Genotype X Environment Interactions of Fodder Barley Genotypes as Estimated by Ammi, Blup and Non Parametric Measures

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Abstract

Field experiments were carried out at six locations in Northern Hill Zone to evaluate twenty three promising fodder barley genotypes in a randomized complete block design (RCBD) during 2020-21 cropping seasons. Using analytic methods Additive Main Effects and Multiplicative Interactions (AMMI), Best Linear Unbiased Predictor (BLUP) along with Non Parametric compared to decipher the GxE interactions under multi environment trials. Highly significant about 67.5% variations accounted by environments, 14.1% of GxE interactions and marginally 3.2% by the genotypes in the total sum square of variations for yield the present study. AMMI1 explained 53.7%, 32.1% by AMMI2, 6.9% for AMMI3, AMMI4 accounted for 4.8% respectively of a total variation. ASV and ASV1 measures considered 85.9% of the total variation identified G4, G5, G9 genotypes. MASV1 exploited 97.7% of interactions favoured for G18, G15, G8 genotypes. BLUP-based settled for G6, G11, G5 genotypes. Non parametric measures found G9, G8, G1 as suitable genotypes. Further non parametric composites measures selected G9, G4, G8 as suitable genotypes. Measures S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7, HMPRVG, ASV1, ASV, accounted more in first principal component whereas $NPi^{(1)}$, $NPi^{(2)}$, $NPi^{(3)}$, $NPi^{(4)}$, PRVG, S_i^1, GM, Mean, Average were major contributors in second principal component. Very tight positive relationships observed for IPC3, IPC1 with BLUP based measures GM, HM, PRVG, HMPRVG, Average in one quadrant. CV closely related to Stdev, IPC2, IPC4 in opposite quadrant. ASV, ASV1 expressed very tight association with Si6, Si7 whereas $NPi^{(1)}$, exhibited close affinity with S_i^1, S_i^4, S_i^2, S_i^5 values. Methods utilized in study showed high to moderate degree of association among themselves, however non parametric measures would be recommended for multi environment trials.

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Introduction

Genotype x Environment interactions of cross over type would introduce inconsistency in the behaviour of genotypes evaluated in the various environmental conditions.[1] Adaptability and stability of various crops under multi-environment field trials studied by number of analytic measures as observed in the literature.[2] Moreover non parametric measures to assess GxE interaction and stability analysis had been also reflected.[6] The components of analysis of variance, the regression models, non-parametric methods, AMMI methods, BLUP based mixed models would be most suitable analytic methods.[3] AMMI stability value (ASV), ASV1, Modified AMMI stability value (MASV) & MASV1) have been registered visibility.[4] Random effects of the genotypes to improve their predictive accuracy had been advocated for Best linear unbiased prediction (BLUP) based measures. The stability and adaptability of genotypes were also highlighted by the harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV), and harmonic mean of relative performance of genotypic values (HMRPGV).[5] Besides that nonparametric measures S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP^{i(3)}$, $NP_i^{(4)}$ have been also utilized for genotypes x environmental conditions.[6] All recent analytic measures have been compared to decipher the Gx E interactions effects for fodder barley genotypes evaluated in northern hills zone of the country.

Materials and Methods

Twenty three fodder barley genotypes were evaluated at six major centers of All India Co-ordinated Research Project at the northern hill zone of the country. To increase the barley production of this zone has been emphasised more to augment the total fodder production of the country. Randomized complete block designs with four replications has been laid out in field trials during 2020-21 cropping season. The environmental conditions of the locations and parentage details of the evaluated fodder barley genotypes reflected in table 1 for ready reference. The phenotypic value of ith genotype in jth environment denoted by X_{ij} where i=1,2, ...k,..,j =, 1,2,...,n while rank of genotypes as per yield values reflected by r_{ij} as the rank of the ith genotype in the jth environment, and average of ranks for the ith genotype by $\bar{r}_i$.

The corrected yield of ith genotype in jth environment reflected as ($X^*_{ij} = X_{ij} - x\bar{i}. + (\bar{x})$ as X^*_{ij}, the corrected mean phenotypic value; ($X_{i.}$ was the overall mean of ith genotype in all environments as $\bar{X}$.

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

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

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

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

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

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

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

$$\bar{r}_{i=} \frac{1}{n}\Sigma_{j=1}^n r_{ij}.$$

However, the composite non parametric measures were also suggested to utilize the ranks of genotypes as per yield and corrected yield in number of environments as $NP^{i(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$. In the formulas, r*ij was the rank of X^*_{ij}, and $\bar{r}_i$ and M_{di} were the mean and median ranks for original (unadjusted) grain yield, where ($\bar{r}_i^*$ and M^*_{di} were the same parameters computed from the corrected (adjusted) data.

$$NP_i^{(1)} = \frac{1}{n}\Sigma_{j=1}^n |r_{ij}^* - M_{di}^*|$$

$$NP_i^{(2)} = \frac{1}{n}\left(\frac{\Sigma_{j=1}^n |r_{ij}^* - M_{di}^*|}{M_{di}}\right)$$

$$NP_i^{(3)} = \frac{\sqrt{\Sigma(r_{ij}^* - \bar{r}_{i.}^*)^2/n}}{\bar{r}_{i.}}$$

$$NP_i^{(4)} = \frac{2}{n(n-1)} \left[\Sigma_{j=1}^{n-1} \Sigma_{j'=j+1}^{m} \frac{|r_{ij}^* - r_{ij'}^*|}{\bar{r}_{i.}} \right]$$

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

ASV1 $\quad ASV1 = [\frac{SSIPC\,1}{SSIPC\,2} (PCI)^2 + (PC2)^2]^{1/2}$

Modified AMMI stability Value

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

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

$HMGV_i$ = 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

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

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

AMMISOFT version 1.0 software utilized for AMMI analysis of data sets and SAS software version 9.3 for further analysis.

Table 1: The location and parentage details of fodder barley genotypes

Code	Genotype	Parentage	Locations	Latitude	Longitude	Altitude
G1	HBL873	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA1/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETU NIA 1 (6th GSBON -2018-19-Ent 87)	Berthein	28.63	77.21	
G2	HBL870	VLB 118 x HBL 712	Majhera	29° 16' N	80° 5' E	1 532
G3	VLB170	VB 1709 INBYT-HI (2016)-12 (CHAMICO/TOCTE//CONGONA/3/PETUNIA 2/4/PENCO/CHEVRON-BAR)	Khudwani	33° 70' N	75°10' E	1590
G4	BHS483	BHS352/BHS366	Malan	32°08 ' N	76°35'E	846
G5	UPB1093	RD2784/RD2035	Rajauri	31.01	75.92	
G6	VLB118	14th EMBSN-9313	Shimla	31°10 ' N	77°17'E	2276
G7	BHS487	BBM593/ BHS169				
G8	BHS400	34th IBON-9009				
G9	BHS486	HBL276/BHS365				
G10	VLB173	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/ PETUNIA1/ 6/GLORIA-BAR/COPAL (IBON-HI-18-91)				
G11	BHS352	HBL240/BHS504//VLB129				
G12	HBL869	DWR 81 x BH 936				
G13	VLB172	ZIGZIG/3/PENCO/CHEVRON-BAR//PETUNIA 1 (INBYT-HI-15-16-20)				

G14	HBL113	SELECTION FROM ZYPHYZE
G15	BHS485	HBL276/BHS369
G16	BHS484	BHS352/BHS 169
G17	HBL872	P.STO/3/LBIRAN/UNA80//LIGNEE640/
		4/BLLU/5/PETUNIA1/6/P.STO/3/LBIRAN/
		UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1
		(6th GSBON-2018-19 -Ent 86)
G18	UPB1092	RD2828/K551
G19	VLB171	BISON 110.3//CANELA/ZHEDAR#2
		(IBON-HI-18-36)
G20	HBL871	TRADITION/6/VMorales/7/LEGACY/
		/PENCO/CHEVRON-BAR
		(IBON 16-17-Ent72 or EIBGN
		2017-18, Ent-49)
G21	BHS380	VOILET/MJA/7/ABN-B6/BA/GAL/
		/ FZA-B /5/DG/DC-B/ PT-BAR /3/
		RA-B/BA /3/4/TRYIGAL…
G22	VLB174	LIMON/BICHY2000//DEFRA/
		DESCONOCIDA-BAR (IBON-HI-18-83)
G23	UPB1091	RD2828/RD2552

Results and Discussion
AMMI Analysis

AMMI analysis observed highly significant variations (P>0.001) due to environments, GxE interactions, and genotypes with corresponding share of 67.5% ,14.1%, marginally 3.2% (Table 2) the total sum square of variation for yield.[7] Further Interaction effects portioned into four significant components accounted for nearly 98% of interactions sum of square variations. First component (AMMI1) contributed 53.7%, followed by 32.1%, 6.9%, 4.8% by AMMI2, AMMI3, AMMI4 respectively. Nearly 85.9% of the total variation contributed by the two AMMI components.[3] G×E signal and noise effects accounted for 25.7% & 74.2% in total G×E. Share of GxE noise effect was 3.2 times the genotypes effects.

Table 2: Interaction principal component analysis of Fodder barley genotypes

Source	Degree of freedom	Mean Sum of Squares	Signifi-cance level	Proportional contribution of factors	GxE inter-action Sum of Squares (%)	Cumulative Sum of Squares (%) by IPCA's
Treatments	137	1148.426	***	84.87		
Genotype (G)	22	269.3139	*	3.20		
Environment (E)	5	25060.03	***	67.59		
GxE interactions	110	237.3574	**	14.08		
IPC1	26	540.1555	*		53.79	53.79
IPC2	24	350.159			32.19	85.98
IPC3	22	82.79075			6.98	92.95
IPC4	20	62.93911			4.82	97.77
Residual	18	32.29291				
Error	138	203.2436				
Total	275	674.1163				

Behaviour Of Genotypes As Per Blup Based Measures

Average higher yield showed by G6, G2, G7 genotypes while lowest yield of G23 (Table 3). IPCA's in the AMMI analysis exploited to know about the stability or adaptability of genotypes. Absolute IPCA-1 scores pointed for G9, G4, G5 while as per IPCA-2, G2, G15, G21 genotypes would be of choice. Values of IPCA-3 favoured G18, G8, G23 genotypes. As per IPCA-4, G17, G7, G10 genotypes would be of stable performance. ASV & ASV1 measures based on two IPCAs and utilized 85.9% of G×E interaction sum of squares would be useful for dynamic concept of stability.[8] Both measures recommended (G4, G5, G9) as of stable performance. Values of MASV1 using 97.7% of GxE interactions sum of squares identified G18, G15, G8 genotypes whereas G18, G8, G5 genotypes be of stable yield as per MASV.[9]

Table 3: Stability measures of fodder barley genotypes as per AMMI analysis

Genotype	Mean	IPC1	IPC2	IPC3	IPC4	MASV1	MASV	ASV1	ASV	Average	Stdev	CV
G1	50.99	1.1403	1.4015	0.5089	0.8949	7.001	3.825	2.37	2.03	48.43	25.75	53.18
G2	52.44	1.9890	-0.1243	-1.9671	0.0828	4.834	4.022	3.33	2.57	51.39	28.50	55.45
G3	47.45	1.4878	-1.0280	1.6536	0.6708	6.216	4.095	2.69	2.18	48.58	25.51	52.51
G4	44.68	0.5333	-1.0650	-0.4442	1.7311	5.448	3.213	1.39	1.27	46.33	26.39	56.95
G5	50.16	0.7677	-0.9705	0.3774	-0.4332	4.824	2.609	1.61	1.39	50.52	23.48	46.47
G6	54.61	-1.1570	1.5170	-0.4005	-2.6186	7.899	4.734	2.46	2.13	51.05	20.39	39.94
G7	51.21	2.0292	0.4155	0.2223	-1.5937	4.247	3.242	3.42	2.66	50.16	26.45	52.73
G8	45.15	-1.3279	0.6956	-0.1237	-0.5554	4.008	2.451	2.33	1.85	44.79	22.13	49.41
G9	48.26	0.2889	1.8028	-0.6271	-0.6508	8.620	4.446	1.87	1.84	46.13	24.98	54.15
G10	41.92	-2.8858	0.7683	-0.7493	0.1256	6.178	4.315	4.88	3.81	42.03	23.12	55.00
G11	49.21	-1.8610	-0.9735	1.8900	-1.4640	6.633	4.690	3.26	2.60	49.53	17.12	34.56
G12	49.69	-1.3804	3.6913	-0.3332	0.7949	17.607	8.977	4.35	4.10	44.65	24.53	54.94
G13	51.45	2.7577	3.1346	0.7342	-0.6483	15.567	8.343	5.57	4.75	47.40	29.88	63.04
G14	51.39	3.0950	1.1854	-0.5153	1.5729	7.834	5.198	5.31	4.17	49.20	32.30	65.65
G15	44.86	-1.6025	0.1838	1.3877	1.1020	3.885	3.226	2.68	2.08	44.83	21.53	48.03
G16	47.21	1.6661	-3.0879	-1.4545	-0.2228	15.062	7.962	4.16	3.76	50.79	25.83	50.86
G17	38.80	-2.7119	-0.2449	-1.7861	0.0511	5.634	4.521	4.54	3.51	40.92	24.38	59.58
G18	49.39	1.5768	0.4732	-0.0800	0.6291	3.514	2.413	2.68	2.09	48.38	26.68	55.14
G19	47.48	1.2225	-2.8947	-1.1421	-0.2967	13.966	7.268	3.54	3.30	50.72	24.80	48.90
G20	45.93	1.2379	-2.0854	2.6700	-0.3688	11.109	6.675	2.94	2.63	48.71	22.99	47.20
G21	38.47	-2.6661	0.1867	1.0613	1.2037	5.056	4.035	4.46	3.45	40.04	23.31	58.21
G22	45.05	-0.8482	-1.3384	-0.6871	-0.8683	6.644	3.629	1.95	1.73	47.04	22.40	47.61
G23	36.06	-3.3513	-1.6431	-0.1952	0.8618	9.612	5.896	5.84	4.63	40.20	23.03	57.29

Table 4: Stability measures of fodder barley genotypesas per BLUP and Non parametric measures

Genotype	Fodder	GM	HM	PRVG	HMPRVG	S_i^1	S_i^2	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
G1	HBL873	41.21	33.37	1.0096	0.9968	5.07	17.47	1.42	4.18	3.00	1.46	7.08	3.00	0.3529	0.4917	0.5961
G2	HBL870	39.91	24.51	1.0232	0.9023	9.13	58.97	4.26	7.68	6.11	2.65	21.31	5.83	1.6667	1.2125	1.4421
G3	VLB170	42.46	36.84	1.0499	1.0178	8.20	45.37	3.28	6.74	5.17	2.24	16.40	5.17	0.7381	0.6415	0.7810
G4	BHS483	38.38	29.84	0.9404	0.9276	6.00	28.67	2.46	5.35	4.11	2.11	12.29	3.67	0.2529	0.4589	0.5143
G5	UPB1093	45.20	39.70	1.1075	1.0932	5.13	17.90	1.23	4.23	3.50	1.45	6.17	3.50	0.5833	0.6044	0.7333
G6	VLB118	46.95	42.41	1.1648	1.1231	9.73	66.27	4.85	8.14	6.44	2.83	24.24	6.33	1.0556	1.2524	1.4974
G7	BHS487	42.81	34.78	1.0503	1.0345	8.60	53.37	3.37	7.31	5.22	1.98	16.85	5.17	0.5439	0.7969	0.9382
G8	BHS400	39.50	33.77	0.9653	0.9573	4.73	17.10	1.80	4.14	3.00	1.89	9.00	2.83	0.2576	0.3817	0.4369
G9	BHS486	37.89	27.69	0.9360	0.9059	3.60	9.07	0.74	3.01	2.11	1.03	3.68	2.00	0.1538	0.2545	0.3042
G10	VLB173	36.22	30.24	0.9033	0.8547	7.20	52.27	6.82	7.23	4.89	3.83	34.09	4.00	0.3077	0.6025	0.6000
G11	BHS352	47.14	44.94	1.2117	1.1006	9.53	61.77	5.08	7.86	6.50	3.21	25.38	6.50	1.4444	1.1227	1.3619
G12	HBL869	37.89	30.55	0.9273	0.9172	6.93	32.27	3.34	5.68	4.44	2.76	16.69	4.33	0.3095	0.5164	0.6303
G13	VLB172	36.60	24.68	0.9282	0.8519	8.40	54.40	3.63	7.38	5.67	2.27	18.13	5.33	0.2807	0.5268	0.6000
G14	HBL113	35.70	20.50	0.9365	0.7866	11.53	100.30	6.92	10.01	8.33	3.45	34.59	7.83	0.7833	0.9245	1.0646
G15	BHS485	40.61	36.84	1.0111	0.9681	7.07	38.27	3.96	6.19	5.22	3.24	19.79	4.33	0.4333	0.5891	0.6730
G16	BHS484	42.48	31.71	1.0502	1.0159	8.20	47.77	3.45	6.91	6.17	2.67	17.27	6.17	1.1212	1.0633	1.2615
G17	HBL872	32.75	22.89	0.8394	0.7507	8.73	58.97	7.53	7.68	6.11	4.68	37.64	5.50	0.3793	0.5688	0.6469
G18	UPB1092	39.85	29.81	0.9853	0.9539	7.33	36.67	2.89	6.06	5.00	2.37	14.47	5.00	0.5556	0.6855	0.8302
G19	VLB171	43.71	35.22	1.0690	1.0591	6.13	25.07	1.75	5.01	4.00	1.67	8.74	4.00	0.6154	0.7905	0.9684
G20	HBL871	44.02	39.78	1.1062	1.0428	9.47	60.27	4.11	7.76	6.11	2.50	20.55	6.00	0.5000	0.7057	0.8606
G21	BHS380	34.93	30.83	0.8780	0.8194	8.93	61.87	8.07	7.87	6.56	5.13	40.35	5.33	0.2735	0.5186	0.5890
G22	VLB174	41.69	35.84	1.0209	1.0086	5.93	24.17	2.23	4.92	3.50	1.94	11.15	3.50	0.4118	0.5267	0.6357
G23	UPB1091	34.83	30.07	0.8860	0.7971	8.93	64.00	8.00	8.00	5.33	4.00	40.00	5.33	0.4444	0.6400	0.7147

Performance of Genotypes as Per Blup and Non Parametric Measures

Average yield of genotypes as per their best linear unbiased predictors[4] pointed towards G2, G6, G16 as high yielders. Consistent yield of G11, G6, G15 recognisedas per lower values of standard deviation while CV values identified G6, G5, G20 genotypes for northern hills zone of the country. More over the values of GM selected G11, G6, G5. Values of measure HM, BLUP-based simultaneous selection, identified G11, G6, G20 while values of PRVG favored G11, G6, G5 and HMPRVG settled for G6, G11, G5 genotypes. Measures HMGV, RPGV and HMRPGV had expressed the same ranking of genotypes as reported.[2,6]

S_i^1 non parametric measure pointed for G9, G8, G1 while S_i^2 selected G9, G8, G1 and values of S_i^3 favoured G9, G5, G1 as suitable genotypes (Table 4). G9, G8, G1selected by values of S_i^4 ,S_i^5 favoured G9, G5, G1,S_i^6 G9, G5, G1and lastly S_i^7 for G3, G5, G1 (Table 4). The stability of genotype over environment in biological concept appreciated by its consistent rank over other environments.[10] Further composite measures $NP_i^{(1)}$ to $NP_i^{(4)}$, considered the ranks of genotypes as per yield and corrected yield

simultaneously. $NP_i^{(1)}$ measure observed suitability of G9, G8, G1 whereas as per $NP_i^{(2)}$, genotypes G9, G4, G8 would be of choice while $NP_i^{(3)}$ identified G9, G8, G1. Last composite measure $NP_i^{(4)}$ found G9, G8, G4 as genotypes of choice for this zone.

Biplot Analysis

Approximately 64.1% of the total variation among the AMMI, BLUP and non parametric measures explained by first two significant PC's in biplot analysis (Table 5) with respective contributions of 35.9% & 28.1% by first and second principal components respectively.[1,11] Measures S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7, HMPRVG, ASV1, ASV, accounted more of share in first principal component whereas $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, PRVG, S_i^1, GM, Mean, Average were major contributors in PC2. The biplot analysis had been established to study the association among measures via graphical presentation. Positive correlation among measures pointed out by acute angles between vectors of measures from the origin in the biplot while negative correlation expressed by obt use or straight line angles. Moreover the right angles between vectors expressed Independent type of relationships.

Table 5: Contribution share of AMMI, BLUP and Non parametric measures

Measure	Principal Component 1	Principal Component 2	Measure	Principal Component 1	Principal Component 2
Mean	0.1376	0.1821	PRVG	0.1850	0.2891
IPC1	0.0719	0.0971	HMPRVG	0.2508	0.2048
IPC2	-0.0388	-0.1072	Si1	-0.2323	0.2345
IPC3	0.0511	0.0654	Si2	-0.2580	0.1921
IPC4	-0.1208	-0.1804	Si3	-0.2917	0.0498
ASV1	-0.2831	0.0071	Si4	-0.2575	0.1997
ASV	-0.2605	0.0051	Si5	-0.2380	0.2231
MASV1	-0.0478	0.0257	Si6	-0.2733	0.0159
MASV	-0.1087	0.0571	Si7	-0.2917	0.0498
Average	0.1635	0.2461	NPi(1)	-0.2067	0.2631
Stdev	-0.1023	-0.0638	NPi(2)	-0.0110	0.3099
CV	-0.1965	-0.1987	NPi(3)	-0.0552	0.3367
GM	0.2232	0.2515	NPi(4)	-0.0353	0.3421
HM	0.1920	0.1722			
			64.12	35.95	28.17

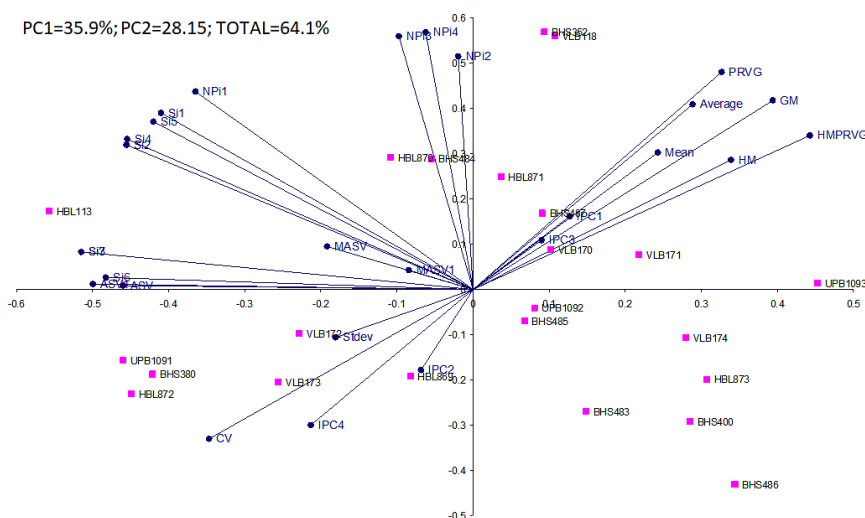PC1=35.9%; PC2=28.15; TOTAL=64.1%

Fig. 1: Association analysis amog AMMI, BLUP and Non parametric measures
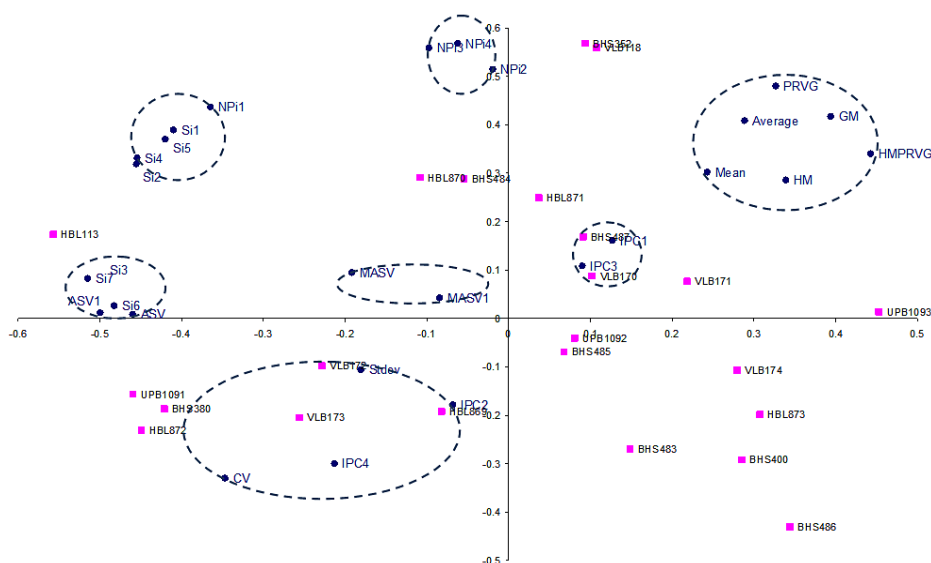

Fig. 2: Clustering pattern of AMMI, BLUP and Non parametric measures

Direct association observed for IPC3, IPC1 with BLUP based measures GM, HM, PRVG, HMPRVG, Average in one quadrant. CV closely related to Stdev, IPC2, IPC4 in opposite quadrant. ASV, ASV1 expressed very tight association with S_i^6, S_i^7. Whereas $NP_i^{(1)}$, exhibited close affinity with S_i^1, S_i^4, S_i^2, S_i^5. Closely related $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ were placed in same quadrant. Group CV with Stdev, IPC2, IPC4 managed right angles with group of BLUP based measures. Nonparametric

measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ showed right angles with BLUP based measures. AMMI based measures also exhibited right angles with BLUP based measures. Overall small and large sizes seven clusters observed among the measures for this study. CV grouped with Stdev, IPC2, IPC4 in first cluster of first quadrant. Third quadrant seen two clusters first former one of IPC1 with IPC3 whereas latter one consisted of BLUP based measures. Last quadrant placed four clusters.

MASV showed affinity with MASV1. Nearby cluster of ASV, ASV1 with S_i^3, S_i^6, S_i^7. Adjacent cluster consisted of $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ measures. While S_i^1, S_i^4, S_i^2, S_i^5 managed with $NP_i^{(1)}$ in last cluster (Fig.2)

Conflict of Interests
No conflict of interests reported by the authors.

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