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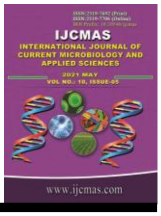

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Feed Barley Genotypes Evaluated for Adaptability under Multi Environment Field Trials of North Eastern Plains Zone of the Country

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ABSTRACT

Keywords

AMMI, ASV, ASV1, HMGV, GAI, HMPRVG, Biplots

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Highly significant effects of the environment (E), genotypes (G), and GxE interaction had been observed by AMMI analysis. GxE interaction accounted for 45.8% whereas Environment explained 27.4% of treatment variations in yield during first year. Ranking of genotype as per IPCA-1 were RD2969, K508. While IPCA-2, selected K508, HUB113 genotypes. Values of ASV1 selected RD2969, K508 and ASV identified K508, HUB113 barley genotypes. Adaptability measures Harmonic Mean of Relative Performance of Genotypic Values (HMPRVG) and Relative Performance of Genotypic Values (RPGV) identified DWRB137, HUB113 as the genotypes of performance among the locations. Biplot graphical analysis exhibited cluster of adaptability measures PRVG, HMPRVG along with mean, GM, HM. During 2019-20 cropping season Environment effects accounted 37.1% whereas GxE interaction contributed for 29.2 % of treatment variations in yield. IPCA-1 scores, desired ranking of genotype was KB1815, DWRB213, RD3021. While IPCA-2 pointed towards RD3019, NDB1748, KB1815 as genotypes of choice. Analytic measures ASV and ASV1 selected KB1815, DWRB213, RD3021 barley genotypes. HMRPGV along with PRVG settled for DWRB213, Lakhan, KB1832. Measures IPC2, IPC3, IPC6 clustered with adaptability measures PRVG, HMPRVG, mean, GM, HM in separate cluster and observed in different quadrant of biplot analysis.

Introduction

Most cosmopolitan crop, Barley (*Hordeum vulgare L.*) grown over the wide range of environmental conditions of the country (Kharub *et al.*, 2017; Bocianowsk *et al.*, 2019). Popularly famous, as "poor man's crop" owing to low requirements of input along with better adaptability to harsh conditions (Kendel *et al.*, 2019). Feed barley is mainly cultivated as a fodder for animal consumption as enriched with nutrients and possess medicinal properties. Traditionally the crop cultivated for grains as crop for human consumption as well feed for animals (Karkee *et al.*, 2020). On yearly basis number of multi-location trials under coordinated system carried out for GxE interaction analysis (Agahi *et al.*, 2020). Breeders select or identify genotypes with stable yield along with broad or narrow adaptation bahaviour of the genotypes (Bocianowsk *et al.*, 2019). Number of adaptability measures based on AMMI stability had observed in literature (Tekdal & Kendal, 2018; Ajay *et al.*, 2019). Analytic measure of adaptability as the harmonic means of the relative performance of the predicted genotypic values (MHPRVG) utilized productivity, stability, and adaptability simultaneously of genotypes (Resende & Durate 2007). Comparative performance of AMMI based measures had been studied with relatively new adaptability measures for feed barley genotypes evaluated under North Eastern Plains Zone of the country in recent past.

Materials and Methods

States of the country Bihar, eastern Uttar Pradesh, Jharkhand, Assam and plains of West Bengal comprises the North Eastern Plains Zone of India. This zone has potential to increase the total production and importance of this zone has been highlighted to ensure food security of the country. Total of six promising genotypes evaluated at five major locations and fifteen genotypes at eight locations of the zone during cropping seasons of 2018-19 and 2019-20 respectively. Field trials were conducted at research centers in randomized complete block designs with three replications. Recommended agronomic practices were followed to harvest good yield. Details of locations and genotype parentage were reflected in tables 1 & 2 for ready reference.

AMMI analysis was performed using AMMISOFT version 1.0, available at https://scs.cals.cornell.edu/people/ hugh-gauch/and SAS software version 9.3. Simple and effective measure for adaptability is calculated as the relative performance of genetic values (PRVG) across environments and MHVG (Harmonic mean of Genetic Values), based on the harmonic mean of the genotypic values across in different environments. Lower the standard deviation of genotypic performance across environments, the greater is the harmonic mean of its genotypic values.

