26' N	80° 19' E	126
G 2	HD 2733	(ATTILA/3/TUI/CARC//CHEN/CHTO/4/ATTILA)	Faizabad	26° 46' N	82° 9' E	97
G 3	PBW 781	(PBW621/4/BW9250*3//Yr10/6* Avocet/3/ BW9250*3//Yr15/6* Avocet/5/2*PBW 621)	Varanasi	25° 19' N	82° 59' E	81
G 4	DBW 257	(HUW640/HD3055)	Gorkhpur	26° 45' N	83° 21' E	84
G 5	DBW 39	(ATTILA/HUI)	IARI Pusa	28°38' N	77°09' E	52
G 6	HD 3277	(CHEN/AEG.SQUARROSA//BCN/3/BAV92/4/BERKUT)	Sabour	25°23' N	87°04' E	46
G 7	RAJ 4529	(PHS 0624/WR1136)	Purnea	25° 46' N	87° 28' E	36
G 8	DBW 187	(NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU)	Banka (RRSS Tilaundha)	24° 53' N	86° 55' E	79
G 9	WH 1239	(TAM200/PASTOR//TOBA97)	RPCAU-Pusa	25°98' N	25°67' E	52
G 10	K0307	(K8321/UP2003)	Ranchi	23° 20'N	85° 18'E	644
G 11	HD 2967	(ALD/CUC//URES/HD2160M/HD2278)	Chianki	23°45'N	85°30'E	215
			Dumka	24°27' N	87°26' E	137
			Kalyani	22° 58' N	88° 26'E	11
			Burdhwan	23° 13' N	87° 51' E	30
			Shillongani	26° 8' N	91° 43' E	86

Table 2. Details of location and parentage of evaluated wheat genotypes (2019-2020).

Code	Genotype	Parentage	Location	Latitude	Longitude	Mean sea level
G 1	PBW804	(SOKOLL/3/PASTOR//HXL7573/2*BAU/4/HUW234+LR34/PRINIA//PBW34 3*2/KUKUNA/3/ROLF07	Kanpur	26° 26'N	80° 19'E	133
G 2	DBW187	(NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU)	Faizabad	26° 46' N	82° 9' E	97
G 3	K1006	(PBW343/HP1731)	Varanasi	25° 19' N	82° 59'E	84
G 4	DBW39	(ATTILA/HUI)	Araul	26° 54'N	80° 01'E	139
G 5	HD3249	(PBW343*2/KUKUNA//SRTU/3/PBW343*2/KHVAKI)	Gorakhpur	26° 45'N	83° 22'E	84
G 6	HD2733	ATTILA/3/TUI/CARC//CHEN/CHTO/4/ATTILA)	IARI Pusa	25°98' N	85°67'E	56
			Sabour	25°23' N	87°04'E	42
			Purnea	25° 46' N	87° 28'E	43
			Banka	24° 53' N	86° 55' E	79
			RPCAU-Pusa	25°98' N	25°67' E	52
			Ranchi	23° 20'N	85° 18'E	644
			Chianki	24° 01' N	84° 10'E	241
			Dumka	24° 16' N	87° 14'E	137
			Coochbehar	26° 34' N	89° 44'E	42
			Kalyani	22° 58' N	88° 26'E	16
			Burdwan	23° 13'N	87° 51'E	38
			Shillongani	26° 8' N	91° 43' E	86

Table 3. AMMI analysis of wheat genotypes for irrigated timely sown trials 2018-2019.

Source	Degree of freedom	Sum of Squares	Mean Sum of Squares	Probability
Treatments	164	37022.65	225.75	0.0000000 ***
Genotypes (G)	10	2519.47	251.95	0.0000000 ***
Environments (E)	14	21994.21	1571.01	0.0000000 ***
Interactions G×E	140	12508.97	89.35	0.0000000 ***
IPC1	23	4362.34	189.67	0.0000000 ***
IPC2	21	2786.12	132.67	0.0000000 ***
IPC3	19	1722.60	90.66	0.0000000 ***
IPC4	17	1256.40	73.91	0.0000000 ***
IPC5	15	838.74	55.92	0.0000000 ***
IPC6	13	690.41	53.11	0.0000104 ***
IPC7	11	420.83	38.26	0.0064488 **
Residual	21	431.52	20.55	0.128013
Error	495	7438.83	15.03	
Total	659	44461.48	67.47	

Table 4. Modified AMMI stability values as per significant IPCAs 2018-2019.

Genotype	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	IPCA6	IPCA7	MASV1	MASV	R _{IPCA1}	R _{MASV1}	R _{MASV}
HD 3249	0.685	0.537	-1.808	0.087	-1.948	-0.137	0.056	4.593	4.209	3	2	1
HD 2733	1.711	2.077	1.557	0.269	0.234	-2.501	-0.185	7.298	6.203	8	11	11
PBW 781	1.324	1.607	0.021	1.182	0.403	1.966	1.277	5.871	5.019	6	6	5
DBW 257	1.034	1.057	-2.548	0.015	0.972	0.040	-0.260	5.269	4.707	5	3	4
DBW 39	-2.494	0.000	-1.632	0.026	0.944	-0.830	-0.392	5.274	4.472	10	4	3
HD 3277	0.470	1.216	1.788	-1.454	0.537	1.414	-1.511	5.687	5.029	2	5	6
RAJ 4529	-3.746	0.277	1.246	2.019	0.099	0.171	0.076	7.246	6.011	11	10	10
DBW 187	0.974	-2.873	-0.215	0.518	0.233	0.304	-1.674	6.038	5.200	4	7	7
WH 1239	-0.324	-0.497	0.604	-0.331	-2.728	0.076	0.056	4.583	4.295	1	1	2
K0307	-1.432	-0.642	0.134	-3.031	0.463	-0.084	1.262	6.206	5.419	7	8	8
HD 2967	1.797	-2.760	0.853	0.701	0.790	-0.419	1.296	6.560	5.610	9	9	9

The analysis showed the greater contribution of environments, G×E interactions, and genotypes to the total sum of squares (SS) as compared to the residual effects. Further SS attributable to G×E interactions was partitioned as attributed to G×E interactions signal and G×E interactions noise. AMMI analysis is appropriate for data sets where-in SS due to interactions were of magnitude at least due to additive genotype main effects (Gauch, 2013). Environments explained significantly about 49.4% of the total sum of squares due to treatments (Table 3) which indicated the diversity of studied locations (Ajay et al., 2020). Genotypes explained only 5.6% of the total sum of squares, whereas G×E interaction accounted for 28.1% of treatment variations in yield. The higher percentage of G×E interaction as compared to genotypes supported the presence of complex G×E interaction for wheat yield. First seven significant interaction principal components (IPCA1, IPCA2..., IPCA7) explained 34.8, 22.2, 13.7, 10, 6.7, 5.5 and 3.3% of G×E interaction sum of squares, respectively.

The total of significant components was 96.5% and the remaining was the residual (Oyekunle et al., 2017).

Ranking of genotypes vis-à-vis number of IPCAs

Values of IPCAs in the AMMI analysis indicate stability or adaptability of genotypes. The greater the IPCA scores reflect the specific adaptation of genotype to certain locations. While values approximate to zero recommends in general adaptations over all the locations, for the genotype. Genotypes as per absolute IPCA-1 scores were WH1239, HD3277, and HD3249. While for IPCA-2, genotypes DBW39, RAJ4529, and WH1239, would be of choice (Table 4). Values of IPCA-3 favored PBW781 K0307, DBW187, wheat genotypes. As per IPCA-4, DBW257 DBW39, and HD3249, genotypes would be of stable performance. RAJ4529, DBW187, and HD2733 genotypes were pointed by IPCA-5 measure. Genotypes DBW257,

Table 5. Weighted average of absolute scores and ranks of wheat genotypes 2018-2019.

Genotype	W1	W2	W3	W4	W5	W6	WAASB	R _{W1}	R _{W2}	R _{W3}	R _{W4}	R _{W5}	R _{W6}	R _{WAASB}
HD 3249	0.685	0.624	0.884	0.763	0.885	0.819	0.773	3	2	2	2	2	2	2
HD 2733	1.711	1.862	1.795	1.563	1.426	1.522	1.442	8	9	9	9	9	10	9
PBW 781	1.324	1.440	1.129	1.137	1.061	1.142	1.150	6	6	5	4	4	7	7
DBW 257	1.034	1.043	1.374	1.167	1.147	1.048	1.001	5	4	6	5	6	4	3
DBW 39	2.494	1.467	1.503	1.279	1.245	1.208	1.159	10	7	8	7	8	8	8
HD 3277	0.470	0.777	0.999	1.068	1.014	1.049	1.077	2	3	4	3	3	5	5
RAJ 4529	3.746	2.318	2.083	2.073	1.870	1.718	1.619	11	11	11	11	11	11	11
DBW 187	0.974	1.756	1.417	1.281	1.173	1.095	1.130	4	8	7	8	7	6	6
WH 1239	0.324	0.395	0.441	0.424	0.662	0.609	0.576	1	1	1	1	1	1	1
K0307	1.432	1.107	0.893	1.218	1.140	1.046	1.059	7	5	3	6	5	3	4
HD 2967	1.797	2.194	1.899	1.717	1.622	1.515	1.502	9	10	10	10	10	9	10

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

WH1239, and K0307 were identified by absolute values of IPCA-6. As per IPCA-7, desirable genotypes would be HD 3249, WH1239, and RAJ4529 for considered locations of the zone. Adaptability measures MASV and MASV1 considered all seven significant IPCAs of the AMMI analysis. Values of MASV1 identifying WH1239, HD3249, and DBW257 genotypes would express stable yield whereas genotypes HD3249, WH1239, and DBW39 would be of stable performance by MASV measure, respectively (Ajay et al., 2019).

To identify how the ranks of evaluated wheat genotype was altered with utilizing numbers of IPCA in the WAASB estimation, the genotype's ranks were obtained while considering 1, 2,..., p IPCAs 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 genotypes varied from WH1239, HD3277, and HD3249, based on W1 to WH1239, HD3249, and HD3277 as per W2 values while WH1239, HD3249, and K0307 by values of W3 (Table 5). Genotypes WH1239, HD3249, and HD3277 were pointed by W4; W5 favored WH1239, HD3249, and HD3277.

