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Experimental and Biological Approaches for Genotype X Environment Interactions Estimation for Wheat Genotypes Evaluated under Multi Locational Trials

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Abstract

Genotypes VL907, HS562, HPW484 were ranked as topped three in comparison to the other during the evaluation of nine wheat genotypes at major locations of the north hills zone of the country under rain fed conditions. The least values of AMMI stability measure (ASV) had expressed the desirability of HPW484, HS562, VL2041 genotypes whereas the genotypes HS562, HPW484, VL2041 had been identified by least values of Modified Ammi Stability Value (MASV). The minimum value of simultaneous selection index measure based on the MASV (ssiMASV) had selected HS562, HPW484, VL2041 wheat genotypes while values of ssiWAASB measure found the suitability of HPW484, HS562, HS691 wheat genotypes. The composite non parametric measure $NP_i^{(2)}$ had favoured the VL892, HS562 genotypes and values of $NP_i^{(3)}$ measure had settled for VL892, HS562 genotypes while VL892, HPW349 wheat genotypes had been pointed by the last composite measure $NP_i^{(4)}$. The Ward's method of Hierarchical Clustering had placed the VL907 genotype in a separate group as compared to others. The shorter rays of measures IPC2, IPC5, IPC3, SD had reflected the less contribution of the joint effects of genotypes and measures in the biplot analysis. Non parametric composite measure $NP_i^{(1)}$ had expressed tight direct relation with S_i^1, S_i^3, S_i^4,S_i^5, S_i^6, S_i^7 values. The values of IPC6 & IPC4 had maintained the direct association with BLUP based analytic measures HMGV, RPGV, HMPRVG*Meanb, GAI, Meanb, RPGV*Meanb values. Moreover the values of CV measure had clustered with S_i^2, S_i^3, S_i^4, S_i^5, S_i^7 measures of this study.

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Keywords

AMMI;
biplot Analysis;
BLUP;
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Introduction

Genotypes and environment effects refers to the different response of genotypes evaluated over number of locations or years and this cross over interactions affects the breeding progress under crop improvement program as makes it difficult to identify

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the really promising genotypes (Karimizadeh *et al.* 2023). The estimation and proper usage of interaction effects had been highlighted by the breeders for the development and release of high-yielding stable genotypes (Azam *et al.* 2023). Moreover, the yield being quantitative trait can be significantly affected by cross over significant genotypes and environment interaction effects (Hossain *et al.* 2023). This demands there searchers to be more careful in evaluation process and identifying genotypes to be better in terms of yield and adaptability particularly for the targeted environmental conditions (Mohammadi *et al.* 2023). On the other hand, this interaction effects also provide opportunities to select genotypes that interact positively with a particular location (specific adaptation) or perform well in most of the environmental conditions (general adaptation) (Taleghani *et al.* 2023). Numerous analytic techniques have been developed over the recent past to take advantage of the genotype × environment interactions and to assist the breeders to identify the cultivars for their better adaptation in specific environmental conditions (Saremirad *et al.* 2022, Saeidnia *et al.* 2023). Broadly there are two approaches for modelling the effects of G, E and their interactions. Parametric methods defined the stability indices considered the interaction effects and the normal distribution of errors, thought their robust assurance might not be applicable for situations when these assumptions are not fulfilled (Pour-Aboughadareh *et al.* 2019; Shojaei *et al.* 2021). Apart from the BLUP based analytic measures good number of non-parametric methods considered the ranks of genotypes as per their performance in each environment had been proposed to interpret and describe the responses of genotypes to various environmental conditions Sharif *et al.* 2021. The current study was carried out to observe association, if any, among the measures considered the Additive Main and Multiplicative Interaction (AMMI), Best Linear Unbiased Predictor (BLUP) and Non parametric approaches for the wheat genotypes evaluated at number of locations in the north hills zone of the country in last cropping season.

