Grain Yield of Dual-Purpose Barley Genotypes Estimated by AMMI, BLUP and Non-Parametric measures after One Cut

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Abstract

AMMI analysis evaluated the total variations in genotypic yield values across the environments and partied the total variations into various components to assess their significance. Environments, GxE interactions, and genotypes effects were highly significant with 69.4%, 24.1%, 3.4% respectively. IPCA-5 favored G11, G6, G8 as per IPCA-6 genotypes would be G5, G4, G17 while IPCA-7 pointed towards G3, G20, G4. First two AMMI components totalled 57.6% and ASV1 & ASV measures recommended (G4, G20, G15). MASV1 & MASV measures considered 98.5% total of seven Interaction principal components and identified G15, G9, G6 genotypes. G21, G17, G10 would be of consistent yield as per least values of standard deviation whereas CV identified G6, G10, G17 genotypes. Non parametric measures S_i^s selected G15, G13, G9 whereas non parametric composite measures selected G15, G13, G20, G16. Biplot analysis observed $S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7$, ASV, ASV1, MASV, MASV1 $NP_i^{(1)}, NP_i^{(3)}, NP_i^{(4)}$ accounted more in first principal component whereas Mean of genotypic yield, Average of BLUP of genotypic yield, PC1, GM, HM , HMPRVG, PRVG, were major contributors for second principal component. AMMI based measures ASV, ASV1, MASV, MASV1 clustered with S_i^6, S_i^7 in first quadrant. Out of two, first comprised of IPC3, IPC6, IPC7 measures while next one consisted of BLUP based measures with mean yield and IPC1. Measures $NP_i^{(2)}, NP_i^{(3)}, NP_i^{(4)}$ formed a cluster with Stdev, CV as this cluster observed adjacent to cluster of MASV1, $NP_i^{(1)}, S_i^1, S_i^4 S_i^2, S_i^5$ in same quadrant.

Keywords: AMMI; BLUP; Biplot analysis; Non parametric composite measures

Introduction

Barley has possessed a tremendous potential and variation for production of large amount of digestible dry matter along with good protein yield per hectare. Morpho-physiological traits of the Barley make it suitable for dual purpose cultivation for fodder and grain production as compared to other cereal crops. The utilization of water and nutrients in limiting conditions have been proved to be highly efficient. Dual-purpose cropping is a method of grazing a cereal crop during the vegetative stage before leaving the crop to flower and set seed as normal. Barley possesses regeneration capacity like other cereals after taking it as fodder before jointing stage. The regeneration ability of barley can be put to use by taking one cutting during the active vegetative growth stage and then leaving the regenerated crop for grain production. Genotype x environment have been estimated under multi-environment trials before the recommendations for wide scale cultivation (Ahakpaz et al., 2021; Anuradha et al., 2022). Additive nmain and multiplicative interaction effects (AMMI) based measures (AMMI stability value (ASV), ASV1, Modified AMMI stability value (MASV) & MASV1) have also gained visibility (Sousa et al., 2020; Pour Aboughadareh et al., 2022). Best linear unbiased prediction (BLUP) based measures, harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV), and harmonic mean of relative performance of genotyp-

ic values (HMRPGV), were also highlighted for the stability and adaptability of genotypes (Gonçalves et al., 2020; Pour-Aboughadareh et al., 2019). Nonparametric measures $S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7, NP_i^{(1)}, NP_i^{(2)}, NP^{(3)}, NP_i^{(4)}$ had been utilized to interpret the genotypes x environmental conditions (Pour-Aboughadareh et al., 2019). Analytic measures have been compared to estimate the GxE interactions effects of dual purpose barley genotypes after taking one cut for fodder in northern hills zone of the country.

Materials and Methods

Twenty three dual purpose barley genotypes were evaluated for grain yield after cut for fodder yield in research field trials at 10 centers of All India Coordinated Research Project across northern hills zone of the country during 2020-21 cropping season. More emphasis had been placed to increase the dual purpose barley cultivation in this zone to augment the total fodder and cereal production of the country. Field trials were laid out in Randomized block designs with four replications. Recommended practices of packages had followed in total to harvest the good yield. Parentage details and environmental conditions were reflected in table 1 for ready reference. Pour-Aboughadareh et al., (2019) recommended various non parametric and parametric measures for assessing GxE interaction and stability analysis. For a two-way dataset with k genotypes and n environments X_{ij} denotes the phenotypic value of it h genotype in jth environment where $i=1,2, ...k, j =, 1,2 ,...,n$ and r_{ij} as the rank of the ith genotype in the jth environment, and $\bar{r_i}$ as the mean rank across all environments for the ith genotype. The correction for yield of ith genotype in jth environment as $(X^*_{ij}= X_{ij}-\bar{x}_{i.}+ \bar{x}_{..})$ as X^*_{ij}, was the corrected phenotypic value; $\bar{X}_{1.}$ was the mean of ith genotype in all environments and was the grand mean.

Code	Genotype	Parentage	Locations	Latitude	Longitude	Altitude
G1	HBL873	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETU-NIA1/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/ PETUNIA 1 (6th GSBON-2018-19-Ent 87)	Almora	29° 35 ' N	79° 39 'E	1610
G2	HBL870	VLB 118 x HBL 712	Berthein	28.63	77.21	
G3	VLB170	VB 1709 INBYT-HI (2016)-12 (CHAMICO/TOCTE//CONGONA/3/PETUNIA 2/4/PENCO/CHEVRON-BAR)	Kangra	32.10	76.27	
G4	BHS483	BHS352/BHS366	Katrain	32.10	77.13	
G5	UPB1093	RD2784/RD2035	Majhera	29° 16' N	80° 5' E	1532
G6	VLB118	14th EMBSN-9313	Khudwani	33° 70' N	75°10' E	1590
G7	BHS487	BBM593/ BHS169	Malan	32°08 ' N	76°35'E	846
G8	BHS400	34th IBON-9009	Rajauri	31.01	75.92	
G9	BHS486	HBL276/BHS365	Ranichauri	28° 43' N	81°02' E	2200
G10	VLB173	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/ PETU-NIA1/6/GLORIA- BAR/COPAL (IBON-HI-18-91)	Shimla	31°10 ' N	77°17'E	2276
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/PETU-NIA1/6/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/CHEV-RON-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				

Table 1: Parentage vis-a-vis location details of dual purpose barley genotypes Cut grain yield NHZ.

$$S_i^{(1)} = \frac{2\Sigma_j^{n-1}\Sigma_{j'=j+1}^{n}|r_{ij} - r_{ij'}|}{[n(n-1)]} \qquad S_i^{(7)} = \frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{\Sigma_{j=1}^{n}|r_{ij} - \bar{r}_i|} \qquad S_i^{(3)} = \frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{\bar{r}_{i.}}$$

$$S_i^{(4)} = \sqrt{\frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{n}} \qquad S_i^{(5)} = \frac{\Sigma_{j=1}^{n}|r_{ij} - \bar{r}_i|}{n} \qquad S_i^{(6)} = \frac{\Sigma_{j=1}^{n}|r_{ij} - \bar{r}_i|}{\bar{r}_{i.}}$$

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

Non parametric composite measures NP$_i$ $^{(1)}$, NP$_i$ $^{(2)}$, NP$_i$ $^{(3)}$ and NP$_i$ $^{(4)}$ based on the ranks of genotypes as per yield and corrected yield of genotypes. 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.

$$NP_i^{(1)} = \frac{1}{n}\Sigma_{j=1}^{n}|r_{ij}^* - M_{di}^*| \qquad NP_i^{(3)} = \frac{\sqrt{\Sigma(r_{ij}^* - \bar{r}_{i.}^*)^2/n}}{\bar{r}_i.}$$

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

ASV

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

ASV1

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

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

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

HMGV$_i$

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

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

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

Geometric Adaptability Index

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

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

Results and Discussion

AMMI analysis

Highly significant variations due to environments, GxE interactions, and genotypes were observed by AMMI analysis (Table 2). Analysis indicated that about 69.4% of the total sum square of variation for yield was due to environments followed by 24.1% of GxE interactions, whereas genotypes accounted marginally 3.4%. Diversity of the testing sites were approved by AMMI analysis (Mehraban et al., 2019). Interaction effects further portioned into seven Interaction principal components totalled for more than 98.5% interactions sum of square variations. AMMI1 explained a total variation of 38.5%, followed by 19.1% for AMMI2, 15.9% for AMMI3, AMMI4 accounted for 11.4% and followed by 8.7%, 2.9% & 1.7% respectively. The first two AMMI components in total showed 57.6% of the total variation indicating the two AMMI components well fit and confirm the use of AMMI model (Pour Aboughadareh et al., 2022). Estimated sums of squares for G×E signal and noise were 90.5% and 9.4% of total G×E respectively. Early IPCs selectively capture signal, and late ones noise. Note that the sum of squares for GxE-signal is 6.27 times that for genotypes main effects. Hence, narrow adaptations are important for this dataset (Vaezi et al., 2018). Even just IPC1 alone is 2.67 times the genotypes main effects. Also note that GxE-noise is 0.65 times the genotypes effects. Discarding noise improves accuracy, increases repeatability, simplifies conclusions, and accelerates progress.

Source	Degree of freedom	Mean Sum of Squares	Significance Level	Proportional contribution of factors	GxE interaction- Sum of Squares (%)	Cumulative Sum of Squares (%) by IPCA's
Treatments	206	112.0935	***	97.02		
Genotype (G)	22	37.62526	***	3.48		
Environment (E)	8	2067.233	***	69.48		
GxE interactions	176	32.53205	***	24.06		
IPC1	29	76.17062	***		38.58	38.58
IPC2	27	40.46131	***		19.08	57.66
IPC3	25	36.44384	***		15.91	73.57
IPC4	23	28.5315	***		11.46	85.03
IPC5	21	23.90849	***		8.77	93.80
IPC6	19	8.99691	***		2.99	96.79
IPC7	17	5.93214	**		1.76	98.55
Residual	15	5.53674	*			
Error	207	3.42976				
Total	413	57.63008				

Table 2: AMMI analysis of dual purpose barley genotypes evaluated under coordinated trials.

Ranking of genotypes as per AMMI based measures

Since the genotypes yield expressed highly significant variations, mean yield was considered as an important measure to assess the yield potential of genotypes. Mean yield of genotypes selected G14, G4, G1 with lowest yield of G21 (Table 3). This measure is simple, but not fully exploiting all information contained in the dataset. Values of IPCA's in the AMMI analysis indicate stability or adaptability of genotypes. The, greater the IPCA scores reflect the specific adaptation of genotype to certain locations. While, the values approximate to zero were recommended for in general adaptations of the genotype. Absolute IPCA-1 scores pointed for G4, G12, G20 as per IPCA-2, G15, G14, G4 genotypes would be of choice. Values of IPCA-3 favored G5, G6, G9 genotypes. As per IPCA-4, G16, G21, G19 genotypes would be of stable performance. IPCA-5 favored G11, G6, G8 as per IPCA-6 genotypes would be G5, G4, G17 while IPCA-7 pointed towards G3, G20, G4. First two IPCAs in ASV & ASV1 measures utilized 57.6% of G×E interaction sum of squares. The two IPCAs have different values and meanings and the ASV and ASV1 parameters using the Pythagoras theorem and to get estimated values between IPCA1 and IPCA2 scores to produce a balanced measure between the two IPCA scores. Also, ASV parameter of this investigation use advantages of cross validation due to computation from first two IPCAs (Silva et al., 2019). Using first two IPCAs in stability analysis could benefits dynamic concept of stability in identification of the stable high yielder genotypes. ASV1 measures recommended (G4, G20, G15) and ASV pointed towards (G4, G20, G15) as of stable performance. Adaptability measures MASV and MASV1considered all seven significant IPCAs of the AMMI analysis using 98.5% of GxE interactions sum of squares (Gerrano et al., 2020). Values of MASV1 identified G15, G9, G6 genotypes would express stable yield whereas genotypes G15, G4, G22 be of stable yield performance by MASV measure respectively.

Genotypes performance as per BLUP and Non parametric measures

Major advantages of BLUP based measures are to account for the random nature of the genotype behavior in changes climatic conditions. At the same time allow ranking genotypes in relation to their performance based on the genetic effects (Sousa et al., 2020). Average yield of genotypes pointed towards G14, G9, G1 as high yielders. Consistent yield of G21, G17, G10 as per least values of standard deviation more over the values of CV identified G6, G10, G17 genotypes for the consistent yield performance for northern hills zone of the country. More over the values of GM favored G9, G14, G1. The BLUP-based simultaneous selections, such as HM identified G9, G1, G6 while values of RPGV favored G14, G9, G1 and HMRPGV settled for G1, G14, G18 genotypes. The evaluation of adaptability and stability of wheat genotypes through these BLUP-based indices was reported by Pour-Aboughadareh et al., (2019). The estimates of HMGV, RPGV, and HMRPGV had the same genotype ranking that was reported (Anuradhaet al., 2022). Non parametric measures ranked the genotypes as per their corrected yield across environments S_i^1 values pointed for G15, G13, G9 while S_i^2 selected G15, G13, G9 and values of S_i^3 favoured G15, G13, G9 as desirable genotypes (Table 4). G5, G1 selected by values of S_i^4, S_i^5, S_i^6 and lastly S_i^7 for G15, G13, G9 (Table 4). The mentioned strategy determines the stability of genotype over environment if its rank is similar over other environments (biological concept). Nonparametric measures of phenotypic stability were associated with the biological concept of stability (Vaezi et al., 2018). Non parametric composite measures $NP_i^{(1)}$ to $NP_i^{(4)}$, consider the ranks of genotypes as per their yield and corrected yield across environments simultaneously. $NP_i^{(1)}$ measure observed suitability of G15, G13, G20 whereas as per $NP_i^{(2)}$, genotypes G15, G16, G20 would be of choice while $NP_i^{(3)}$ identified G15, G13, G16. Last composite measure $NP_i^{(4)}$ found G15, G13, G20 as genotypes of choice for this zone.

Genotype	Mean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	ASV1	ASV	MASV1	MASV	Average	Stdev	CV
G1	17.37	0.58	0.91	1.29	0.94	-0.79	-0.81	-0.20	1.48	1.23	4.39	3.58	17.30	7.60	43.93
G2	16.10	1.69	0.96	-0.65	-0.42	1.36	-0.50	0.12	3.54	2.58	5.87	4.15	16.18	9.72	60.09
G3	16.28	0.60	1.21	1.23	0.50	0.41	-0.32	0.06	1.70	1.47	3.48	3.01	16.29	7.82	48.01
G4	16.42	-0.13	-0.07	0.49	-1.07	0.78	0.18	-0.23	0.28	0.20	3.15	2.41	16.38	7.39	45.10
G5	17.09	1.17	0.33	0.18	-1.23	1.39	0.14	-0.11	2.38	1.69	5.36	3.77	17.03	9.19	53.99
G6	16.35	-0.65	-0.82	0.12	-0.72	-0.20	0.70	1.44	1.54	1.23	3.02	2.66	16.21	6.34	39.10
G7	15.84	0.81	-0.38	1.52	1.19	1.02	-0.56	0.22	1.68	1.21	4.99	3.92	15.92	6.93	43.53
G8	14.75	-1.37	-2.05	1.83	-1.04	-0.61	-0.02	-0.53	3.44	2.82	5.87	5.02	14.91	6.60	44.25
G9	17.77	1.05	0.30	-0.18	0.25	-0.29	0.78	0.91	2.14	1.52	3.00	2.34	17.54	8.27	47.14
G10	14.73	-1.68	0.37	-1.25	0.98	0.79	0.38	0.53	3.42	2.42	5.10	3.89	14.67	5.79	39.51
G11	15.44	-0.82	-0.07	-1.56	1.86	0.00	0.77	-0.76	1.66	1.17	4.70	4.16	15.32	6.33	41.30
G12	16.54	-0.30	1.39	-1.37	-1.39	-0.70	-0.50	0.25	1.52	1.46	4.65	4.01	16.47	8.71	52.89
G13	17.07	0.81	-0.22	1.25	1.05	0.22	1.18	0.30	1.65	1.17	4.04	3.43	16.90	7.49	44.31
G14	18.99	1.74	0.02	-0.33	-0.93	-1.90	0.75	-0.49	3.51	2.47	7.23	4.94	18.74	10.43	55.67
G15	14.46	-0.73	0.00	-0.68	-0.59	0.32	0.30	-0.26	1.47	1.03	2.42	1.92	14.57	6.87	47.16
G16	16.38	1.44	-0.84	-0.90	-0.06	0.86	0.26	-1.35	3.04	2.22	4.68	3.56	16.38	9.03	55.14
G17	13.05	-1.66	0.54	-0.23	0.81	-0.43	-0.72	-0.04	3.40	2.42	4.21	3.16	13.30	5.33	40.04
G18	17.20	0.93	0.12	-0.25	0.27	-1.02	0.51	0.19	1.89	1.33	3.87	2.63	17.07	8.24	48.30
G19	15.46	1.09	-1.24	-1.07	-0.25	-0.30	-1.50	0.59	2.53	1.98	4.69	3.92	15.65	7.87	50.28
G20	15.69	0.38	-0.51	0.40	0.55	-1.05	-0.41	-0.16	0.91	0.74	3.71	2.60	15.79	6.82	43.21
G21	12.80	-1.46	-2.44	-0.55	-0.07	0.65	-0.30	0.12	3.82	3.20	5.34	4.47	13.09	5.24	40.02
G22	14.85	-0.94	0.51	-0.35	0.43	-0.76	-0.55	-0.25	1.96	1.43	3.45	2.50	14.93	6.14	41.14
G23	14.91	-2.54	1.96	1.05	-1.05	0.26	0.28	-0.35	5.50	4.11	6.57	5.23	14.90	8.01	53.74

Table 3: AMMI based measures of dual purpose barley genotypes.

Genotype	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	15.66	13.99	1.09	1.07	7.47	38.27	3.10	6.19	4.56	2.22	15.51	4.33	0.62	0.77	0.93
G2	13.65	11.48	0.97	0.92	10.07	72.17	5.22	8.50	7.50	3.25	26.08	7.50	0.56	0.63	0.75
G3	14.52	12.74	1.01	0.99	7.27	36.57	2.85	6.05	4.56	2.13	14.25	4.17	0.31	0.50	0.60
G4	14.72	12.98	1.02	1.01	7.67	38.57	3.45	6.21	5.17	2.78	17.27	5.17	0.57	0.64	0.79
G5	14.72	12.60	1.03	1.00	9.60	65.87	5.20	8.12	7.00	3.32	26.00	7.00	0.93	0.77	0.91
G6	15.05	13.89	1.06	1.02	8.60	52.17	4.82	7.22	5.89	3.26	24.08	5.50	0.48	0.70	0.83
G7	14.53	13.06	1.02	0.99	7.73	39.20	2.80	6.26	5.00	2.14	14.00	5.00	0.31	0.46	0.57
G8	13.53	12.14	0.96	0.91	8.87	53.77	4.54	7.33	5.50	2.79	22.72	5.50	0.38	0.54	0.65
G9	15.74	14.06	1.10	1.07	6.20	28.57	2.07	5.34	4.44	1.93	10.33	3.83	0.51	0.55	0.64
G10	13.75	12.93	0.98	0.91	8.87	52.17	5.13	7.22	5.83	3.44	25.66	5.83	0.49	0.64	0.78
G11	14.02	12.59	1.00	0.93	7.67	41.37	3.22	6.43	5.11	2.39	16.12	4.83	0.32	0.45	0.54
G12	14.34	12.24	1.02	0.95	9.07	55.47	5.94	7.45	6.00	3.86	29.71	6.00	1.50	1.02	1.24
G13	15.20	13.35	1.06	1.03	5.87	23.87	1.63	4.89	4.00	1.64	8.14	4.00	0.35	0.40	0.48
G14	15.69	12.71	1.11	1.05	12.07	99.90	7.99	9.99	8.17	3.92	39.96	8.17	1.26	1.11	1.34
G15	13.06	11.52	0.91	0.89	4.27	13.07	1.35	3.61	2.67	1.66	6.76	2.67	0.20	0.25	0.29

G16	14.00	11.70	0.99	0.94	7.93	50.70	3.07	7.12	5.67	2.06	15.36	4.83	0.25	0.43	0.48
G17	12.34	11.42	0.87	0.83	7.87	43.60	4.84	6.60	5.33	3.56	24.22	5.33	0.41	0.45	0.53
G18	15.10	13.14	1.05	1.03	7.13	35.37	2.69	5.95	4.78	2.18	13.43	4.50	0.38	0.54	0.65
G19	14.03	12.60	0.98	0.95	8.47	46.57	3.83	6.82	5.17	2.55	19.14	5.17	0.38	0.55	0.68
G20	14.21	12.47	0.99	0.97	7.07	37.47	2.96	6.12	4.44	2.11	14.79	4.00	0.31	0.46	0.53
G21	12.26	11.54	0.88	0.81	10.93	85.60	8.56	9.25	7.67	4.60	42.80	7.67	0.51	0.63	0.75
G22	13.72	12.51	0.96	0.93	7.53	38.97	3.29	6.24	5.17	2.62	16.46	5.17	0.34	0.47	0.57
G23	13.20	11.75	0.96	0.85	8.33	59.77	7.32	7.73	4.94	3.63	36.59	4.83	0.60	0.81	0.88

Table 4: BLUP based and Non parametric measures of dual purpose barley genotypes cut grain plot yield.

Biplot analysis

The first two significant principal components (PC's) has explained about 65.3% of the total variation in the AMMI, BLUP and non parametric measures considered for this study in biplot analysis (Table 5) with respective contributions of 39.1 & 26.1% by first and second principal components respectively (Ahakpaz et al., 2021). Measures S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7, ASV, ASV1, MASV, MASV1 $NP_i^{(1)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, accounted more of share in first principal component whereas Mean, Average, PC1, GM, HM , HMPRVG, PRVG, were major contributors in PC2. The association analysis among measures had been explored with the biplot analysis. In the biplot vectors of measures expressed acute angles would be positively correlated whereas those achieved obtuse or straight line angles would be negatively correlated. Independent type of relationships had expressed by right angles between vectors.

Measure	Principal Component 1	Principal Component 2
Mean	0.0168	0.3516
IPC1	0.0336	0.2581
IPC2	0.0048	0.0995
IPC3	0.0569	0.0456
IPC4	0.1449	-0.0680
IPC5	0.0008	-0.1018
IPC6	0.0335	0.1045
IPC7	0.0378	0.0575
ASV1	-0.2047	-0.1256
ASV	-0.2126	-0.1349
MASV1	-0.2462	0.0173
MASV	-0.2283	-0.0222
Average	0.0151	0.3515
Stdev	-0.0867	0.2647
CV	-0.1202	0.1543
GM	0.0703	0.3376
HM	0.1180	0.2373
PRVG	0.0385	0.3384
HMPRVG	0.1000	0.3278
S_i^1	-0.2728	0.0424
S_i^2	-0.2800	0.0344
S_i^3	-0.2797	-0.0405

S_i^4	-0.2792	0.0312
S_i^5	-0.2582	0.0506
S_i^6	-0.2621	-0.0658
S_i^7	-0.2797	-0.0405
$NP_i^{(1)}$	-0.2618	0.0338
$NP_i^{(2)}$	-0.1893	0.1849
$NP_i^{(3)}$	-0.2181	0.1899
$NP_i^{(4)}$	-0.2118	0.1965
Per cent contribution	39.16	26.17

Table 5: Loadings of AMMI, BLUP and non parametric measures.

Positive relationships of CV observed for $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. AMMI based measures MASV1 closely associated with, S_i^1, S_i^2, S_i^4, S_i^5, $NP_i^{(1)}$. Strong direct relationship of MASV exhibited with S_i^3, S_i^7, S_i^6, ASV, ASV1 values. BLUP based measures exhibited very tight relationship with mean, IPC1, IPC3, IPC6, IPC7 in separate quadrant. This group of measures expressed no relationship with IPC5 measures as evident from straight line angle. Moreover group S_i^7 S_i^6 & MASV, ASV, ASV1 maintained right angles with BLUP based measures. Stdev also exhibited right degree angles with IPC3, IPC7 measures. IPC4 showed straight line angle with MASV1, S_i^1, S_i^2, S_i^4 S_i^5, $NP_i^{(1)}$ measures (Fig. 1). Total six clusters of small and medium sizes were observed in various quadrants of biplot analysis. AMMI based measures ASV, ASV1, MASV, MASV1 clustered with, S_i^6 S_i^7 in first quadrant. Second cluster of IPC5 & IPC4 found in next quadrant. Out of two, first comprised of IPC3, IPC6, IPC7 measures while next one consisted of BLUP based measures with mean yield and IPC1. Measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ formed a cluster with Stdev, CV as this cluster observed adjacent to cluster of MASV1, $NP_i^{(1)}$, S_i^1, $S_i^4 S_i^2$, S_i^5 in same quadrant (Fig. 2).
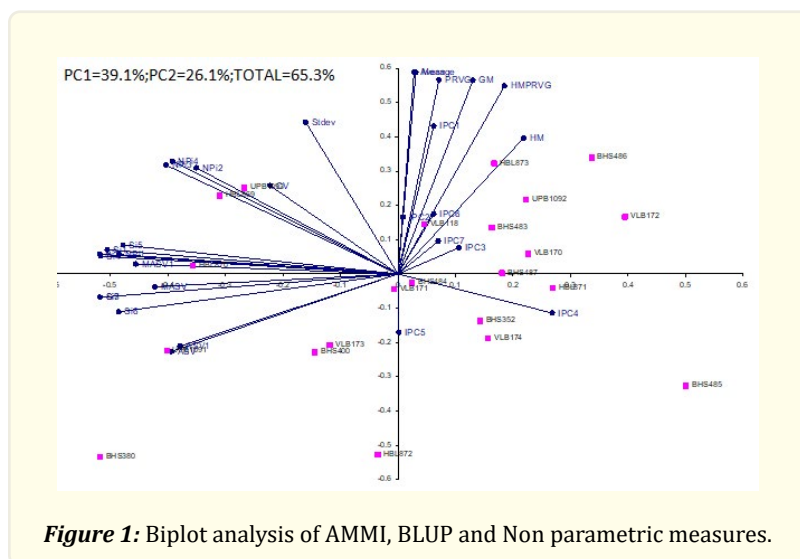

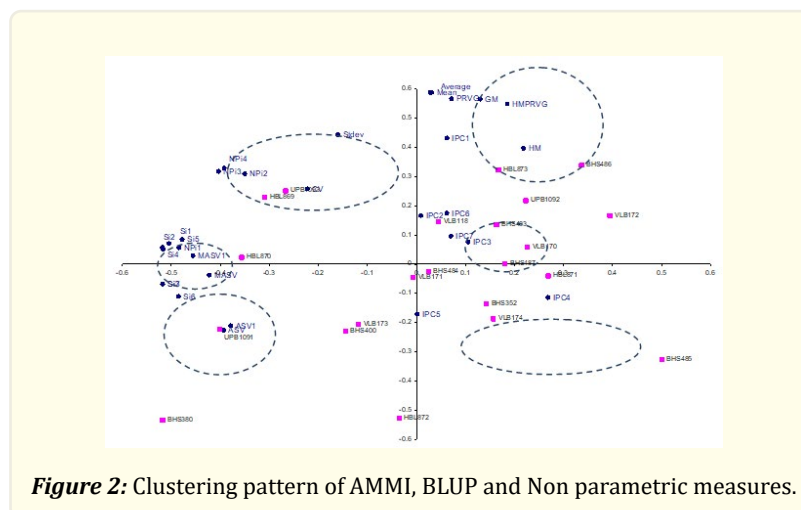***Figure 1:*** Biplot analysis of AMMI, BLUP and Non parametric measures.

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

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Conflict of Interests

No conflict of interests reported by the authors.

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