As per W6 measure, the genotypes WH1239, HD3249 and K0307 got higher ranks for their stable performance. Stability measures WAASB based on seven significant IPCAs simultaneously and settled for WH1239, HD3249, and DBW257 genotypes for considered locations of the zone for stable high yield. The genotype's ranking was altered utilizing a greater number of IPCAs in the stability estimation (Olivoto et al., 2019).

Productive and broadly adapted genotypes (AMMI + BLUP)

Mean yield of genotypes as per their BLUP estimates

selected DBW187, WH1239, and HD3249 wheat genotypes (Table 6). This method is simple, but not fully exploiting all information contained in the dataset. Geometric mean was also recommended to study the adaptability of genotypes (Mohamadi and Amri, 2008). Geometric mean showed higher values of DBW187, WH1239, and HD3249 as the top-ranked genotypes. As proposed by Resende (2007), the harmonic mean of genetic values (HMGV) considered the yield and stability simultaneously for the ranking of genotypes for their performance. Harmonic mean found maximum values by DBW187, WH1239, and HD3249 genotypes. Moreover, the Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) method proposed by Resende (2007a) is similar to the methods of Lin and Binns (1988) and Annicchiarico (1992). 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 DBW187, WH1239, and HD3249 with the performance of the genotypes among the locations. While considering the yield and adaptability simultaneously, the recommended approach was to calculate the relative performance of genetic values (RPGV) overcrop years. Relative performance of genotypic values settled for DBW187, WH1239, and HD3249 wheat genotypes.

While assigning 65 and 35 weights to yield and stability, the superiority index pointed out WH1239, DBW187, and HD3249 genotypes would maintain high yield and stable performance. SI measure, considered GM and stability WH1239, DBW187, and HD3249 selected genotypes. Values of SI, using HM and stability, favored the same set of wheat genotypes WH1239, DBW187, and HD3249. Analytic measures of adaptability RPGV and MHRPGV pointed out DBW187, WH1239, and HD3249 would be more adaptable genotypes.

Table 6. Superiority index and analytic adaptability measures based on BLUPs of genotypes 2018-2019.

Genotype	AMu	Rk	SI au	Rk	GMu	Rk	SI gu	Rk	HMu	Rk	SI hu	Rk	RPGVu	Rk	MHRPGVu	Rk
HD 3249	48.53	3	67.40	3	48.22	3	69.65	3	47.89	3	71.97	3	1.0289	3	1.0249	3
HD 2733	47.86	4	36.38	5	47.31	4	35.34	5	46.73	4	34.32	5	1.0115	4	1.0037	4
PBW 781	46.56	7	29.55	6	45.98	7	27.79	6	45.39	6	26.49	6	0.9819	7	0.9766	7
DBW 257	45.48	11	20.74	9	45.05	11	20.74	8	44.60	10	21.16	8	0.9628	10	0.9561	11
DBW 39	46.03	9	22.49	8	45.54	8	21.85	7	45.05	8	21.77	7	0.9747	8	0.9646	8
HD 3277	46.93	6	36.75	4	46.49	5	36.87	4	46.01	5	37.10	4	0.9925	5	0.9876	5
RAJ 4529	46.09	8	7.87	11	45.34	9	3.72	11	44.57	11	0.00	11	0.9733	9	0.9572	10
DBW 187	50.57	1	81.40	2	50.04	1	81.40	2	49.52	1	81.40	2	1.0688	1	1.0628	1
WH 1239	49.87	2	91.05	1	49.43	2	92.11	1	48.97	2	92.76	1	1.0552	2	1.0505	2
K0307	45.52	10	19.28	10	45.06	10	18.93	9	44.61	9	19.35	9	0.9623	11	0.9573	9
HD 2967	47.10	5	24.64	7	46.18	6	18.67	10	45.22	7	12.56	10	0.9879	6	0.9794	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.

Table 7. Superiority index and analytic adaptability measures based on BLUEs of genotypes 2018-2019.

Genotype	AMe	Rk	SI ae	Rk	GMe	Rk	SI ge	Rk	HMe	Rk	SI he	Rk	RPGVe	Rk	MHRPGVe	Rk
HD 3249	48.81	3	67.12	3	48.49	3	69.50	3	48.16	3	72.86	3	1.0358	3	1.0300	3
HD 2733	48.16	4	37.45	4	47.53	4	36.12	5	46.86	4	36.34	5	1.0170	4	1.0076	4
PBW 781	45.93	7	22.37	6	45.34	7	21.26	6	44.76	7	23.45	8	0.9690	8	0.9625	7
DBW 257	45.33	11	20.74	7	44.88	10	21.03	7	44.40	10	24.55	6	0.9602	11	0.9512	10
DBW 39	45.79	8	20.63	9	45.34	8	20.96	8	44.88	6	24.47	7	0.9710	7	0.9597	8
HD 3277	47.06	5	37.40	5	46.54	5	37.25	4	45.98	5	39.12	4	0.9945	5	0.9881	5
RAJ 4529	45.67	9	3.77	11	44.85	11	0.00	11	44.04	11	0.00	11	0.9646	9	0.9455	11
DBW 187	51.17	1	81.40	2	50.61	1	81.40	2	50.07	1	81.40	2	1.0814	1	1.0747	1
WH 1239	50.41	2	91.54	1	49.95	2	92.57	1	49.46	2	93.46	1	1.0665	2	1.0615	2
K0307	45.50	10	20.65	8	44.97	9	20.13	9	44.45	9	23.21	9	0.9615	10	0.9543	9
HD 2967	46.71	6	19.30	10	45.65	6	12.94	10	44.51	8	8.95	10	0.9785	6	0.9660	6

AMe, GMe, HMe = Arithmetic, Geometric, Harmonic Mean for BLUE values; SI ae, SI ge, SI he = Superiority index as per Arithmetic, Geometric, Harmonic Mean; RPGVe, MHRPGVe = Relative performance and Harmonic mean of Relative Performance as per BLUE of genotypes; Rk = Rank of genotypes.

Productive and broadly adapted genotypes (AMMI + BLUE)

Mostly employed average of a genotype across environments identified DBW187, WH1239, and HD3249 wheat genotypes (Table 7). Genotypes with higher values of DBW187, WH1239, and HD3249 would be recommended. Wheat genotypes DBW187, WH1239, and HD3249 were selected by the harmonic mean measure. For adaptability analysis, the Relative Performance of Genotypic values had been measured across environments, and genotypes DBW187, WH1239, and HD3249 would be of choice.

The superiority index measures by assigning 65:35 weights to yield and stability pointed out WH1239, DBW187, and HD3249 genotypes would maintain high yield and stable performance. Moreover, for SI values,

GM and stability were considered selected WH1239, DBW187, and HD3249 genotypes. Moreover, the values of SI based on HM along with stability favored the same set of wheat genotypes WH1239, DBW187, and HD3249. Surprisingly the same genotypes WH1239, DBW187, and HD3249 observed as more adaptable to considered locations by RPGV and MHRPGV measures also.

Biplot analysis of measures BLUP

The first two significant PCs explained about 74.7% of the total variation (Table 8) with 54.5 and 20.1 contributions by PC1 and PC2 (Mohammadi et al., 2015). Random effects of wheat genotypes had been considered for stability measures. A group comprised stability measures by utilizing two or more number of

Table 8. Loadings of BLUP based measures as per first two significant Principal Components (2018-2019).

Measure	PC1	PC2
IPCA1	0.0898	0.0780
IPCA2	-0.0346	-0.1942
IPCA3	-0.0599	0.2130
IPCA4	-0.0717	0.2315
IPCA5	-0.2078	-0.0460
IPCA6	0.0494	-0.1601
IPCA7	-0.0924	-0.1393
MASV1	-0.2134	0.2308
MASV	-0.1976	0.2329
W1	-0.2287	0.0924
W2	-0.2143	0.2640
W3	-0.2254	0.2203
W4	-0.2505	0.1807
W5	-0.2460	0.1868
W6	-0.2482	0.1934
WAASB	-0.2465	0.1959
Amu	0.2080	0.2981
SI au	0.2572	0.1642
Gmu	0.2212	0.2716
SI gu	0.2616	0.1444
Hmu	0.2320	0.2434
SI hu	0.2649	0.1240
RPGVu	0.2158	0.2829
MHRPGVu	0.2264	0.2595
% variation explained	54.54	20.19

interaction principal components (Figure 1). Adaptability measures as per arithmetic, geometric and harmonic means along with the corresponding values of RPGV and MHRPGV expressed bondage with each other. The cluster is seen in different quadrants. Moreover, this group maintained the right angle with MASV, MASV1 and stability measures. Superiority indexes were based on the mean yield of wheat genotypes placed in the same quadrant. The performance difference of genotypes would be very less by superiority indexes and adaptability measures.

BLUE

Table 9 reflects the loadings of the stability measures as per the first two significant principal components while considering the fixed effects of genotypes. Two significant PCs have explained 74.7% of the total variation with respective contributions of 55.4 and 19.2% (Table 9). The first group comprised MASV, MASV1 (Ajay et al., 2020), and stability measures by

utilizing two or more number of interaction principal components (Figure 2). Adaptability measures as per arithmetic, geometric and harmonic means and their corresponding values expressed deviation from all already mentioned measures and observed in a different quadrant. However, this group maintained the right angle with MASV, MASV1, and stability measures. The cluster of superiority indexes as per averages of wheat genotypes yield was placed in the same quadrant. Performance of genotypes would not be different by superiority indexes and adaptability measures.

Second-year 2019-2020 AMMI analysis

Highly significant effects of environment (E), genotypes (G), and G×E interaction were observed by AMMI analysis of wheat genotypes evaluated under multi-location trials. The environment had explained significantly portion 64.2% of the total sum of squares due to treatments (Table 10). Genotypes explained only

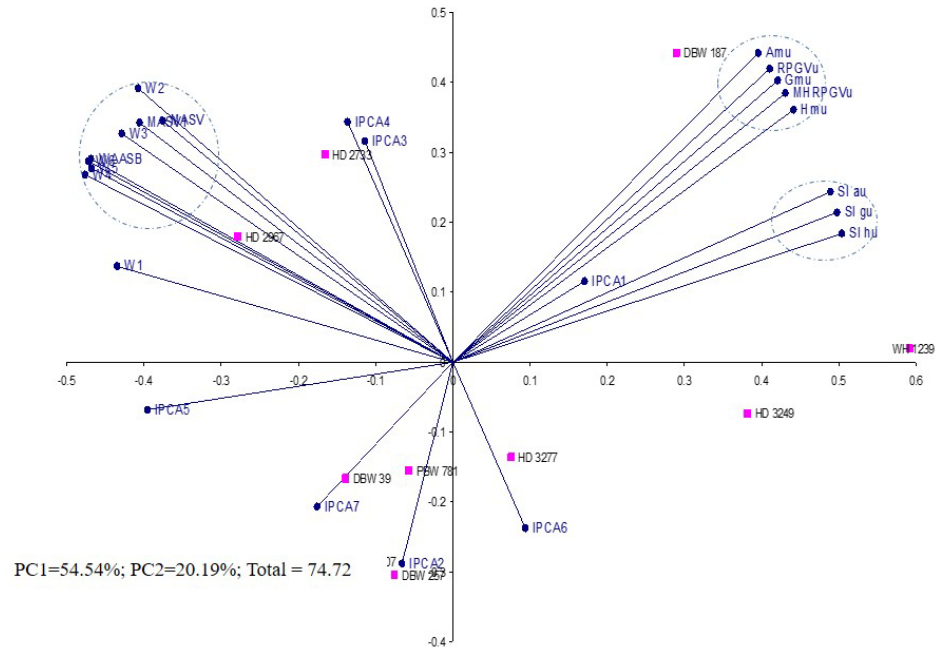


Figure 1. Biplot analysis of BLUP based measures as per first two significant PCAs (2018-2019).

Table 9. Loadings of BLUE based measures as per first two significant Principal Components (2018-2019).

Measure	PC1	PC2
IPCA1	-0.0851	0.0722
IPCA2	0.0302	-0.1908
IPCA3	0.0613	0.2178
IPCA4	0.0808	0.2084
IPCA5	0.2040	-0.0460
IPCA6	-0.0424	-0.1892
IPCA7	0.0970	-0.1660
MASV1	0.2118	0.2375
MASV	0.1955	0.2422
W1	0.2276	0.0881
W2	0.2168	0.2577
W3	0.2253	0.2200
W4	0.2495	0.1803
W5	0.2454	0.1854
W6	0.2478	0.1919
WAASB	0.2466	0.1933
Ame	-0.2115	0.2951
SI ae	-0.2558	0.1653
Gme	-0.2236	0.2682
SI ge	-0.2599	0.1453
Hme	-0.2332	0.2400
SI he	-0.2635	0.1203
RPGVe	-0.2186	0.2796
MHRPGVe	-0.2283	0.2562
% variation explained	55.46	19.26

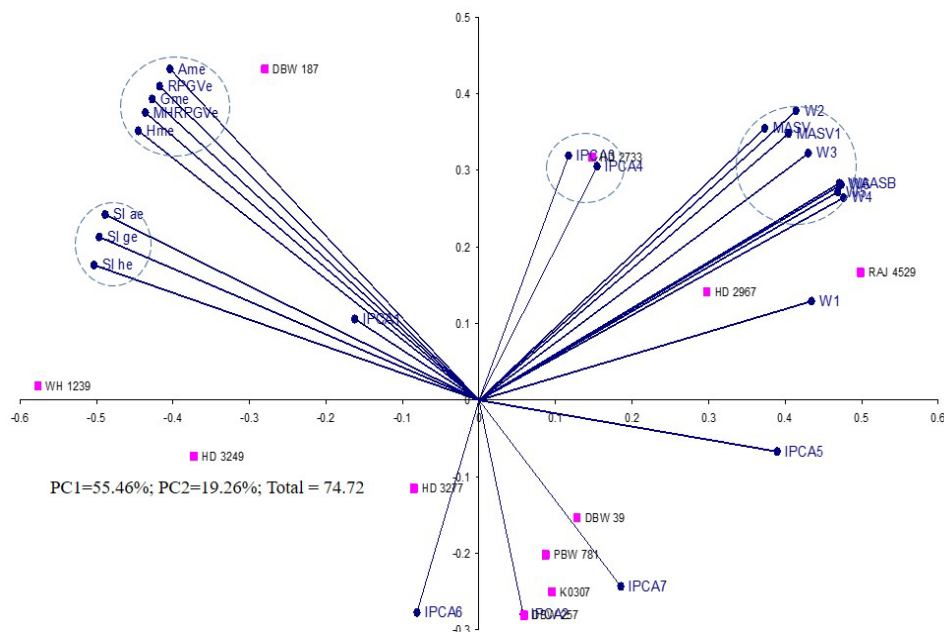


Figure 2. Biplot analysis of BLUE based measures as per first two significant PCAs (2018-2019).

Table 10. AMMI analysis of wheat genotypes for irrigated timely sown trials 2019-2020.

Source	Degree of freedom	Sum of Squares	Mean Sum of Squares	Probability
Treatments	101	35777.26	354.23	0.000000 ***
Genotypes (G)	5	1211.27	242.25	0.000000 ***
Environments (E)	16	26098.57	1631.16	0.000000 ***
Interactions G×E	80	8467.43	105.84	0.000000 ***
IPC1	20	2849.21	142.46	0.000000 ***
IPC2	18	1969.55	109.42	0.000000 ***
IPC3	16	1719.78	107.49	0.000000 ***
IPC4	14	1077.83	76.99	0.000000 ***
Residual	12	851.06	70.92	0.0000013 ***
Error	306	4865.79	15.90	
Total	407	40643.04	99.86	

2.9% of the total sum of squares, whereas G×E interaction accounted for 20.8% of treatment variations in yield. First four significant interaction principal components (IPCA1, IPCA2, IPCA3 and IPCA4) explained 33.6, 23.2, 20.3, and 12.7% of G×E interaction sum of squares, respectively. The total significant component was 89.9% of total variation which was accounted for by four interaction terms and the remaining leftover was the residual.

Ranking of genotypes vis-à-vis number of IPCAs

As per absolute IPCA-1 scores, genotypes were ranked

as HD2733 and HD3249. While for IPCA-2, genotypes PBW804 and DBW39 would be of choice (Table 11). Values of IPCA-3 favored PBW804 and K1006 wheat genotypes. As per IPCA-4, HD2733, and DBW187, genotypes would be of stable performance. Adaptability measures MASV and MASV1 considered all significant IPCAs of the analysis simultaneously. Values of MASV1 identified genotypes K1006 and HD3249 would express stable yield whereas genotypes K1006 and DBW39 would be of stable performance by MASV measure, respectively.

Values of stability measure W1 preferred HD2733 and HD3249 genotypes and HD3249 and DBW39 as per W2 values, while HD3249 and K1006 by values of

Table 11. Modified AMMI stability values as per significant IPCAs 2019-2020.

Genotype	IPCA1	IPCA2	IPCA3	IPCA4	MASV1	MASV	R _{IPCA1}	R _{MASV1}	R _{MASV}
PBW804	-3.957	-0.665	0.180	1.467	6.004	5.083	6	5	4
DBW187	1.131	-2.638	-3.045	-0.635	7.213	6.422	3	6	6
K1006	1.733	1.845	0.452	-0.870	3.954	3.596	4	1	1
DBW39	2.421	-0.695	1.696	2.557	5.489	4.850	5	3	2
HD3249	-0.728	-0.995	2.370	-2.562	5.466	4.902	2	2	3
HD2733	-0.600	3.148	-1.654	0.043	5.776	5.375	1	4	5

Table 12. Weighted average of absolute scores and ranks of genotypes 2019-2020.

Genotype	W1	W2	W3	WAASB	R _{W1}	R _{W2}	R _{W3}	R _{WAASB}
PBW804	3.957	2.527	1.825	1.762	6	6	5	4
DBW187	1.131	1.785	2.162	1.893	3	5	6	6
K1006	1.733	1.782	1.384	1.293	4	4	2	1
DBW39	2.421	1.671	1.679	1.834	5	2	3	5
HD3249	0.728	0.844	1.301	1.523	2	1	1	3
HD2733	0.600	1.707	1.691	1.400	1	3	4	2

Table 13. Superiority index and analytic adaptability measures based on BLUPs of genotypes 2019-2020.

Genotype	AMu	Rk	SI _{au}	Rk	GMu	Rk	SI _{gu}	Rk	HMu	Rk	SI _{hu}	Rk	RPGVu	Rk	MHRPGVu	Rk
PBW804	46.07	5	16.96	5	44.99	5	6.75	5	43.92	5	11.55	5	0.970	5	0.961	5
DBW187	47.80	3	35.76	4	46.90	3	36.21	3	46.00	3	37.05	4	1.010	3	1.002	3
K1006	48.34	2	78.97	2	47.64	2	47.75	2	46.93	2	86.91	1	1.026	2	1.019	2
DBW39	45.46	6	3.44	6	44.56	6	0.00	6	43.67	6	3.44	6	0.960	6	0.952	6
HD3249	49.72	1	86.58	1	48.75	1	65.00	1	47.75	1	86.58	2	1.050	1	1.043	1
HD2733	46.25	4	40.83	3	45.67	4	17.31	4	45.11	4	51.72	3	0.984	4	0.976	4

W3 (Table 12). Stability measures WAASB based on all significant IPCAs settled for K1006 and HD2733 genotypes for considered locations of the zone for stable high yield. It was observed that the genotype ranking was altered by the extent to which IPCAs are included in the WAASB estimation.

Productive and broadly adapted genotypes (AMMI + BLUP)

An average yield of genotypes as per BLUP values of genotypes yield selected HD3249 and K1006 wheat genotypes (Table 13). Geometric mean observed higher values for HD3249 and K1006 as top-ranked genotypes. Harmonic mean of yield expressed higher values for HD3249 and K1006 genotypes. Values of HMRPGV ranked HD3249 the genotypes performance among the locations. Relative Performance of Genotypic Values settled for HD3249 and K1006 wheat genotypes.

While assigning 65 and 35 weights to yield and stability, superiority indexes pointed out HD3249 and K1006 genotypes would maintain high yield and stable performance. Analytic measures of adaptability RPGV and MHRPGV pointed out HD3249 and K1006 would be more adaptable genotypes.

Productive and broadly adapted genotypes (AMMI + BLUE)

The arithmetic means identified HD3249 and K1006 wheat genotypes (Table 14). Geometric mean selected HD3249 and K1006 genotypes with high values. HD3249 and K1006 genotypes were selected by measure of Harmonic mean. For 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. Wheat genotypes HD3249 and K1006

Table 14. Superiority index and analytic adaptability measures based on BLUEs of genotypes 2019-2020.

Genotype	AMe	Rk	SI ae	Rk	GMe	Rk	SI ge	Rk	HMe	Rk	SI he	Rk	RPGVe	Rk	MHRPGVe	Rk
PBW804	45.57	5	8.12	5	44.48	6	7.64	5	43.39	6	7.64	5	0.960	5	0.948	6
DBW187	47.92	3	33.55	4	46.99	3	35.18	4	46.07	3	37.50	4	1.013	3	1.003	3
K1006	48.48	2	76.34	2	47.74	2	80.59	2	46.99	2	85.30	2	1.029	2	1.020	2
DBW39	45.54	6	3.44	6	44.49	5	3.63	6	43.47	5	4.61	6	0.960	6	0.949	5
HD3249	50.16	1	86.58	1	49.12	1	86.58	1	48.04	1	86.58	1	1.058	1	1.050	1
HD2733	45.98	4	34.94	3	45.40	4	41.58	3	44.82	4	48.88	3	0.979	4	0.969	4

Table 15. Loadings of BLUP based measures as per first two significant Principal Components (2019-2020).

Measure	PC1	PC2
IPCA1	-0.0549	-0.0058
IPCA2	-0.0660	0.3788
IPCA3	-0.0805	0.2369
IPCA4	0.2742	0.1753
MASV1	0.1470	-0.4112
MASV	0.1236	-0.4133
W1	0.1934	0.1571
W2	0.2164	0.1069
W3	0.2100	-0.2975
W4	0.2126	-0.2942
WAASB	0.2126	-0.2942
AMu	-0.2738	-0.1694
SI au	-0.2972	0.0011
GMu	-0.2832	-0.1486
SI gu	-0.2833	-0.1480
HMu	-0.2890	-0.1261
SI hu	-0.2952	0.0270
RPGVu	-0.2832	-0.1476
MHRPGVu	-0.2841	-0.1444
% variation explained	58.40	21.25

were selected by this measure. The Relative Performance of Genotypic Values found HD3249 and K1006 genotypes would be of choice.

Superiority index while assigning 65 and 35 weights to various averages yield and stability pointed out HD3249 and K1006 genotypes would maintain high yield and stable performance.

Biplot analysis of measures BLUP

The first two significant PCs jointly explained 79.6% of the total variation (Table 15) with 58.4 and 21.2 contributions by PC1 and PC2. A group comprised MASV, MASV1 and nearby group contained stability measures by utilizing three or more number of interaction principal components (Figure 3). As stability measures, the first two interaction principal components were placed

with IPCA4 measure. Adaptability measures as per arithmetic, geometric and harmonic means along with the corresponding values of RPGV and MHRPGV expressing bondage and placed in a different quadrant. Superiority indexes as per yield of wheat genotypes placed in another cluster occupied place in a separate quadrant. However, this group maintained right angle with AMMI based measures. The performance difference of genotypes would be very more by superiority indexes and stability measures.

BLUE

Loadings of the stability measures as per BLUE of genotypes were tabulated and the first two significant PC has explained 80% of the total variation with respective contributions of 58.9 and 21.1% (Table 16).