Materials and Methods

Promising nine wheat genotypes were evaluated under advanced varietal trials at major nine locations of the north hills zone of the country during 2022-23 cropping season under rain fed conditions reflected in table 1. Randomised Block deigns with four replications were laid out in research fields of plot size 3.5 x 1.20 meter to accommodate ample number of plants as inner six rows were harvested for yield recording. Sowing of seeds in fields were completed during second fortnight of October and recommended dose of fertilizers 60:30:20 (N:P:K) for the zone was applied thoroughly in fields. The recent analytic measures as per BLUP, Non parametric measures and AMMI based measures had been mentioned below for ready reference as (Zali *et al.* 2012, Olivoto *et al.* 2019; Vineeth *et al.* 2022)

AMMI Stability Value

$$\mathrm{ASV} = [(\frac{SSIPC\ 1}{SSIPC\ 2} PCI)^2 + (PC2)^2]^{1/2}$$

Modified AMMI stability Value

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

Harmonic Mean Genotypic Value

HMGV = Number of environments / $\sum_{j=1}^{k} \frac{1}{GV_{ij}}$

GV_{ij} genetic value of ith genotype in jth environments

Relative performance of genotypic values across environments

$RPGV_{ij} = \sum\ GV_{ij} / \sum\ GV_j$

Harmonic mean of Relative performance of genotypic values

$HMRPGV_{i\cdot}$ = Number of environments /$\sum_{j=1}^{k} \frac{1}{RPGV_{ij}}$

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

Simultaneous selection index SSI = R (AMMI stability indices) + RY

Weighted Average of Absolute Scores

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

Superiority index $\mathrm{SI} = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(\theta_Y + \theta_S)}$;|

Non parametric measures based on the ranks

$$S_i^{(1)} = \frac{2\Sigma_j^{n-1}\Sigma_{j'=j+1}^{n}|r_{ij} - r_{ij'}|}{[n(n-1)]}$$

$$S_i^{(2)} = \frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_{i'})^2}{(n-1)}$$

$$S_i^{(3)} = \frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{\bar{r}_{i.}}$$

$$S_i^{(4)} = \sqrt{\frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{n}}$$

$$S_i^{(5)} = \frac{\Sigma_{j=1}^{n}|r_{ij} - \bar{r}_i|}{n}$$

$$S_i^{(6)} = \frac{\Sigma_{j=1}^{n}|r_{ij} - \bar{r}_i|}{\bar{r}_{i.}}$$

$$S_i^{(7)} = \frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{\Sigma_{j=1}^{n}|r_{ij} - \bar{r}_i|}$$

Recent and popular software's viz. Meta-R, AMMIsoft 1.0 and SAS 9.3 software's were used to analyse the research data generated under multi location evaluation of wheat genotypes.

Table 1: Detail about the parentage of evaluated wheat genotypes and locations of the field trials

Code	Genotype	Parentage	Location	Latitude	Longitude	Altitude	Soil type
NHRF101	VL907	DYBR1982-838 42ABVD50/VW9 365//PBW343	Malan	32°08 ' N	76°35'E	846	Silty clay loam
NHRF102	VL2041	NESSER/SAUL SKU32/MACS62 40//HS507	Shimla	31°10 ' N	77°17'E	2276	Silty clay loam
NHRF103	VL3028	SUP152/BAJ#1/ 4/BAJ#1/3/KIRITA TI//ATTILA*2/PAS TOR/5/SUP152/ BAJ#1	Bajaura	31°50'N	77°9'E	1103.85	Silty clay loam
NHRF104	HPW484	PBW677mutant/ G W322//BAJ#1 (Trombay)	Almora	29° 35 ' N	79° 39 'E	1610	Silty clay loam
NHRF105	HPW349	NAC/TH.AC//3* MIR LO/BUC/4/ 2*PASTOR	Majhera	29° 16' N	80° 5' E	1532	
NHRF106	HS691	HS484/KLE/BE R/2*FL-8/DONS K-POLL	Gaja				
NHRF107	VL892	WH542/PBW226	Khudwani	33° 70' N	75°10' E	1590	
NHRF108	HS692	ZANDER-33/HD 2932//HS484	Wadura	21° 18' N	77° 41' E	508	
NHRF109	HS562	OASIS/SKUAZ //4*BCN/3/2*P ASTOR	Imphal	24°81° N	93°93 E	786	

Results and Discussion

ANOVA has partitioned the total sum of squares into effects of environments, interactions and genotypes with respective shares of 21.3%, 12.7% and 2.6% respectively (Table 2). Interaction effects were further partitioned into three components and first two components had accounted for 93.5% of total interactions sum of squares in AMMI analysis of nine genotypes at nine locations (Mohammadi *et al.* 2020a).

Table 2: ANOVA for yield and significance of interaction principal components by AMMI

Source	Degree of freedom	Sum of squares	Mean Sum of squares	Share of factors (%)	IPCA's share (%)	Cumulative total of interaction components
Treatments	80	81762.79	1022.03	36.6		
Genotypes (G)	8	5851.72	731.46	2.62		
Environments (E)	8	47605.43	5950.68	21.31		
GxE interactions	64	28305.64	442.28	12.67		
IPC1	15	24897.37	1659.82		87.96	87.96
IPC2	13	1570.65	120.82		5.55	93.51
IPC3	11	1274.59	115.87		4.5	98.01
IPC4	9	340.85	37.87			
IPC5	7	162.23	23.18			
IPC6	5	51.04	10.21			
IPC7	3	8.88	2.96			
Residual	1	0.04	0.04			
Error	396	141656.33	357.72			
Total	476	223419.12	469.37			

Performance of Genotypes Based on Simultaneous Selection Index

Measures from the AMMI analysis were compared with the average yield for each genotype in all environments; these are shown in Table 3. VL907, HS562, HPW484 genotypes had achieved the higher yield as compared to other ones as ranked in top three genotypes. Least values of IPC1 had been observed for HS691, HPW484, VL2041 whereas genotypes HS562, HS692, VL907 had exhibited minimum values of IPC2 in the recent study. Lower values of IPC3 measure had pointed by HS562, HPW349,VL3028 genotypes. AMMI analysis based measure while considering first two interactions components had expressed the desirability of HPW484, HS562, VL2041as least values would be suitable for stable performance of wheat genotypes (Mohammadi *et al.* 2020b). Moreover the genotypes HS562, HPW484, VL2041 had been identified by least values of MASV measure as observed from the table3 (Jędzura *et al.* 2023). Moreover, simultaneous selection index (SSI) was also computed by considering yield and stable behaviour of the evaluated genotypes. The genotypes were ordered as per the SSI values for each of the indices derived from the AMMI analysis, with the highest ranking going to the genotype with the highest yield and stability and the lowest ranking going to the genotype with the lowest yield and instability (Hilmarsson *et al.* 2021). Simultaneous selection index while considering the higher yield values with their stable performance had ranked the evaluated genotypes. HS562, HPW484, VL2041 were found as least ranked genotypes. The genotypes with stable performance may not be high-yielders as stability alone is not a suitable selection criterion therefore Simultaneous Selection Index, a single non-parametric measure is suggested as the phenotypic characteristics and stability both included in a single selection measure by summing the rankings of the stable performance measure and average yield of genotypes. High SSI is seen to be least stable with low yield, whereas low SSI is thought to be most stable with high yield. Values of ssiMASV had selected HS562, HPW484, VL2041 while ssiWAASB measures found the suitability of HPW484, HS562, HS691 wheat genotypes. Ranks of the evaluated genotypes as per the superiority index mentioned the minimum values of HPW484, HS691, HS562 genotypes.

Table 3: Simultaneous selection indexes as per AMMI and superiority measures

	Mean	rMean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	ASV	rASV	ssiASV	MASV	rMASV	ssiMASV	W2	W3	W4	W5	WAASB	rWAASB	ssiWAASB
VL907	35.36	1	7.36	-0.44	-0.67	-0.13	0.00	-0.10	-0.01	29.29	9	10	29.34	9	10	3.69	6.51	6.38	6.31	6.27	9	10
VL2041	30.23	4	-0.65	-0.66	1.35	1.43	-0.79	-0.85	-0.31	2.67	3	7	5.50	3	7	0.35	0.69	0.71	0.71	0.71	4	8
VL3028	28.61	5	-1.28	-0.83	-0.56	0.79	1.57	0.03	-0.13	5.17	6	11	6.43	6	11	0.67	1.21	1.20	1.21	1.20	6	11
HPW484	30.24	3	-0.25	-0.92	1.56	0.12	0.57	0.84	0.14	1.36	1	4	4.55	2	5	0.16	0.37	0.37	0.37	0.37	1	4
HPW349	25.13	8	-1.61	-1.73	0.53	-1.95	-0.20	-0.51	0.16	6.64	7	15	7.93	7	15	0.87	1.55	1.56	1.54	1.54	7	15
HS691	27.22	6	0.22	3.08	1.49	-0.71	0.32	-0.05	-0.24	3.20	4	10	5.87	4	10	0.22	0.48	0.48	0.48	0.48	2	8
VL892	22.50	9	-1.22	1.23	-1.26	0.46	0.08	-0.50	0.78	5.00	5	14	6.11	5	14	0.65	1.22	1.21	1.19	1.19	5	14
HS692	27.13	7	-1.90	0.23	-2.34	-0.41	-0.28	0.18	-0.60	7.55	8	15	9.19	8	15	0.96	1.82	1.79	1.77	1.76	8	15
HS562	30.61	2	-0.67	0.04	-0.11	0.39	-1.25	0.96	0.20	2.65	2	4	4.51	1	3	0.33	0.59	0.59	0.60	0.60	3	5