Results and Discussion

AMMI analysis of barley genotypes

First year of study 2018-19

AMMI based measures evaluate the adaptability performance after reduction of the noise from the GxE interaction effects (Gauch, 2013). Highly significant effects of the environment (E), genotypes (G), and GxE interaction had been observed by 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 (Kamila *et al.*, 2016). Environment explained about significantly 27.4% of the total sum of squares due to treatments indicating that diverse environments caused most of the variations in genotypes yield. Genotypes explained only 13.5% of a total sum of squares, whereas GxE interaction accounted for 45.8% of treatment variations in yield. Further bifurcation of GxE interaction observed the significant three multiplicative terms explained 99 % of interaction sum of squares and the remaining 1.0% was the residual / noise, which was not interpretable and discarded (Oyekunle *et al.*, 2017).

Second year 2019-20

Analysis observed the greater contribution of environments, GxE interactions, and genotypes to the total sum of squares (SS) as compared to the residual effects. Environment explained about significantly 37.1%, GxE interaction accounted for 29.2 whereas

Genotypes explained only 10.5% % of the total sum of squares due to treatments. Partitioning of GxE interaction revealed that only first three out of six multiplicative terms were significant and explained of interaction sum of squares.

Ranking of genotypes as per descriptive measures

First year of study 2018-19

An average yield of genotypes selected DWRB137, HUB113 genotypes (Table 5). This method is simple, but not fully exploiting all information contained in the dataset. Geometric mean is used to evaluate the adaptability of genotypes. Geometric mean observed DWRB137, HUB113 were top-ranked genotypes. Harmonic mean of genetic values (HMGV) yield expressed higher values for DWRB137, HUB113genotypes.

Consistent yield performance judged by lower values of Coefficient of Variation and genotypes DWRB137, RD 2552would be suitable for considered locations of this zone of the country. Minimum values of standard deviation of yield values selected DWRB137, RD 2552, barley genotypes. Analytic measures PRVG, MHVG, and MHPRVG, had showed consensus for classification of genotypes as per raking of genotypes vis-à-vis analytic measures (Table 4). Presence of significant cross over interactions has been validated by differences among ranks of genotypes vis-à-vis locations of the zone.

Second year 2019-20

An average yield of genotypes selected Lakhan, DWRB213, KB1832 genotypes (Table 9). Geometric mean observed Lakhan, DWRB213, KB1832, were with top-rank. Harmonic mean of genetic values (HMGV) expressed higher values for Lakhan, DWRB213, HUB69 genotypes.

Consistent yield performance of Lakhan, DWRB213, HUB270 judged by lower values of Coefficient of Variation. Minimum values of standard deviation of yield values selected Lakhan, HUB270, NDB1748 barley genotypes. Analytic measures PRVG, MHVG, and MHPRVG, had showed consensus for classification of genotypes as per raking of genotypes vis-à-vis analytic measures (Table 6). Presence of significant cross over interactions has been validated by differences among ranks of genotypes vis-à-vis locations of the zone.

Adaptability behaviour of genotypes

First year of study 2018-19

The IPCA scores of a genotype in AMMI analysis indicate the stability or adaptation over environments. The greater the IPCA scores, either negative or positive (as it is a relative value), the more specifically adapted is the genotype to certain environments. The more the IPCA scores approximate zero, the more stable or adapted the genotypes are over the entire environments sampled (Ajay *et al.*, 2019). Kendal and Tekdal, 2016 stated that genotypes having PC1 scores > 0 were recognized as high-yielding and those having PC1 scores < 0 were regarded as low-yielding. The IPCA scores of genotypes in the AMMI analysis are an indication of stability or adaptability over environments. The ranking of genotype as per absolute IPCA-1 scores were RD2969, K508(Table 4). While for IPCA-2, genotypes K508, HUB113would be of choice. Values of IPCA-3 favored RD 2552, K1055barley genotypes. