## Wheat genotypes evaluated for Stability, adaptability analysis for Northern Hills by AMMI & BLUP Tools

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*Abstract* : Environment effects explained 78% & 66.8%, GxE interaction accounted for 5.9% & 15.4 and genotypes explained only 2.4% & 4.0% of sum of squares during 2018-19 and 2019-20 respectively. More than 98% of variations had been accounted for by three interaction principal components for the first year. Ranking of genotypes had altered with the utilization of the number of IPCA's for AMMI-based and WAASB measures. Superiority indexes as per arithmetic, geometric, and the harmonic mean as well adaptability measures had identified HS562, HS652, VL907 genotypes. Graphical analysis utilized 83.7% variations accounted by PC1 & PC2's observed deviation of Adaptability measures from others and maintained the right angle with MASV1 and stability measures. Cluster of Superiority indexes was placed in the quadrant of adaptability measures. Wheat genotypes HPW349, VL907, HS507 selected by Superiority indexes and adaptability measures the second year of study. Biplot considered 85.1% of variability accounted by two PC's. Cluster of Adaptability measures was placed in a seperate quadrant. However, this group maintained nearly the right angle with stability measures. Superiority indexes as per averages of the yield of wheat genotypes were clustered in the quadrant.

Keywords: AMMI model, MASV, WAASB, SI, SSI, Graphical analysis

## **1** Introduction

Genotypes have been recommended/identified for large area cultivation on the basis of multi location trials [1]. An efficient analytic mechanism for GxE interactions had been attracted utmost importance in crop breeding trials [3]. AMMI analysis had been employed mostly even large number of other statistical procedures for the stability analyses has been validated in literature [2]. Recently the effects of genotypes, environments, or both to be advocated as of random nature. BLUP's have improved the predictive accuracy of random effects under mixed model approach [14][12]. Both BLUP and AMMI, approaches, seperated the pattern from the random error components in GxE interactions analysis [5]. Simultaneous use of stability and yield would assist in suitable selection of productive stable genotypes. This approach had lowered the ill effects of interaction thereby more precise and reliable selection [6]. These two approaches have been

used separately in the field evaluation of genotypes under multi location trials [17]. Desirable advantages of AMMI and BLUP, had been confunded to Superiority Index measure for stability and adaptability of genotypes [12]. The current study dealt with the relative evaluation of the merits of the analysis of GxE interaction and yield stability through AMMI with BLUP techniques to study the stability & adaptability of evaluated wheat genotypes.

### 2 Material and methods

The cropping seasons of 2018-19 and 2019-20 tested five advanced wheat genotypes at ten research stations of the Northern Hiils of India zone and six genotypes at eleven locations were evaluated. Fields were well prepared with recommended inter culture operations before randomized complete block designs with four replications in field layout. Tables 1 & 2 used to mention the fine details of locations and wheat genotypes.

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

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

the weighted average of absolute scores of the ith genotype (or environment) denoted by WAASB<sub>i</sub>: Interaction principal compoents of the *i*th genotype (or environment) in the *k*th IPCA expressed by IPCA<sub>ik</sub> where the amount of the variance explained by the *k*th IPCA was by EP<sub>k</sub>. Superiority index SI =  $\frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(rG_i \times \theta_Y)}$  $(\theta_Y + \theta_S)$ considered variable weights to yield and stability while rescaled values for yield & WAASB were  $rG_i$  and  $rW_i$  respectively.  $\theta Y$  and  $\theta S$  were the weights for yield and stability assigned in 65:35 for study,

[11] Geometric  
Adaptability  
Index  
[18] Modified  
AMMI  

$$MASV$$

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

MASV1 [2] MASV1  $\left|\sum_{n=1}^{N-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}}PC_n\right)^2 + (PC_{n+1})^2\right|$  $PRVG_{ij} = VG_{ij} / VG_i$ [16] Relative

performance of genotypic values across environments

stab

MHPRVG<sub>i.</sub> = Number of environments [16] Harmonic  $\sum_{j=1}^{k} \frac{1}{PRVG_{ij}}$ mean of Relative performance of genotypic values  $\mathbf{SI} = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(rW_i \times \theta_S)}$ [12] Superiority  $(\theta_Y + \theta_S)$ Index

AMMISOFT software with version 1.0 for AMMI analysis and SAS software version 9.3. was for Stability measures. Measures of adaptability PRVG and MHPRVG (Mendes et al., 2012) assessed against SI [9].

### **3 Results and discussion**

### 3.1 First-year of study (2018-19)

Environment (E), GxE interaction, and genotypes (G) effects were significant in 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 is appropriate for data sets where-in SS due to were of magnitude at least of due to additive genotype main effects [7]. The SS for GxE interactions Signal was higher compared to main effects. indicated genotype appropriateness of AMMI analysis. Significant environments explained about 78%, GxE interaction accounted for 5.9% more than the genotypes contribution of 2.4% [3]. AMMI model observed that 98.4 % of interaction sum of squares managed by the first three significant multiplicative terms [13].

### 3.2 Ranking of genotypes vis-à-vis number of **IPCA's**

Stability or adaptability of genotypes under multi location trials had been assessed by IPCA's in the AMMI analysis. The specific adaptation of genotypes reflected by higher IPCA scores. The more stable or adapted genotypes to all the locations assessed by lower the scores of IPCA. The ranking of genotypes as per the absolute value of IPCA-1 measure was HS507, VL907 (Table 4). While for IPCA-2, genotypes VL907, HS562 would be of choice. Values of IPCA-3 favored HS507, HS652 wheat genotypes.

adaptability Measures of MASV and MASV1considered all significant three IPCAs of the analysis. Values of MASV and MASV1 measure pointed towards VL907. HS562 genotypes would express stable yield [2].

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. Genotypes preferences varied as VL907, HS562 based on W1 values whereas VL 907, HS562 as per W2 values while VL907, HS562 by values of W3.

Stability measure WAASB based on all three significant IPCA's settled for VL907, HS562 genotypes [12].

## 3.3 Stable productive genotypes by AMMI & BLUP

An average yield of genotypes selected HS562, HPW349 wheat genotypes (Table 5). Geometric mean found HS562, HS652 genotypes with higher the adaptability index. Harmonic Mean of yield expressed higher values for HS562, HS652 genotypes. Similar to the established Lin and Binns and Annicchiarico methods, Resende proposed Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) The genotypes could [4][8][15]. be simultaneously sorted by yield and stability using the harmonic means of the yield and genotypic performance with smaller the standard deviation among the locations would recommended/identified.Values be of MHRPGV ranked HS562, HS652 the genotype's performance among the locations. The yield and adaptability of genotypes had been simultaneously considered by relative performance of genetic values (RPGV). Relative Performance of Genotypic Values had settled for wheat genotypes HS562, HS652 selected by RPGV measure.

Considering the 65:35 ratio to yield and stability, the Superiority index pointed out HS562, VL907 genotypes would maintain high yield and stable performance. SI considered GM and stability selected HS562, VL907 genotypes. The SI while using HM and stability favored the same set of wheat genotypes HS562, VL907. Analytic adaptability measures RPGV and MHRPGV pointed out HS562, HS652 genotypes would be more adaptable.

### 3.4 Graphical analysis of measures

Principal components analysis was performed to study the relationships among the stability & adaptability measures [10]. Loadings of the studied measures were tabulated as the first two significant PC as explained 83.6% of the total variation in the original variables with respective contributions were 57.6 & 26 percent (Table 6). Four groups of measures were observed in graphical Biplot analysis (Fig. 1). The smallest group comprised of measures. The nearby group clustered stability measures by utilizing two and three interaction principal components. Adaptability measures as per arithmetic, geometric and harmonic means and their corresponding values expressed bondage in the group placed in a different quadrant. However, this group maintained the right angle with MASV & MASV1 measures. This quadrant also showed a cluster of Superiority indexes as per averages yield of wheat genotypes. Performance of genotypes would be different by Superiority indexes as compared to their behavior as per values of W2 & WAASB measures.

### 3.5 Second-year of study (2018-19)

Highly significant effects of Environment (E), GxE interaction, and genotypes (G) were showed by AMMI analysis. Environments explained about 66.8% while Genotypes explained only 4.0% of the total sum of squares (Table 3) while 15.4%, accounted by GxE interactions. About 89.8 % of the interaction sum of squares accounted by four multiplicative terms and the remaining was residual.

## **3.6 Ranking of genotypes vis-à-vis number of IPCA's**

Wheat genotypes VL907, HPW349 were ranked as per the absolute value of IPCA-1 While for IPCA-2. measure (Table 7). genotypes HS562, HPW349 would be of choice. Values of IPCA-3 favored HS507, VL907 wheat genotypes. As per IPCA-4, VL907, genotypes would be of stable HS668 performance. Analytic measures of adaptability MASV and MASV1considered all significant four IPCAs of the analysis. Values of MASV pointed towards genotypes HPW349, HS562 would express stable yield whereas genotypes HPW349, VL907 be of stable performance by MASV1 measure respectively. Genotypes preferences varied as VL907, HPW349 based on W1 values whereas HPW349, HS562 as per W2 values while HPW349, VL907 by values of W3. Stability measure WAASB based on all four significant IPCA's settled for VL907, HPW349 genotypes for considered locations of the zone.

# 3.7 Stable Productive genotypes by AMMI & BLUP

Mean yield of genotypes, as per their BLUP estimates, selected HPW349, HS562 wheat genotypes (Table 8). Geometric mean observed HPW349, VL2036 were of top-ranked genotypes. Harmonic Mean of yield expressed higher values for HS507, VL2036 genotypes. Values of MHRPGV ranked HPW349, VL2036 the performance of the genotypes among the locations. Relative Performance of Genotypic Values had settled for HPW349, HS507 wheat genotypes. While assigning 65 and 35 weights to yield and stability, the Superiority index pointed out HPW349, HS562 genotypes would maintain high yield and stable performance. SI considered GM and stability selected HPW349, VL907 genotypes. The SI while using HM and stability favored the same set of wheat genotypes HPW349, VL907. Adaptability measure RPGV pointed out HPW349, HS507, and MHRPGV or HPW349, VL2036 genotypes would be more adaptable.

### 3.8 Graphical analysis of measures

Principal components analysis was performed to study the relationships among the stability & adaptability measures of wheat genotypes. Loadings of the considered measures were tabulated as the first two significant PC as explained 85.2% of the total variation in the original variables with respective contributions were 62.6 & 22.6 percent (Table 9). Three groups of measures were observed in graphical Biplot analysis. A separate group comprised of MASV, MASV1 & stability measures by utilizing the varying number of interaction principal components (Fig. 2). Adaptability measures as per arithmetic, geometric and harmonic means and their corresponding values expressed bondage in the group placed in a different quadrant. However, this group maintained the right angle with stability measures. This quadrant also showed a cluster of Superiority indexes as per averages of the vield of wheat genotypes. Performance of genotypes would be different by Superiority indexes as compared to their behavior as per values of MASV & MASV1 measures.

### 4 Conclusions

AMMI model has been established for GxE interaction in multi-loation trials. In the present study, the main advantages of AMMI and BLUP had been combined to increase the reliability of multi-locations trials analysis. The Superority Indexes provided opportunity to different weights as per the objectives of breeding trials. Since the superiority index of genotype considered more of IPCA's has the potential to provide reliable estimates of performance and stability even by biplots graphical analysis.

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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	HPW 349	(NAC/TH.AC//3*MIRLO/BUC/4/2*PASTOR)	Bajaura	31°50'N	77°9'E	1103.85
G 2	VL 907	(DYBR1982-83842ABVD50/VW9365//PBW343)	Shimla	31°10' N	77°17'E	2276
G 3	HS 507	(KAUZ/MYNA/VUL//BUC/FLK/4/MILAN)	Berthin	31°50'N	77°9'E	1103
G 4	HS 652	(HD2888/EC463658//VL906)	Malan	32°08' N	76°35'E	846
G 5	HS 562	(OASIS/SKUAZ//4*BCN/3/2*PASTOR)	Dhaulakuan	28°59 N	77°16 E	468
			Akrot	31°4 ' N	76°1' E	425
			Khudwani	33° 70' N	75°10' E	1590
			Wadura	21° 18' N	77° 41' E	508
			Almora	29° 35' N	79° 39'E	1610
			Majhera	29° 16' N	80° 5' E	1532

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

Code	Genotype	Parentage	Location	Latitude	Longitude	Mean sea level
G 1	HS507	(KAUZ/MYNA/VUL//BUC/FLK/4/MILAN)	Bajaura	31°50'N	77°9'E	1103.85
G 2	HS562	(OASIS/SKUAZ//4*BCN/3/2*PASTOR)	Shimla	31°10 ' N	77°17'E	2276
G 3	HPW349	(NAC/TH.AC//3*MIRLO/BUC/4/2*PASTOR)	Berthin	31°50'N	77°9'E	1103
G 4	HS668	(VL906/FLW13)	Malan	32°08' N	76°35'E	846
G 5	VL907	(DYBR1982-83842ABVD50/VW9365//PBW343)	Dhaulakuan	28°59 N	77°16 E	468
G 6	VL2036	(SW89.5277/BORL95//SKAUZ/3/PRL/2*PASTOR/4/HEILO/5/W	Akrot	31°4 ' N	76°1'E	425
		HEAR/SOKOLL)				
			Khudwani	33° 70' N	75°10' E	1590
			Wadura	21° 18' N	77° 41' E	508
			Almora	29° 35' N	79° 39'E	1610
			Majhera	29° 16' N	80° 5' E	1532
			Ranichauri	28° 43' N	81°02' E	2200

Table 3: AMMI analysis of wheat genotypes for irrigated timely sown trials 2018-19 and 2019-20

Source	DF	DF	MSS	MSS	Level of significance	Level of significance
	(18-19)	(19-20)	(18-19)	(19-20)	2018-19	2019-20
Treatments	49	65	626.47	526.72	.0000000 ***	.0000000 ***
Genotypes (G)	4	5	217.22	318.57	.0000000 ***	.0000000 ***
Environments (E)	9	10	3079.51	2651.38	.0000000 ***	.0000000 ***
Interactions GxE	36	50	58.68	122.60	.0000002 ***	.0000000 ***
IPC1	12	14	83.87	167.93	.0000002 ***	.0000000 ***
IPC2	10	12	84.02	118.67	.0004497 ***	.0000000 ***
IPC3	8	10	29.03	106.95	0.4699921	.0000000 ***
IPC4		8		82.96		.0000000 ***
Residual	6	6	5.60	103.58	0.9412371	.0000026 ***
Error	250	330	19.29	16.39		
Total	299	395	118.80	100.37		

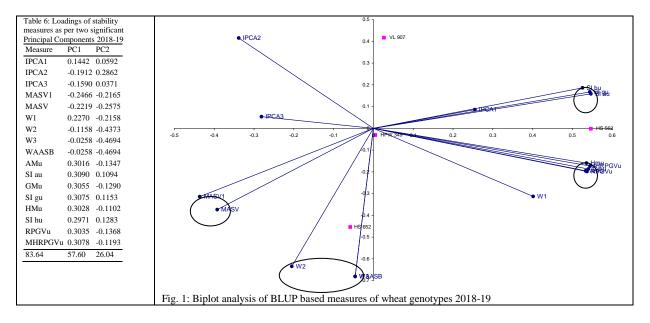
### Table 4: Modified AMMI and WAASB stability measures 2018-19

Genotype	IPCA1	IPCA2	IPCA3	MASV1	MASV	W1	W2	W3	WAASB	R IPCA1	R MASV1	R MASV	$R_{W1}$	$R_{W2}$	$R_{W3}$	R <sub>WAASB</sub>
HPW 349	1.886	-0.760	1.718	4.025	3.144	1.886	1.323	1.381	1.381	4	3	3	4	3	4	4
VL 907	-1.363	0.519	0.245	2.553	1.879	1.363	0.941	0.838	0.838	2	1	1	2	1	1	1
HS 507	-0.287	2.668	-0.024	10.021	5.742	0.287	1.478	1.264	1.264	1	5	5	1	4	3	3
HS 652	-2.045	-1.893	-0.154	7.519	4.646	2.045	1.969	1.701	1.701	5	4	4	5	5	5	5
HS 562	1.809	-0.533	-1.785	3.448	2.901	1.809	1.170	1.261	1.261	3	2	2	3	2	2	2
Rw1, Rw2, Rw3,	w1, Rw2, Rw3, Rw4, Rw5, Rw6, RwAASB = Rank of genotypes as per number of IPCA's in WAASB values															

#### Table 5: 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	AMu	Rk	SI au	Rk	GMu	Rk
HPW 349	39.74	2	52.42	2	47.07	3	38.03	3	43.22	3	41.09	3	36.19	4	31.38	4	33.39	4	0.994	3	0.997	3
VL 907	38.68	4	26.93	4	52.51	2	37.56	4	31.50	4	55.48	2	36.32	3	34.46	3	57.40	2	0.983	4	0.984	4
HS 507	37.57	5	0.00	5	17.73	5	36.29	5	0.00	5	17.73	5	34.95	5	0.00	5	17.73	5	0.947	5	0.953	5
HS 652	39.61	3	49.21	3	31.99	4	38.41	2	52.70	2	34.25	4	37.03	2	52.39	2	34.05	3	1.003	2	1.008	2
HS 562	41.71	1	100.00	1	82.86	1	40.32	1	100.00	1	82.86	1	38.91	1	100.00	1	82.86	1	1.054	1	1.057	1

AMu, GMu, HMu = Arithmetic, Geometric, Harmonic Mean for BLUP values; SI au, SI au, 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: Modified AMMI and WAASB stability measures 2019-20

Genotype	IPCA1	IPCA2	IPCA3	IPCA4	MASV1	MASV	W1	W2	W3	WAASB	R <sub>IPCA1</sub>	R <sub>MASV</sub>	R <sub>MASV1</sub>	$R_{W1}$	$R_{W2}$	$R_{W3}$	$R_{WAASB}$
HS507	2.698	2.131	-0.391	-1.192	8.261	5.726	2.698	2.463	1.900	1.777	6	6	6	6	6	5	6
HS562	-1.625	-0.608	-1.413	-1.595	5.235	3.881	1.625	1.204	1.261	1.319	4	2	3	4	2	3	3
HPW349	-0.444	1.040	-1.502	2.459	4.203	3.832	0.444	0.691	0.911	1.181	2	1	1	2	1	1	2
HS668	-2.635	1.222	1.921	-0.261	7.941	5.544	2.635	2.050	2.015	1.709	5	5	5	5	5	6	5
VL907	0.402	-2.509	-0.774	-0.069	5.120	4.302	0.402	1.274	1.138	0.952	1	3	2	1	3	2	1
VL2036	1.604	-1.276	2.158	0.658	6.076	4.725	1.604	1.468	1.656	1.482	3	4	4	3	4	4	4

#### Table 8: Superiority index and adaptability measures of genotypes 2019-20

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Ge	notype	AMu	Rk	SI au	Rk	GMu	Rk	SI gu	Rk	HMu	Rk	SI hu	Rk	MHRPGVu	Rk	RPGVu	Rk	AMu R	s SI au	Rk	GMu	Rk
HS	507	34.66	4	86.98	4	56.54	5	33.78	3	95.91	3	62.34	5	32.91	1	100.00	1	65.00 5	1.039	2	1.018	3
HS	562	34.99	2	93.27	2	80.06	2	33.31	4	87.68	4	76.42	3	31.44	5	77.78	5	69.99 4	1.021	4	1.009	4
HP	W349	35.34	1	100.00	1	90.30	1	34.02	1	100.00	1	90.30	1	32.50	3	93.86	3	86.31 1	1.041	1	1.032	1
HS	668	30.12	6	0.00	6	2.85	6	28.21	6	0.00	6	2.85	6	26.28	6	0.00	6	2.85 6	0.871	6	0.848	6
VI	.907	33.21	5	59.26	5	73.52	3	32.41	5	72.24	5	81.96	2	31.50	4	78.73	4	86.18 2	0.990	5	0.985	5
VI	.2036	34.97	3	92.96	3	72.92	4	33.83	2	96.80	2	75.42	4	32.63	2	95.84	2	$74.80 \ 3$	1.038	3	1.023	2