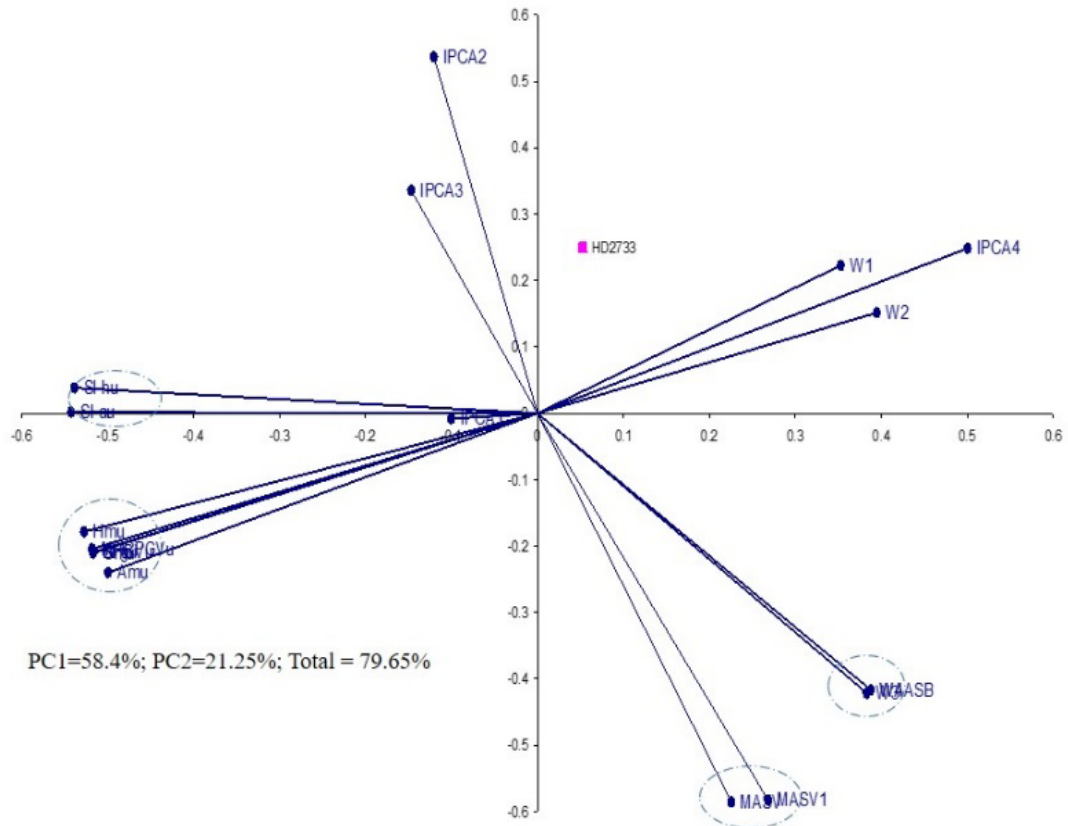


Figure 3. Biplot analysis of BLUP based measures as per first two significant PCAs (2019-2020).

Table 16. Loadings of BLUE based measures as per first two significant Principal Components (2019-2020).

Measure	PC1	PC2
IPCA1	0.0696	0.0335
IPCA2	0.0693	-0.3815
IPCA3	0.0867	-0.2256
IPCA4	-0.2671	-0.1782
MASV1	-0.1531	0.4041
MASV	-0.1287	0.4087
W1	-0.1967	-0.1735
W2	-0.2224	-0.1300
W3	-0.2143	0.2873
W4	-0.2125	0.2939
WAASB	-0.2125	0.2939
AMe	0.2689	0.1828
SI ae	0.2965	0.0182
GMe	0.2779	0.1662
SI ge	0.2964	0.0051
HMe	0.2833	0.1491
SI he	0.2945	-0.0077
RPGVe	0.2777	0.1661
MHRPGVe	0.2787	0.1637
% variation explained	58.97	21.09

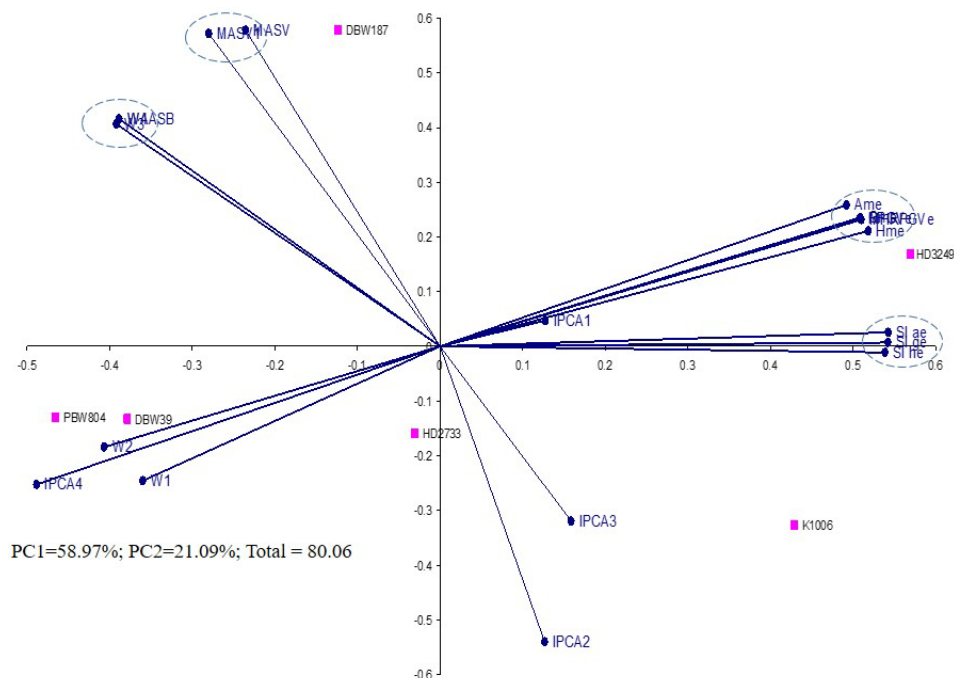


Figure 4. Biplot analysis of BLUE based measures as per first two significant PCAs (2019-2020).

The first group comprised MASV and MASV1 and the second nearby cluster of stability measures by utilizing three or more interaction principal components (Figure 4). Adaptability measures as per arithmetic, geometric and harmonic means and their corresponding values expressed deviation from all already mentioned measures and placed in a different quadrant. Moreover, this group maintained the right angle with stability measures. The cluster of superiority indexes as per averages yield of wheat genotypes were placed in the same quadrant. Right angles were expressed by superiority indexes with AMMI-based measures, that is, MASV and MASV1. Performance of genotypes would not be different by superiority indexes and adaptability measures.

Conclusions

Stability measures considering stability and yield simultaneously would be more appropriate to recommend/identify high-yielding wheat genotypes with stable performance. In the present study, the main advantages of AMMI and BLUP had been combined to increase the reliability of multi-locations trials analysis. An interesting advantage was provided by superiority indexes to assign variable weights to the yield and stability performance of genotypes. Researcher may prioritize the productivity of a genotype rather than its stability or vice-versa as per the goal of a crop

improvement trial.

The superiority index has the potential to provide reliable estimates in future studies with the possibility of joint interpretation of performance and stability in a biplot graphs while utilizing number of IPCAs.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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