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Stability and adaptability analysis of wheat genotypes by AMMI & BLUP for Northern Hills Zone

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ABSTRACT

Environment (E), GxE interaction, and genotypes (G) effects were highly significant by AMMI analysis of wheat genotypes evaluated in the North Eastern zone of the country during 2018-19 and 2019-20. Environments explained 64.1% & 74.4%, GxE interaction accounted for 19.6% & 11.1% Genotypes explained only 3.8% & 1.3% of total sum of squares due to treatments respectively. Genotypes preference ranking had altered with the number of IPCA's in AMMI and WAASB based measures. Superiority indexes as per various averages along with adaptability measures had identified HS490, VL3020, VL892 VL3021 wheat genotypes. Biplot analysis based on 69.8% variations accounted by two PC's observed deviation of adaptability measures and the right angle with MASV1 and stability measures. Cluster of Superiority indexes placed in the same quadrant. Wheat genotypes HS490, VL3023, VL3022,HS680 selected by Superiority indexes and adaptability measures for the second year of study. About 70.6% of variability considered estimators explained by two PC's. Adaptability measures as per various averages clustered in a different quadrant in Biplot analysis. Superiority indexes as per various averages seen in the same quadrant.

1. Introduction

GxE interaction has been assessed by the differential expression of genotypes over the environments (Ajay *et al.,* 2020). This complicate the selection of a genotype for a target trait as various genotypes respond in a different way under varied environmental conditions (Agahi *et al.,* 2020).Research studies observed the better performance of AMMI model than linear regression models and other multivariate procedures (Bocianowski *et al.,* 2019).AMMI stability parameters permit to evaluate yield stability after reduction of the noise from the GxE interaction effects (Gauch 2013; Oyekunle *et al.,* 2017). Several of AMMI based stability measures are available in literature (Zali *et al.,* 2012; Ajay *et al.,* 2019).Very stable varieties are generally not highly productive and to that end it is imperative that the use of appropriate methods and approaches to combine productivity with a stability in a measure (Kang, 1993). Reseachers have introduced different selection criteria for simultaneous selection of yield and stability (Rao & Prabhakaran 2005; Farshadfar, 2008; Farshadfar *et al.,* 2011). In this regard, since ASV takes into account both IPCA1 and IPCA2, most of the variation in the GxE interaction is justified (Mohammadi *et al.,* 2015). BLUP and AMMI, two distinct approaches, utilized to distinguish the pattern from the random error components in GxE interactions (Piepho *et al.,* 2008; Mendas *et al.,* 2012). The benefits of two important techniques AMMI and BLUP amulgated into a Superiority Index measure for stability and adaptability of genotypes (Olivoto *et al.,* 2019).

2. Materials and Methods

Northern hills zone encompasses the hilly terrain of Northern region extending from Jammu & Kashmir to North Eastern States. NHZ comprises 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. During cropping seasons of 2018-19 and 2019-20, ten promising wheat genotypes in advanced trials evaluated at nine major locations and eleven genotypes at eleven locations were evaluated under field trials respectively. Field trials were conducted at research centers in randomized complete block designs with three replications. Recommended agronomic practices were followed to harvest good yield. Details of locations and

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parentage of evaluated wheat genotypes were reflected in tables 1 & 2 for ready reference.

Stability measure as 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 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).

Mohamadi & 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	$\mathrm{MASV1} = \sqrt{\sum_{n=1}^{N-1} (\frac{SSIPC_n}{SSIPC_{n+1}} PC_n)^2 + (PC_{n+1})^2}$
Resende & Durate, 2007	Relative performance of genotypic values across environments	$PRVG_{ij} = VG_{ij} / VG_i$
Resende & Durate, 2007	Harmonic mean of Relative performance of genotypic values	$MHPRVG_{i.}$ = Number of environments / $\sum_{j=1}^{k} \frac{1}{PRVG_{ij}}$
Oliveto *et al.,* 2019	Superiority Index	$SI = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(\theta_Y + \theta_S)}$

3. Results and discussion

First-year 2018-19

AMMI analysis seen highly significant effects of Environment (E), genotypes (G), and GxE interaction. 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 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 compared to genotype main effects, indicated appropriateness of AMMI analysis. Environment explained significantly about 64.1% of the total sum of squares due to treatments indicating that diverse environments caused most of the variations in genotypes yield (Ajay *et al.,* 2020) (Table 3). Genotypes explained only 3.8% of the total sum of squares, whereas GxE interaction accounted for 19.6% of treatment variations in yield. Six significant interaction principal components explained 98.3 % and the remaining 1.7% was the residual or noise, discarded (Oyekunle *et al.,* 2017).

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

The stability or adaptability of genotypes in the AMMI analysis was indicated by values of IPCA. Then, the specific adaptation of genotype to certain locations was judged by greater IPCA scores. More of the IPCA score approximate to zero, the genotype would be more adapted over all the locations. The ranking of genotypes as per absolute IPCA-1 scores wereHPW467, HPW468, VL3019 (Table 4). While for IPCA-2, genotypes HPW467, VL3020, VL3021, would be of choice. Values of IPCA-3 favoured VL3021, VL3019, HS674, wheat genotypes. As per IPCA-4, VL892, HS674, VL3019, genotypes would be of stable performance. UP 3041 HS673, HS674 genotypes pointed by IPCA-5 measure. Genotypes HPW468, VL892, VL3019, identified by absolute values of IPCA-6. Analytic measures of adaptability MASV and MASV1 consider all six significant IPCAs of the analysis. Values of MASV1 identified genotypes HS674, VL3019, VL3020, would express stable yield whereas genotypes HS 674 VL3020, VL3019 be of stable performance by MASV measure respectively (Ajay *et al.,* 2019).

To identify whether and how the ranks of genotype are altered when different numbers of IPCA are used in the WAASB estimation, the genotype's ranks were obtained considering the WAASB estimated with 1, 2,..., *p* IPCA. When using only one IPCA, WAASB = |IPCA1|. The ranking was increasing; so, the genotype with the smallest WAASB value had the first-order rank. Preferences of genotypes varied as HPW467, HPW468, VL3019 based on W1 whereas HPW 467, HPW468, VL3020 as per W2 values while VL3021, HPW467, VL3020 by values of W3 (Table 5). Genotypes VL3021 HPW467, VL3020 were pointed by W4; W5 favoured HPW467, VL 3021, VL3020. Stability measure WAASB based on all significant IPCA's settled for HPW 467, VL3021, VL3020 genotypes for considered locations of the zone for stable high yield. It is observed that the genotype ranking was altered by the extent to which IPCAs are included in the WAASB estimation (Olivoto *et al.,* 2019).

Productive and broadly adapted genotypes by AMMI + BLUP tools

An average yield of genotypes as per BLUP values of genotypes yield selected HS490, VL892, VL3020 wheat genotypes (Table 6). This method is simple, but not fully exploiting all information contained in the dataset. Geometric mean is used to evaluate the adaptability of genotypes and genotypes with high values wereHS490, VL3020, VL892. As proposed by Resende (2007), 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 was calculated as genotypes with greater values would be recommended. Harmonic Mean of yield expressed higher values for HS490, VL3020, VL3021 genotypes. Moreover, the Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) method proposed by Resende (2007) that used Restricted Maximum Likelihood (REML) or Best Linear Unbiased Prediction (BLUP) as similar to the methods of Lin and Binns (1988) and Annicchiarico (1992). 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 HS490, VL3020, VL892 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) over crop years. For adaptability analysis, the Relative Performance of Genotypic Values had been measured across environments. Wheat genotypes HS490, VL3020, VL892 identified by this measure.

While assigning 65 and 35 weights to yield and stability, the Superiority index pointed out HS 490, VL892, VL3020 genotypes would maintain high yield and stable performance. SI measure, considered GM and stability, HS490, VL3020, VL892 selected genotypes. Values of SI, using HM and stability, favoured the same set of wheat genotypes HS490, VL3020, VL 3021. Analytic measures of adaptability RPGV and MHRPGV pointed out HS490, VL3020, VL892 would be more adaptable genotypes.

Biplot analysis of measures

The first two significant PC's jointly has explained 70.3% of the total variation (Table 7) with 37.6 & 32.7 contributions by PC1 & PC2. A group comprised of IPCA4, MASV, MASV1 & nearby group contains stability measures by utilizing two or more number of interaction principal components (Fig. 1). 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. Superiority indexes as per averages of the yield of wheat genotypes placed in the same cluster. However, this group maintained the right angle with stability measures. The performance difference of genotypes would be very less by Superiority indexes and adaptability measures.

Second-year 2019-20

Environment (E), genotypes (G), and GxE interaction effects were highly significant as mentioned by the AMMI analysis. Genotypes explained 1.3% of the total sum of squares, whereas GxE interaction accounted for 11.1% of treatment variations in yield (Table 3). The environment significantly explained about 74.4% of the total sum of squares due to treatments. Seven interaction principal components explained 97.8 of GxE interaction sum of squares and the remaining 8.3% was discarded.

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

The ranking of genotype as per absolute IPCA-1 scores wasVL3024, HS681, VL3022 (Table 8). While for IPCA-2, genotypes VL3023, HS679, VL3024 would be of choice. Values of IPCA-3 favoured HS679, UP3069, VL3022 wheat genotypes. As per IPCA-4, HS681, HPW474, HS679 genotypes would be of stable performance. VL3023, HPW473, HS679, genotypes pointed by IPCA-5 measure. Genotypes HS679, VL3023, VL892 identified by absolute values of IPCA-6. Lastly, IPCA-7 settled for HS681, HPW474, VL3024 genotypes for the studied locations of the zone. Analytic measures of adaptability MASV and MASV1consider all significant IPCAs of the analysis. Values of MASV1 & MASV measures identified genotypes HS679, VL3022, VL3023 be of stable performance.

Preferences of wheat Genotypes varied as VL3024, HS681, VL3022 based on W1 whereas VL3024, HS681, VL3023 as per W2 values while HS681, HS679, VL3022 by values of W3 (Table 9). Genotypes HS681, HS679, VL3022 were pointed by W4; W5 favoured HS679, VL3022 HS681, and lastly by W6 genotypes of choice would be HS679 VL3022, VL3023. Stability measure WAASB based on all significant IPCA's settled for HS679, VL3022, VL3024 genotypes for considered locations of the zone for stable high yield. It is observed that the genotype ranking was altered by the extent to which IPCAs are included in the WAASB estimation.

Productive and broadly adapted genotypes by AMMI + BLUP tools

Average yield of genotypes selected HS680, HS490, VL3023 wheat genotypes (Table 10). Geometric mean observed HS680, VL3023, HS490, were top-ranked genotypes. Harmonic Mean of yield expressed higher values for HS680, VL3023, VL3022 genotypes. Values of HMRPGV ranked HS680, VL3023, HS490as the performance of the genotypes among the locations. Relative Performance of Genotypic Values had settled for HS680, VL3023, HS490 wheat genotypes.

While assigning 65 and 35 weights to yield and stability, the Superiority index settled for VL3023, VL3022, and HS680 genotypes would maintain high yield and stable performance. SI measure considered GM and stability, selected VL3023, HS680, VL3022 genotypes. Values of SI, using HM and stability, favoured the same set of wheat genotypes VL3023, HS680, VL3022. Analytic measures of adaptability RPGV and MHRPGV pointed out HS680, VL3023 and HS490 would be more adaptable genotypes.

Biplot analysis of measures

The first two significant PC's jointly has explained 70.6% of the total variation (Table 11) with 41.5 & 29.1 contributions by PC1 & PC2. A group comprised of MASV, MASV1& stability measures by utilizing the number of interaction principal components (Fig. 2). Adaptability measures as per arithmetic, geometric and harmonic means along with the corresponding values of RPGV & MHRPGV expressed bondage with others and placed in a different quadrant. However, this group maintained the right angle with MASV, MASV1 & 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 less by Superiority indexes and adaptability measures.

4. Conclusions

GxE interaction study in multi-environment trials had been carried out by a well-established AMMI model. The simultaneous consideration of stability measures and yield would be more appropriate to recommend high-yielding stable wheat genotypes. In the present study, the main advantages of AMMI and BLUP had been 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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6. Conflict of interest

The authors declared no conflict of interests.

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

Code	Genotype	Parentage	Location	Latitude	Longitude	Mean sea level
G 1	VL 892	(WH542/PBW226)	Bajaura	31°50'N	77°9'E	1103.85
G 2	HS 490	(HS364/HPW114//HS240//HS346)	Dhaulakuan	28°59 N	77°16 E	468
G 3	HPW 468	(BOW/URES//KEA/3/SITE)	Shimla	31°10' N	77°17'E	2276
G 4	HS 673	(HD2888/FRTL/AGRI/NAC//FLW3)	Malan	32°08' N	76°35'E	846
G 5	VL 3020	(PHS0728/HS490//HS490)	Una	31°46' N	76°27° E	369
G 6	UP 3041	(VHW6140P-1)	Almora	29° 35' N	79° 39'E	1610
G 7	HPW 467	(HP155/VL864)	Majhera	29° 16' N	80° 5' E	1532
G 8	HS 674	(WBM2112/FLW13)	CAU-Imphal	24°81° N	93°93 E	786
G 9	VL 3019	(VW0865/KANACI//GW385)	Kalimpong	27° 4 ' N	88° 28' E	1121
G 10	VL 3021	(SOKOLL/3/PASTOR//HXL7573/2*BAU/4/BECARD)				

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

Code	Genotype	Parentage	Location	Latitude	Longitude	Mean sea level
G 1	HS681	(HEINESVII/HPW251//HS507)	Bajaura	31°50'N	77°9'E	1103.85
G 2	VL3022	(SW89-3218//AGRI/NAC/HS507//QLD 39)	Dhaulakuan	28°59 N	77°16 E	468
G 3	HS680	(VL616/HD2733)	Shimla	31°10' N	77°17'E	2276
G 4	VL3023	(PHS822/ISFRA)	Malan	32°08' N	76°35'E	846
G 5	HPW474	(S308/HD29P2)	Almora	29° 35' N	79° 39'E	1610
G 6	UP3069	(VHW6278P-9)	Majhera	29° 16' N	80° 5' E	1532
G 7	HPW473	(HPW155/PBW486)	Ranichauri	28° 43' N	81°02' E	2200
G 8	VL892	(WH542/PBW226)	Gangtok	27° 20' N	88° 36' E	1509
G 9	VL3024	(ZANDER33/VL907//QLD40)	CAU-Imphal	24°81° N	93°93 E	786
G 10	HS490	(HS364/HPW114//HS240//HS346)	Umiam			
G 11	HS679	(VL907/DL640)	Kalimpong	27° 4 ' N	88° 28' E	1121

Table 3. AMMI analysis of wheat genotypes for restricted irrigated late sown trials during 2018-19& 2019-20

Source	Degree of freedom 18-19	Degree of freedom19-20	Mean Sum of Squares18-19	Mean Sum of Squares19-20	Level of significance 18-19	Level of significance 19-20
Treatments	79	120	286.66	557.96	.0000000 ***	.0000000 ***
Genotypes (G)	9	10	109.40	99.84	.0000000 ***	.0000000 ***
Environments (E)	7	10	2370.50	5740.30	.0000000 ***	.0000000 ***
Interactions GxE	63	100	80.45	85.54	.0000000 ***	.0000000 ***
IPC1	15	19	125.02	162.34	.0000000 ***	.0000000 ***
IPC2	13	17	98.36	136.22	.0000000 ***	.0000000 ***
IPC3	11	15	84.81	80.77	.0000000 ***	.0000000 ***
IPC4	9	13	54.55	46.16	.0000000 ***	.00000***
IPC5	7	11	33.18	48.92	.00000 ***	.0000 ***
IPC6	5	9	34.73	39.89	.0001 ***	.00519 **
IPC7		7		37.08		0.0521
Residual	3	9	28.19	20.57		0.2788
Error	400	605	8.06	16.84		
Total	479	725	54.01	106.41		

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_{MASV1}	R_{MASV}
VL 892	-1.832	-1.407	-0.801	-0.361	-1.403	0.307	4.708	4.071	9	5	8

