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Full Research Article

Performance of Dual Purpose Barley Genotypes for Green Fodder by AMMI Analysis

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Abstract

Highly significant effects were observed for green fodder yield of dual purpose barley for environments, genotypes and interactions. Environmental effects accounted for the major portion of the total variance as of 82.3%. Significant interaction effects were partitioned further into IPCA1, IPCA2, IPCA3, IPCA4; which explained 30.4, 19.4, 14.8, 13.2% respectively. MASV indicated that genotypes UPB 1035, BH 970, RD 2035, UPB 1034, RD 2857 and KB 1238 were stable; whereas, genotypes RD 2857 and RD 2035 were the stable genotypes with relatively more average yield. SIPC4 identified AZAD, RD 2856, UPB 1034, BH 970 and RD 2858 as stable genotypes. AMMI distance ranked genotypes in order of preference as RD 2035<BH 970<RD 2857<UPB 1035<UPB 1034. Least ASV score associated with UPB 1035, followed by UPB 1034, UPB 1036 and BH 971. Positive and negative IPCA1values had been observed for large number of genotypes. Genotype AZAD had large negative IPCA1 score along with positive IPCA4 as this reflected crossover type G×E interaction. RD 2715, RD 2857 and RD 2859 genotypes expressed yields greater than the overall mean and positive IPCA1 scores. Lower MASV observed for Vijapur, Banswara and Bikaner conditions where SIPC4 pointed towards Hisar, Bikaner and Varanasi as favorable locations. AMMI distance values identified Vijapur, Udaipur and Varanasi locations.

1. Introduction

Barley crop can be harvested as green fodder in rain fed, arid to semiarid conditions where other crops viz., barseem, oats, sugarcane etc. cannot be grown due to water shortage (Kharub et al., 2013). The crop had shown advantageous over oats due its dual utilization as green fodder for animal feed and grain crop for human consumption (Kumar et al., 2014). Dual barley cultivation provides nutrition to the livestock through its green fodder and grains can be harvested from regenerated crop (Kharub et al., 2013).

Methods to study Genotype-environment interaction varied from univariate to multivariate such as the additive main effect and multiplicative interaction (AMMI) analysis (Bavandpori et al., 2015). AMMI model is a hybrid model separates the additive variance from the multiplicative variance. The principal component analysis (PCA) applied to the interaction explains it in more detail the interaction pattern (Mortazavian et al., 2014). AMMI stability value (ASV) based on only two significant IPC's scores as well as the respective sum of squares (Sabaghnia et al., 2008). ASV observed useful for situations with relatively high total variation explained by two significant IPCA's (Sabaghnia et al., 2012). Modified AMMI's stability value (MASV) benefited from four significant IPCs whenever, total of IPC1 and IPC2 variances were low.

Mohammadi et al. (2015) highlighted several advantages of MASV as compared to other AMMI based estimates. ASV and MASV had high significant correlation with grain yield (Karimizadeh et al., 2012). ASV and MASV parameters offer reliable statistic to describe G×E interaction (Adugna and Labuschange, 2003).

The prime objective of the present study was to stratify dual purpose barley genotypes by AMMI analysis based on their green fodder yield.

2. Materials and Methods

Sixteen barley genotypes (12 varieties and 4 checks) were evaluated under national varietal trials carried out under the All India coordinated wheat and barley improvement programme at eleven locations. The experiments were conducted during the crop season 2012–13 across locations, viz., Banswara, Bikaner, Durgapura, Faizabad, Hisar, Jalore, Kanpur, Kota, Udaipur, Varanasi and Vijapur. Details of studied genotypes and environmental conditions were presented in Table

1 for reference. The randomized complete block design employed, with four replications. Cultural practices as zone^{-1} recommendations were followed to harvest good yield. AMMI analysis was carried out by Genstat software version 17.1 (VSN International).