Meanb : Average of BLUP ; rASV, rMASV and rWAASB: Rank of genotypes for ASV, MASV and WAASB values; ssiASV, ssiMASV and ssiWAASB : Simultaneous selection index based on ranks of yield and of ASV, MASV and WAASB simultaneous

Table 4: Performance of multi location evaluation of wheat genotypes as per BLUP and non-parametric measures

	Meanb	CV	GAI	HMGV	RPGV *Meanb	RPGV GV*Meanb	HMRPGV	HMRP	S_i^1	S_i^2,	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	Z1	Z2	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
VL907	27.69	38.61	25.29	22.28	1.01	27.77	0.99	27.20	2.53	2.91	1.60	2.83	2.44	4.60	8.00	1.48	0.75	2.33	0.49	0.56	0.53
VL2041	29.99	36.11	27.50	24.26	1.09	29.99	1.08	29.76	1.87	3.29	1.61	2.80	2.12	5.38	7.86	3.77	0.67	2.11	0.59	0.74	0.53
VL3028	28.29	38.53	26.04	23.53	1.03	28.40	1.03	28.19	1.56	2.50	0.93	2.11	1.58	3.28	4.44	4.84	0.83	1.56	0.36	0.46	0.36
HPW484	29.91	38.46	27.22	23.92	1.08	29.69	1.07	29.46	1.64	2.98	1.83	3.06	2.79	7.06	9.36	4.53	0.73	2.67	0.75	0.81	0.46
HPW349	25.19	45.14	22.13	18.29	0.89	24.53	0.85	23.48	2.31	3.22	1.63	3.00	2.49	3.37	9.03	2.24	0.68	2.33	0.35	0.42	0.35
HS691	26.90	38.01	24.83	22.50	1.00	27.38	0.97	26.56	2.89	3.32	1.92	3.20	2.74	4.72	10.25	0.25	0.66	2.56	0.49	0.58	0.55
VL892	22.69	42.24	20.61	18.40	0.82	22.51	0.81	22.28	0.62	2.72	1.55	2.69	2.37	2.56	7.25	8.05	0.78	2.33	0.28	0.30	0.07
HS692	26.66	40.90	24.53	22.37	0.98	26.90	0.96	26.39	2.49	3.27	1.91	3.06	2.54	4.29	9.36	1.63	0.67	2.44	0.46	0.54	0.47
HS562	30.05	35.89	27.77	25.01	1.10	30.19	1.10	30.16	1.20	1.16	0.25	1.09	0.91	2.64	1.19	6.06	1.09	0.89	0.29	0.33	0.39
											χ^2 =	18.54	12.59		Sum =	32.86	6.87				

SD: Standard deviation; GAI: Geometric Adaptability Index; HMGV: Harmonic mean of Genotypic values; RPGV: Relative performance of genotypic values; HMRPGV: Harmonic mean of relative performance of genotypic values