HS 490	0.961	1.216	-0.789	1.178	-0.518	1.157	4.335	3.599	5	4	4
HPW 468	-0.571	-0.924	-1.624	1.173	0.825	-0.226	4.980	4.010	2	7	6
HS 673	-2.507	1.187	1.098	0.658	-0.068	-0.870	5.126	4.263	10	10	9
VL 3020	1.181	0.205	0.905	-1.018	-1.128	-0.384	4.032	3.296	7	3	2
UP 3041	0.946	2.034	-1.410	-0.729	0.023	-0.440	5.109	4.328	4	9	10
HPW 467	0.416	0.107	2.108	0.844	0.332	0.831	5.079	4.043	1	8	7
HS 674	1.612	-0.936	0.290	0.536	0.293	-1.292	3.462	2.983	8	1	1
VL 3019	0.820	-1.905	0.144	-0.615	0.333	0.372	3.809	3.350	3	2	3
VL 3021	-1.025	0.424	0.078	-1.665	1.312	0.545	4.803	3.865	6	6	5

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

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

Genotype	W1	W2	W3	W4	W5	WAASB	R_{W1}	R_{W2}	R_{W3}	R_{W4}	R_{W5}	R_{WAASB}
VL 892	1.832	1.645	1.413	1.254	1.267	1.189	9	9	8	8	9	9
HS 490	0.961	1.073	0.995	1.023	0.980	0.995	5	5	6	7	6	7
HPW 468	0.571	0.727	0.974	1.004	0.989	0.927	2	2	4	6	7	5
HS 673	2.507	1.926	1.698	1.542	1.418	1.374	10	10	10	10	10	10
VL 3020	1.181	0.751	0.793	0.827	0.852	0.814	7	3	3	3	3	3
UP 3041	0.946	1.425	1.421	1.317	1.208	1.146	4	8	9	9	8	8
HPW 467	0.416	0.280	0.783	0.792	0.754	0.760	1	1	2	2	1	1
HS 674	1.612	1.315	1.033	0.958	0.902	0.934	8	7	7	5	5	6
VL 3019	0.820	1.298	0.980	0.926	0.876	0.835	3	6	5	4	4	4
VL 3021	1.025	0.761	0.573	0.737	0.785	0.766	6	4	1	1	2	2

Table 6. Superiority index and adaptability measures of genotypes 2018-19

Genotype	AMu	Rk	SI au	Rk	GMu	Rk	SI gu	Rk	HMu	Rk	SI hu	Rk	MHRPGVu	Rk	RPGVu	Rk
VL 892	27.96	2	56.68	2	26.67	3	49.52	3	25.24	6	43.20	6	1.016	3	1.036	3
HS 490	28.54	1	65.35	1	27.85	1	65.35	1	27.12	1	65.35	1	1.067	1	1.077	1
HPW 468	24.19	10	0.32	10	22.99	10	0.32	10	21.63	10	0.32	10	0.869	10	0.898	10
HS 673	26.40	7	33.47	7	25.86	7	38.85	7	25.26	5	43.41	5	0.986	7	1.005	7
VL 3020	27.89	3	55.51	3	27.04	2	54.43	2	26.12	2	53.42	2	1.036	2	1.046	2
UP 3041	25.45	8	19.18	8	24.88	8	25.67	8	24.32	8	32.21	8	0.950	8	0.966	8
HPW 467	26.73	6	38.13	6	25.95	6	39.76	6	25.12	7	41.60	7	0.992	6	1.005	6
HS 674	27.19	4	45.02	4	26.35	5	45.18	5	25.59	4	47.24	4	1.010	5	1.019	5
VL 3019	25.23	9	15.73	9	23.86	9	11.89	9	22.50	9	10.62	9	0.912	9	0.925	9
VL 3021	27.16	5	44.55	5	26.48	4	46.86	4	25.75	3	49.01	3	1.016	4	1.023	4

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 BLUP based measures as per first two significant Principal Components (2018-19)

Measure	PC1	PC2
IPCA1	0.0322	-0.2238
IPCA2	0.1050	0.1160
IPCA3	0.1176	-0.0846
IPCA4	-0.0378	0.0616
IPCA5	-0.1811	-0.1347
IPCA6	0.0639	-0.1447
MASV1	-0.0858	0.1511
MASV	-0.0942	0.2070
W1	0.1186	0.2806
W2	0.0139	0.3102
W3	-0.0320	0.3505
W4	-0.0325	0.3583
W5	-0.0179	0.3619
W6	0.0092	0.3623
WAASB	0.0092	0.3623
AMu	0.3342	-0.0122
SI au	0.3342	-0.0106
GMu	0.3387	0.0045
SI gu	0.3387	0.0059
HMu	0.3322	0.0153
SI hu	0.3322	0.0165
RPGVu	0.3381	0.0150
MHRPGVu	0.3389	-0.0052
70.39	37.63	32.76

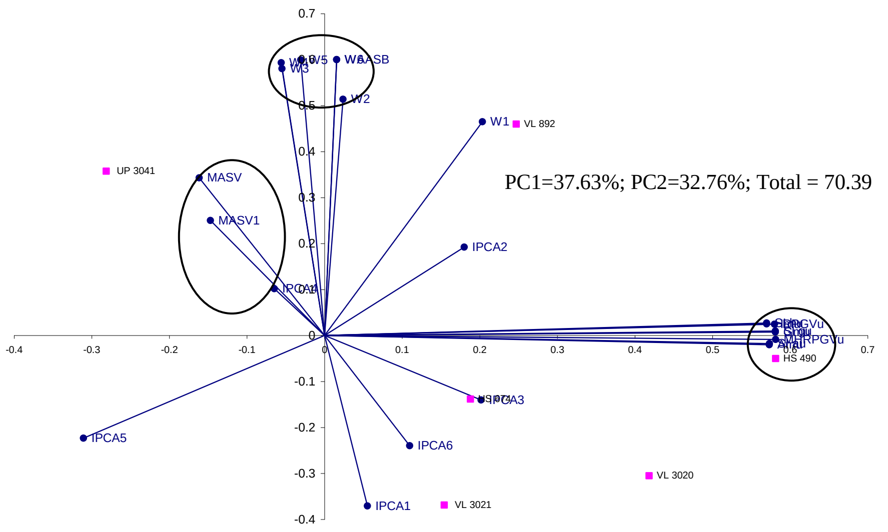

Fig. 1: Biplot analysis of measures as per first two significant PCA's (2018-19)

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}
HS681	-0.174	0.571	0.712	-0.056	1.811	-1.882	0.166	5.015	4.381	2	7	7
VL3022	-0.284	0.890	0.271	0.869	0.449	0.421	-1.054	2.860	2.504	3	2	2
HS680	2.609	0.769	0.368	0.976	-1.010	-0.662	-0.307	4.726	4.111	11	5	6
VL3023	-0.687	-0.145	-1.580	-0.655	0.143	-0.087	1.452	4.095	3.363	4	3	3
HPW474	-1.952	-2.477	1.557	-0.061	-1.294	-0.566	-0.201	7.350	5.937	9	11	11
UP3069	-0.934	-1.038	-0.270	1.184	1.337	1.302	-0.303	4.573	4.010	5	4	4
HPW473	1.250	0.807	1.603	0.229	-0.253	1.024	1.368	4.909	4.047	7	6	5
VL892	2.525	-2.070	-0.407	-1.645	0.504	0.358	-0.569	6.300	5.335	10	10	10
VL3024	-0.080	0.152	-2.380	0.708	-0.942	-0.396	-0.281	5.780	4.572	1	8	8
HS490	-1.332	2.392	0.277	-1.774	-0.425	0.467	-0.767	6.247	5.241	8	9	9
HS679	-0.939	0.149	-0.151	0.225	-0.319	0.022	0.495	1.573	1.384	6	1	1

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}
HS681	0.174	0.355	0.431	0.391	0.537	0.641	0.609	2	2	1	1	3	5	4
VL3022	0.284	0.561	0.499	0.539	0.530	0.521	0.557	3	4	3	3	2	2	2
HS680	2.609	1.769	1.471	1.417	1.375	1.320	1.252	11	8	8	8	8	8	8
VL3023	0.687	0.440	0.683	0.680	0.624	0.583	0.641	4	3	5	5	4	3	5
HPW474	1.952	2.192	2.056	1.840	1.784	1.689	1.589	9	10	11	10	11	11	11
UP3069	0.934	0.981	0.830	0.868	0.917	0.946	0.903	5	6	6	6	6	6	6
HPW473	1.250	1.048	1.166	1.064	0.981	0.984	1.010	7	7	7	7	7	7	7
VL892	2.525	2.318	1.911	1.882	1.740	1.633	1.561	10	11	10	11	10	10	10
VL3024	0.080	0.113	0.596	0.608	0.642	0.623	0.600	1	1	4	4	5	4	3
HS490	1.332	1.816	1.488	1.519	1.406	1.333	1.295	8	9	9	9	9	9	9
HS679	0.9391	0.5787	0.4877	0.4592	0.4448	0.4120	0.418	6	5	2	2	1	1	1

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	MHRPGVu	Rk	RPGVu	Rk
HS681	27.94	5	61.99	5	26.25	6	57.71	4	24.66	7	53.71	5	0.987	6	0.996	6
VL3022	28.59	4	76.49	2	26.95	4	74.73	3	25.44	3	74.56	3	1.016	4	1.020	4
HS680	29.55	1	75.08	3	27.91	1	75.08	2	26.30	1	75.08	2	1.047	1	1.062	1
VL3023	28.82	3	78.65	1	27.27	2	79.21	1	25.87	2	82.51	1	1.027	2	1.033	2
HPW474	26.31	11	0.00	11	24.95	11	0.00	11	23.67	11	0.00	11	0.932	11	0.954	11
UP3069	27.05	9	35.28	9	26.02	7	43.88	8	25.09	5	55.66	4	0.978	7	0.988	7
HPW473	27.23	7	35.84	8	25.49	9	29.07	10	23.77	10	19.92	10	0.955	10	0.970	9
VL892	27.75	6	29.68	10	26.60	5	37.08	9	25.44	4	44.45	8	0.998	5	1.012	5
VL3024	27.15	8	46.50	6	25.64	8	44.75	7	24.29	8	44.89	7	0.965	8	0.972	8
HS490	29.41	2	70.95	4	27.14	3	56.81	5	24.94	6	40.07	9	1.017	3	1.032	3
HS679	26.87	10	46.30	7	25.40	10	44.94	6	24.09	9	45.37	6	0.958	9	0.961	10

Table 11 : Loadings of BLUP based measures as per first two significant Principal Components (2019-20)

Measure	PC1	PC2
IPCA1	0.0203	-0.1960
IPCA2	-0.1785	-0.0995
IPCA3	0.1447	0.0235
IPCA4	-0.1153	0.1281
IPCA5	-0.1239	0.0172
IPCA6	0.0327	0.0080
IPCA7	-0.0583	0.1227
MASV1	0.2454	-0.0674
MASV	0.2435	-0.0874
W1	0.2228	-0.1981
W2	0.2688	-0.1748
W3	0.2912	-0.1409
W4	0.2822	-0.1653
W5	0.2873	-0.1576
W6	0.2883	-0.1530
WAASB	0.2862	-0.1594
AMu	-0.1187	-0.3328
SI au	-0.2500	-0.2106
GMu	-0.1171	-0.3507
SI gu	-0.2572	-0.2203
Hmu	-0.1167	-0.3239
SI hu	-0.2500	-0.2000
RPGVu	-0.0933	-0.3599
MHRPGVu	-0.1382	-0.3398
70.60	41.53	29.06

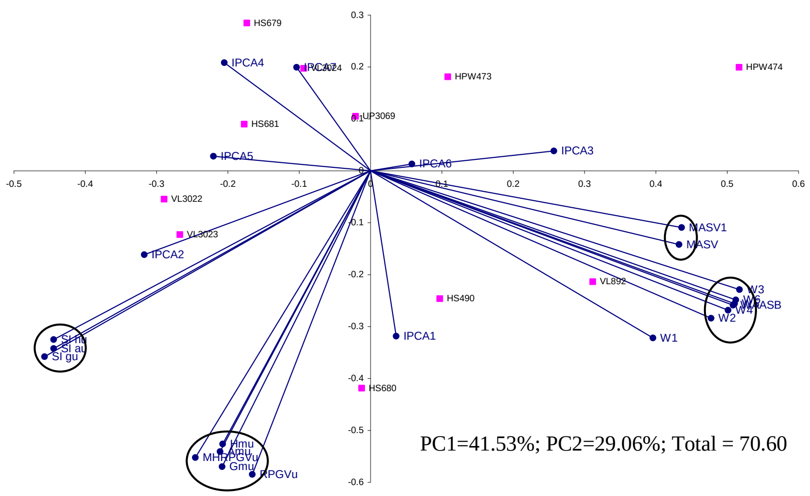

Fig. 2: Biplot analysis of measures as per first two significant PCA's (2019-20)