Adugna and Labuschange (2002) introduced modified AMMI's stability value (MASV), based on all significant IPCs, for AMMI models for effective interpretation of G×E interactions as follows:

$$\text{MASV} = \sqrt{\sum_{N=1}^{N-1} \left(\frac{\text{SSIPC}_n}{\text{SSIPC}_{n+1}}\right)\left(\text{IPC}_n^2 + \text{IPC}_{n+1}^2\right)} \quad \text{(i)}$$

Where, SSIPC_n and SSIPC_{n+1} are sum of squares by the IPC_n, IPC_{n+1} respectively

SIPC4 (sum of IPC scores) proposed by Sneller et al., 1997 based on AMMI analysis to identify stable genotypes as:

$$\text{SIPC} = \sum_{N=1}^{N-1} \gamma_{in} \lambda_n^{0.5} \quad \text{(ii)}$$

Where, g_{in} is the genotype eigen value for axis n and λn is the eigen value of the IPC analysis axis n as four significant IPC's were retained in the AMMI model.

AMMI stability value (ASV) based on the AMMI model's IPC1 and IPC2 scores for each genotype was calculated as follows (Purchase et al., 2000):

$$\text{AMMI Stability Value (ASV)} = \sqrt{\left[\frac{\text{SSIPCA1}}{\text{SSIPCA2}} \times \text{IPCA1 score}\right]^2 + \text{IPCA2 score}^2} \quad \text{(iii)}$$

Where, SSIPCA1 and SSIPCA2 are sum of squares by the IPCA1, IPCA2 respectively. The lowest ASV value associated with stable performance of genotypes.

The AMMI distance statistic coefficient (D) (Zhang et al., 1998) was calculated as the distance of the Interaction Principal Component (IPC) point from the origin in space, for the significant IPCs, and γ_{is} is the score of i-th genotype in IPC. The genotype with the lowest value of D considered as the most stable.

$$\text{AMMI Distance } (D_i) = \sqrt{\sum_{i=1}^{n} \gamma_{i3}^2} \quad (i=1,2,3,..n) \quad \text{(iv)}$$

Yield stability index (YSI) incorporate mean yield and stability index of genotypes in single criteria and calculated as (Farshadfar et al., 2011):

$$\text{YSI}=\text{RASV}+\text{RY} \quad \text{(v)}$$

Where, RASV is the rank of AMMI stability value and RY is the rank of mean yield of genotypes (RY) across environments. Low values of index show desirable genotypes with high mean yield and stability.

3. Results and Discussion

3.1. Analysis of variance

Analysis revealed variances due to environments, genotypes and interactions were highly significant at $p<0.01$. Nearly

Table 1: Parentage details of dual barley purpose genotypes along with environmental conditions

Code	Genotype	Parentage	Code	Locations	Latitude	Longitude	Altitude (m)
G_1	RD 2859	K-551/PL-604//RD 2552	E_1	Banswara	23°55´N	74°45´E	216.4
G_2	RD 2552 ©	RD 2035/DL 472	E_2	Bikaner	28° 02´N	73°31´E	225.3
G_3	RD 2035©	RD 103/PL 101	E_3	Durgapura	26°51´N	75°47´E	390
G_4	UPB 1036	JYOTI/(CABUYA/JAZMIN//PETUNIA. 1)	E_4	Faizabad	26°47´N	82°12´E	113
G_5	RD 2715 ©	RD 387/BH 602//RD 2035	E_5	Hisar	29°10´N	75°46´E	215.2
G_6	UPB 1034	RD 2624/DWR 46	E_6	Jalore	25°34´N	72° 62´E	170.5
G_7	BH 971	HBL 405/RD/2683	E_7	Kanpur	26°29´N	80°18´E	125.9
G_8	KB 1238	K603/RD2552	E_8	Kota	25°21´N	75° 86´E	259.7
G_9	BH 970	HBL 276/RD/2683	E_9	Udaipur	24°34´N	70°42´E	582
G_{10}	RD 2858	RD 2035/UBL-9//VMORALIS	E_{10}	Varanasi	25°20´N	83°03´E	75.5
G_{11}	NDB 1570	NDB 1020/LAKHAN	E_{11}	Vijapur	23°35´N	72°55´E	41.1
G_{12}	UPB 1035	LAKHAN/(GIORIA-BAR/4/SOTOL//2762/BC-B/3/11012.2/…)					
G_{13}	RD 2857	RD 2620/NDB 1173//RD 2522					
G_{14}	AZAD ©	K12/K19					
G_{15}	RD 2856	RD 2620/NDB 1173//RD 2634					
G_{16}	NDB 1566	BCB 128/NDB 940					

82.3% of the total sum of squares was attributable to environmental effects, 10.2% to G×E interaction and 2.9% to genotypic effects in AMMI analysis of variance for green fodder yield of sixteen dual purpose barley genotypes tested in eleven environments (Table 2). The large sum of squares for environments indicated that the environments were diverse, with differences among environmental means causing variation in forage yield (Abdipur and Vaezi, 2014). Highly significant G×E interaction for green fodder yield indicated the different performance of genotypes across environments. In spite of this high significance, the magnitude of the G×E interaction sum of squares was larger than that of genotypes, indicating the presence of large variation among the genotypes over environments.

The G×E interaction was partitioned into four significant interaction principal component analysis axis (IPCAs). First two IPCAs explained 30.4% and 19.4% of the variability and jointly accounted for only 49.8% of the interaction sum of squares.

3.2. Modified AMMI stability value (MASV)

Biplot visual interpretation of G×E interaction is not valid for more than two significant IPCs (Gauch et al., 2008). AMMI analysis indicated more complex G×E interaction and the graphical visualization of the genotypes in low dimensions is not valid to interpret G×E interaction by two IPCA's (Sabaghnia et al., 2012).

Table 2: AMMI analysis of green fodder yield for dual barley genotypes

Source of variation	DF	MSS	VR	TSS %	G×E %
Treatments	175	14983	67.97^{***}	95.47	
Genotypes	15	5454	24.74^{***}	2.98	
Environments	10	226077	487.68^{***}	82.31	
Block	33	464			
Interactions	150	1863	8.45^{***}	10.18	
IPCA1	24	3537	16.04^{***}		30.37
IPCA2	22	2465	11.18^{***}		19.40
IPCA3	20	2063	9.36^{***}		14.76
IPCA4	18	2046	9.28^{***}		13.18
Residuals	66	944			
Error	495	220			
Total	703	3907			

DF: Degree of freedom; MSS: Mean Sum of squares; VR: Variance ratio; TSS: percentage of total sum of squares; G×E: percentage of G×E total sum of squares; ***denotes significant at (p=0.001) level of significance

MASV used all four significant IPCs. The results of MASV indicated that genotypes G_{12}, G_9, G_3, G_6, G_{13} and G_8 were most stable; whereas, genotypes G_{13}, and G_{13} were the stable genotypes which had relatively more average yield (Table 3). MASV introduced some of the high yielding genotypes (G_3 and G_{13}) as the most stable ones.

3.3. SIPC4

This would be useful in identifying stable genotypes as AZAD, RD 2856, UPB 1034, BH 970 and RD 2858 were the stable genotypes whereas RD 2715 and RD 2859 as unstable genotype (Table 3). It is interesting that high yield genotypes AZAD and RD 2858 had been identified by this parameter.

3.4. AMMI stability index (D) incorporates

The scores of significant four IPCA's towards the interaction sum of squares. The lower value of D associated stability across the tested environments and vice versa for instability (Zhang et al., 1998). The ranking of genotypes in ascending order of D values are those in G_3 (3.07)<G_9 (3.35)<G_{13} (3.47)<G_{12} (3.73)<G_6 (3.79) (Table 3). Genotype G_{14} (AZAD), G_{15} (RD 2856) and G_4 (UPB 1036) showed larger D values. More over the largest the negative value of IPCA1 score (-7.03) also exhibited by G_{14} (AZAD).

3.5. AMMI stability value (ASV)

ASV value is the distance from origin in a two dimensional scatter graph of IPCA1 against IPCA2 scores. Least ASV score associated with stable genotypes, accordingly genotype G_{12} (UPB 1035), followed by G_6 (UPB 1034), G_4 (UPB 1036) and G_7 (BH 971) were stable (Table 3), while genotypes G_{14} (AZAD), G_{15} (RD 2856) and G_2 (RD 2552) were undesirable for green fodder yield.

3.6. Yield stability index (YSI)

The least YSI is considered as the most stable with high yield. Based on the YSI the most desirable genotype for selection is G_{13} (RD 2857), G_5 (RD 2715) followed by G_{11} (NDB 1570) and G_1 (RD 2859).

3.7. IPCAs interaction (crossover and non-crossover interactions)

Green fodder yield of dual purpose barley genotype ranged from 169.8 to 127.5 q ha^{-1} with genotype RD2715 recorded highest yield and lowest yield shown by UPB 1035.

Nearly 50% of genotypes showed positive and negative IPCA1 values for green fodder yield. Genotype G_{14} (AZAD) has large negative IPCA1 score also showed positive IPCA4 value (Table 3). This type of response is referred to as crossover G×E interaction. On the other hand, same sign or near zero scores represent a non-crossover interaction or a proportionate genotype response (Silveira et al., 2013). The genotypes with

Table 3: AMMI estimates of green fodder yield for dual purpose barley genotypes

Code	Genotype	Gm	R_{Gm}	IPCA1	IPCA2	IPCA3	IPCA4	MASV	R_{MASV}	ASV	R_{ASV}	D	R_D	SIPC4	R_{SIPC4}	YSI
G_1	RD 2859	162.5	3	3.876	2.204	1.678	4.275	7.68	11	5.33	13	6.40	13	12.03	16	16
G_2	RD 2552	154.5	9	-4.153	1.717	2.348	-1.181	6.85	8	5.47	14	5.21	9	-1.27	9	23
G_3	RD 2035	158.0	6	-2.440	1.763	-0.409	0.434	4.13	3	3.53	6	3.07	1	-0.65	10	12
G_4	UPB 1036	146.7	11	-1.036	2.447	-5.457	3.563	9.56	15	2.77	3	7.04	14	-0.48	11	14
G_5	RD 2715	169.8	1	3.276	1.649	3.520	1.485	7.18	9	4.42	10	5.30	10	9.93	15	11
G_6	UPB 1034	141.3	15	1.211	0.127	-2.046	-2.954	4.46	4	1.52	2	3.79	5	-3.66	3	17
G_7	BH 971	142.5	14	-0.077	-2.905	-2.554	3.423	6.71	7	2.91	4	5.17	8	-2.11	6	18
G_8	KB 1238	152.8	10	3.195	-0.256	-0.404	-3.998	5.70	6	4.01	8	5.14	7	-1.46	8	18
G_9	BH 970	144.4	12	-2.360	0.271	0.920	-2.175	3.93	2	2.97	5	3.35	2	-3.34	4	17
G_{10}	RD 2858	156.6	7	3.730	-0.401	-4.231	-2.000	8.01	12	4.68	11	6.00	12	-2.90	5	18
G_{11}	NDB 1570	162.4	4	-1.181	-4.021	3.741	1.415	8.44	13	4.28	9	5.79	11	-0.05	12	13
G_{12}	UPB 1035	127.5	16	0.341	0.956	0.309	-3.572	3.91	1	1.05	1	3.73	4	-1.97	7	17
G_{13}	RD 2857	168.1	2	2.873	0.981	1.351	1.014	4.48	5	3.73	7	3.47	3	6.22	14	9
G_{14}	AZAD	158.7	5	-7.033	-1.785	-1.281	0.447	9.41	14	8.98	16	7.38	16	-9.65	1	21
G_{15}	RD 2856	156.3	8	1.506	-6.989	0.729	0.052	10.85	16	7.24	15	7.19	15	-4.70	2	23
G_{16}	NDB 1566	144.2	13	-1.728	4.241	1.785	-0.228	7.29	10	4.76	12	4.92	6	4.07	13	25

Gm: Genotype mean yield; ASV: AMMI stability value; D: AMMI Distance; YSI: Yield stability index; R_{Gm}: Genotype ranking based on Gm; R_D: Genotype ranking based on D; R_{ASV}: Genotype ranking based on ASV

lower IPCA1 scores would produce a lower absolute G×E interaction effect than those with higher absolute IPCA1 scores and have less variable yields (more stable) across genotypes (Oliveira et al., 2014). Genotypes G_5 (RD 2715), G_{13} (RD 2857) and G_1 (RD 2859) with yields greater than the overall mean and positive IPCA1 scores.

3.8. Environments classification based on AMMI analysis

Environmental mean yields varied from 283.8 to 187 q ha^{-1} as variability observed both in main and interactions effects (Table 4). Five out of eleven environments show negative IPCA1 scores while Jalore and Faizabad showed maximum positive IPCA1 scores (Table 4), while Bikaner and Faizabad had larger negative IPCA2 score and Kanpur and Varanasi possessed high negative IPCA3 scores. Kota and Jalore environments showed positive values for all IPCA's values with good green fodder yield. Lower MASV observed for Vijapur, Banswara and Bikaner conditions where, SIPC4 pointed towards Hisar, Bikaner and Varanasi as favorable locations. AMMI distance values identified Vijapur, Udaipur

Table 4: AMMI analysis of environments

Code	Environment	Em	IPCA1	IPCA2	IPCA3	IPCA4	MASV	ASV	D	SIPC4
E_1	Banswara	283.8	-3.658	-1.076	0.063	4.837	6.86	4.70	6.16	0.17
E_2	Bikaner	88.0	-0.334	-4.199	0.870	-2.041	7.03	4.22	4.76	-5.70
E_3	Durgapura	179.3	-1.382	7.280	0.075	-3.750	23.60	7.43	8.31	2.22
E_4	Faizabad	145.0	4.247	-3.787	0.537	-4.180	18.27	13.43	7.08	-3.18
E_5	Hisar	105.2	-8.869	-0.409	0.127	-0.174	27.20	27.18	8.88	-9.33
E_6	Jalore	178.7	4.417	0.791	0.109	5.745	11.85	9.14	7.29	11.06
E_7	Kanpur	150.8	1.633	2.179	-6.518	-0.906	20.07	10.25	7.12	-3.61
E_8	Kota	187.0	2.996	3.361	5.684	0.678	28.36	12.43	7.28	12.72
E_9	Udaipur	161.8	-0.846	-2.612	3.296	-1.357	12.06	3.14	4.50	-1.52
E_{10}	Varanasi	143.7	1.133	-2.420	-3.826	0.417	7.65	5.34	4.69	-4.70
E_{11}	Vijapur	58.3	0.663	0.893	-0.416	0.733	2.35	0.95	1.40	1.87

Em: Environment mean; MASV: Modified AMMI stability value; SIPC4: Sum of 4 IPC's; ASV: AMMI stability value and Varanasi locations.

4. Conclusion

Sixteen dual barley genotypes were evaluated for green fodder yield under coordinated system at eleven locations across the country. Highly significant effects were observed for environments, genotypes and interactions. AMMI analysis indicated more complex G×E interaction and the graphical visualization by biplots would not interpret G×E interaction. MASV and SIPC4 based on four significant IPCs were useful and identified relatively the high yielding genotypes as the genotypes stable performance. Environments Vijapur, Banswara and Bikaner showed lower MASV while SIPC4 pointed towards Hisar, Bikaner and Varanasi as the favorable locations.

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