Behaviour of Genotypes as per BLUP and Non Parametric Measures

The BLUP values of the genotypes over the locations had been utilized for calculation of analytic measures i.e. HMGV, RPGV, and HMRPGV to determine the degree of agreement among the analytic measures for choosing stable and high-yielding genotypes (Taleghani *et al.* 2023). More average values as per the BLUP of genotypes had expressed by HS562, VL2041, HPW484 while the consistent yield exhibited by HS562, VL2041, HS691 genotypes as evident from the CV measure. Large values of GAI measure had obtained by HS562, VL2041, HPW484 genotypes whereas the next measure HMGV also settled for these genotypes. Measures RPGV and RPGV*Meanb had found the suitability of HS562, VL2041, HPW484 genotypes based on their BLUP at individual locations. Last two analytic measures HMRPGV and HMRPGV*Meanb had favour the HS562, VL2041, HPW484 genotypes in the present study. Non parametric measure S_i^1 pointed for VL892, HS562, VL3028 whereas as per S_i^2 measure HS562, VL3028, VL892 while values of S_i^3 had settled for HS562, VL3028, VL892 and genotypes HS562, VL3028, VL892 pointed by S_i^4. Measure S_i^5 had observed the suitability of HS562, VL3028, VL2041 genotypes. Measures Z1 and Z2 represented the normalised values of Si1 & S_i^2 as tests for their significance had been put forward in literature. Significant differences among the genotypes ranks as per their yield performance across the locations had been express by sum of Z1 values and non significant differences among the genotypes ranks as per Z2 values as observed by Saremirad and Taleghani, 2022. Next composite non parametric measures considered the ranks of genotypes as per yield and their corrected yield values for ranking their behaviour among the considered locations of the zone (Pour-Aboughadareh *et al.* 2019). Lower values of $NP_i^{(1)}$ had selected HS562, VL3028 genotypes whereas $NP_i^{(2)}$ had favoured VL892, HS562 and $NP_i^{(3)}$ had settled for VL892, HS562 genotypes while VL892, HPW349 wheat genotypes had been pointed by last measure $NP_i^{(4)}$.

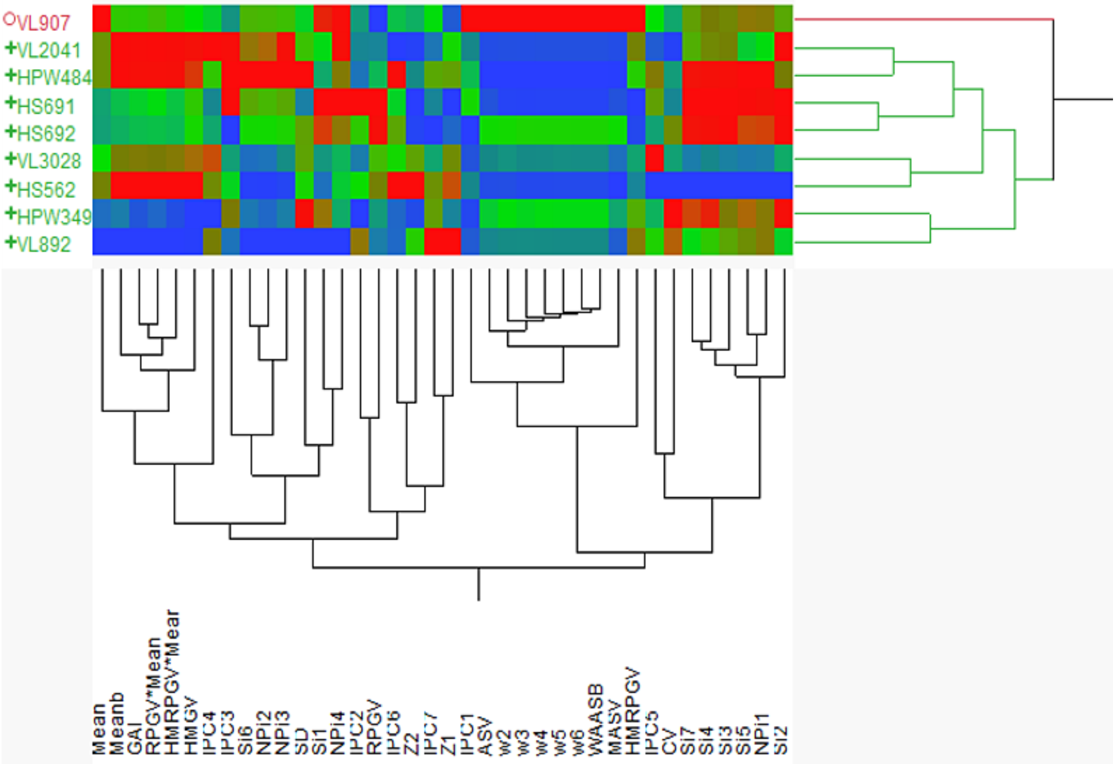

Fig. 1: Two ways Hierarchical clustering based on Ward’s method

Multivariate Hierarchical Clustering as Per Ward's Method

The advantage of two ways hierarchical cluster analysis, based on genotypes and various measures has been discussed. By dividing genotypes and measures into homogeneous groups, interactions within groups would be minimized as mentioned by Mostafavi and Saremirad, 2021. Multivariate hierarchical clustering of evaluated and considered measures had been carried out as per Ward's method as similar performers were grouped together in same group (Khalid *et al.* 2023). One genotype VL907 was placed in separate group and others performed in similar fashion as per considered measures of this study. Measure Interaction principal component IPC1 had divided others in two groups at the first node of bifurcation. ASV, MASV, WAASB, HMPRGV, non parametric measures along with composite non parametric measure were placed together while analytic measure as per BLUP of genotypes i.e. Meanb, GAI, HMGV, RPGV, HMGV*Meanb, RPGV*Meanb, interaction principal components IPC2, IPC3, IPC4, IPC5, IPC6, IPC7, non parametric measures along with composite non parametric. Further at the second node of classification the measures in first group had been further in five clusters while the measures of bigger group had partitioned into seven clusters.

Biplot analysis based on first two Principal Components

First two significant components had accounted for 55.5% of the total variation among the evaluated genotypes and considered measures in the study (Table 5). Respective share of these components were 30.5% and 25% whereas the MASV, ASV, WAASB were major contributors for the first while the more share had augmented by RPGV*Mean, Mean, Meanb, GAI, HMRPGV*Mean, $NP_i^{(4)}$ for second one. Wheat genotypes VL907, HS562 and VL892 VL907 had more contributions in respective components.

Table 5: Loadings of measures and wheat genotypes based on principal components

Measure	PC1	PC2	Measure	PC1	PC2	Genotype	PC1	PC2
Mean	0.069	0.302	GAI	-0.114	0.297	VL907	0.701	0.379
IPC1	0.199	0.158	HMGV	-0.127	0.281	VL2041	-0.091	0.284
IPC2	-0.017	-0.081	RPGV	-0.126	-0.023	VL3028	-0.236	0.048
IPC3	-0.049	0.105	RPGV*Mean	-0.106	0.300	HPW484	-0.077	0.266
IPC4	-0.119	0.118	HMRPGV	0.156	0.033	HPW349	0.189	-0.383
IPC5	0.047	-0.037	HMRPGV*Mean	-0.121	0.293	HS691	0.032	-0.052
IPC6	-0.125	0.133	S_i^{1}	0.171	0.102	VL892	-0.019	-0.707
IPC7	-0.039	-0.171	S_i^{2}	0.192	-0.052	HS692	0.123	-0.060
ASV	0.236	0.085	S_i^{3}	0.197	-0.060	HS562	-0.622	0.225
MASV	0.240	0.102	S_i^{4}	0.205	-0.065	% share of measures (55.50%)	30.47%	25.03%
W2	0.233	0.082	S_i^{5}	0.203	-0.070			
W3	0.236	0.082	S_i^{6}	0.075	0.183			
W4	0.236	0.081	S_i^{7}	0.196	-0.057			
W5	0.236	0.082	Z1	-0.171	-0.102			
W6	0.236	0.082	Z2	-0.192	0.052			
WAASB	0.236	0.082	$NP_i^{(1)}$	0.201	-0.072			
Meanb	-0.106	0.297	$NP_i^{(2)}$	0.068	0.187			
SD	-0.004	0.163	$NP_i^{(3)}$	0.065	0.197			
CV	0.118	-0.252	$NP_i^{(4)}$	0.073	0.260			

The symmetrical singular value partitioning method was used to display the biplot of PC1 against PC2 for both genotypes and measurements as this method is useful for understanding how genotypes and adaptability or stability measures would interact. In the biplot graph, close genotypes and environments show positive relations and stable genotypes are located close to the biplot's origin (Saeidnia *et al.* 2023). Shorter rays of measures IPC2, IPC5, IPC3, SD contribute less to joint effects of genotypes and measures effects as comparison to CV, Z1, IPC1, HMGV, RPGV*Meanb, GAI, Meanb (Figure 2). Genotypes observed at far places VL892, HS562, VL902 from the origin in biplot analysis would express the least stable behaviour as compared to genotypes placed near to origin. The nature of G × E is governed by the angle between the genotype and the environmental vectors: it is positive for acute angles, insignificant for straight angles, and negative for obtuse angles (Taleghani *et al.* 2023). Z1 measure showed direct association with RPGV, IPC2, IPC7 measures while NPi (1) expressed tight direct relation with S_i^1, S_i^3, S_i^4 ,S_i^5, S_i^6, S_i^7 measures. WAASB, ASV, MASV measures had exhibited very tight association as rays corresponding to these measures overlapped. The direct association maintained with HMPRVG, S_i^1 and IPC1 values. Direct tight association of $NP_i^{(4)}$ had observed with mean, $NP_i^{(2)}$, $NP_i^{(3)}$ and S_i^6, $NP_i^{(1)}$. IPC6 & IPC4 had maintained the direct association with Z2 values of genotypes on one side and tight relation with BLUP based analytic measures HMGV, RPGV, HMPRVG*Meanb, GAI, Meanb, RPGV*Meanb values. AMMI analysis based measures ASV, MASV had maintained ninety degree angles with BLUP based analytic measures. CV showed straight line angles with BLUP based analytic measures whereas values of Z1 expressed with ASV, MASV measures. IPC7, IPC2 had same type of relation with $NP_i^{(4)}$ and mean values of genotypes over the locations in this study.

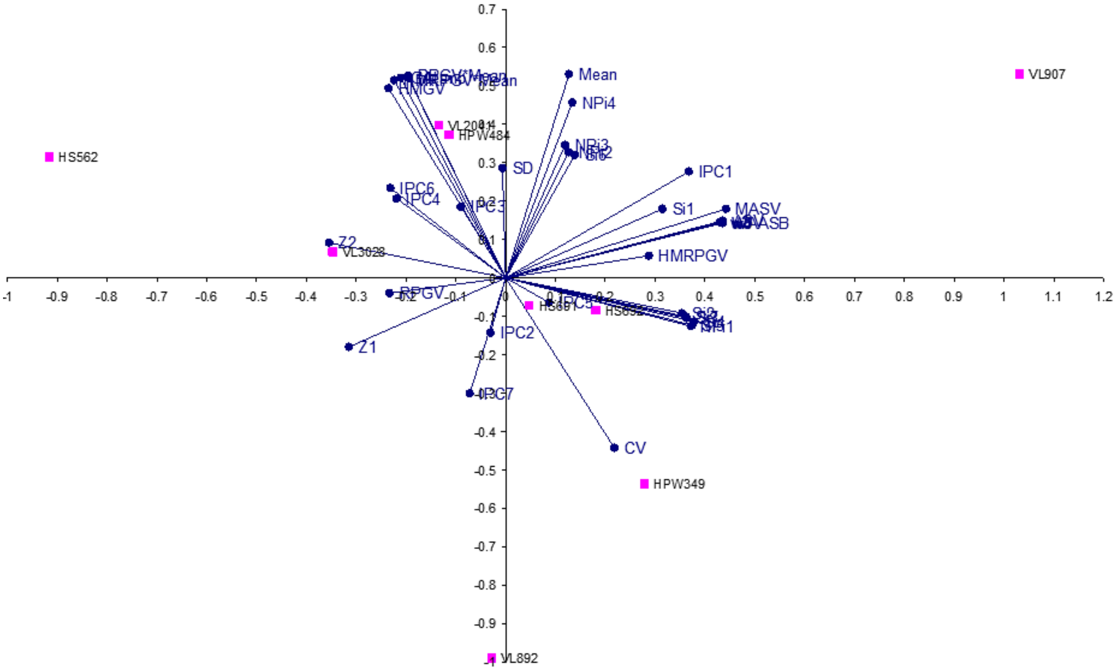

Fig. 2: Biplot analysis of measures and evaluated wheat genotypes

Biplot analysis of measures and genotypes based on first two components had observed the five clusters of the measures (Figure 3). Measures IPC2, IPC7, RPGV and Z1 had placed in first cluster in the first quadrant. Second quadrant had found the clustering of CV measure with non parametric measures S_i^2, S_i^3, S_i^4, S_i^5, S_i^7 along with first composite non parametric measure $NP_i^{(1)}$ of this study. Composite non parametric measures observed with average yield of genotypes with S_i^6 and second adjacent cluster was consisted of ASV, MASV, HMPRVG, WAASB, IPC1, Si1 measures. Fifth and largest cluster grouped BLUP based analytic measures Meanb, GAI, RPGV*Meanb, HMPRVG*Meanb, Z2, IPC3, IPC4, IPC6, SD etc.

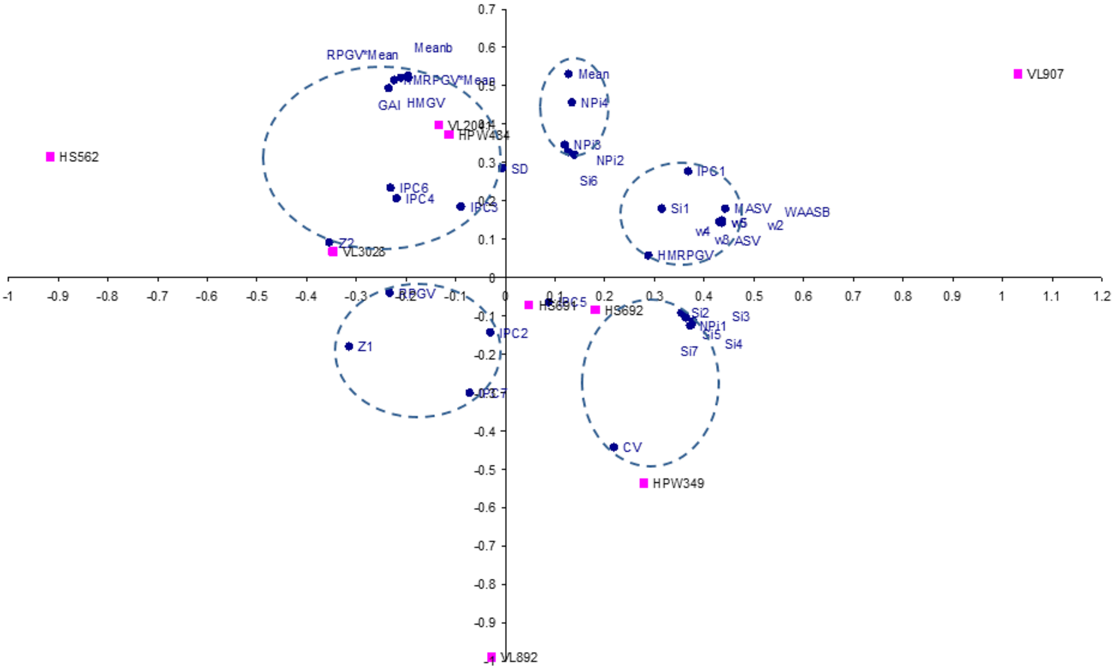

Fig. 3: Grouping of studied measures as per principal components

Conclusions

ANOVA has partitioned the total sum of squares into environments, interactions and genotypes effects for nine wheat genotypes evaluation under advanced varietal trials at major locations of the north hills zone of the country under rain fed conditions. Least values of AMMI stability measure had expressed the desirability of HPW484, HS562, VL2041 whereas HS562, HPW484, VL2041 had been identified by least values of Modified AMMI Stability Value. Higher values of BLUP based analytic measures had found the suitability HS562, VL2041, HPW484 genotypes. Composite non parametric measure $NP_i^{(2)}$ had favoured VL892, HS562 and $NP_i^{(3)}$ had settled for VL892, HS562 genotypes while VL892 HPW349 wheat genotypes had been pointed by last measure $NP_i^{(4)}$. Ward's method of hierarchical clustering had placed VL907 in separate group as compared to others. Shorter rays of measures IPC2, IPC5, IPC3, SD contribute less to joint effects of genotypes and measures effects in the biplot analysis as comparison to CV, Z1, IPC1, HMGV, RPGV*Meanb, GAI, Meanb. $NP_i^{(1)}$ expressed tight direct relation with S_i^1, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7 measures in the biplot analysis. PC6 and PC4 had maintained the direct association with BLUP based analytic measures. CV measure had clustered with non parametric measures S_i^2, S_i^3, S_i^4, S_i^5, S_i^7 along with $NP_i^{(1)}$ whereas the adjacent cluster was consisted of ASV, MASV, HMPRVG, WAASB, IPC1, S_i^1 measures.

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Conflict of Interest

Authors disclosed no conflict of interest including any financial, personal or other relationships with other people or organizations that can influence their work.

Data Availability

Data used uploaded on website

Ethics Statement

No animals or humans used in experimentatons

Authors' Contribution

Ajay Verma Field layout, Data Analysed, manuscript preparation,G Singh: Mobilised resources, manuscript preparation, B S Tyagi : Monitored field trials and execution, manuscript preparation.

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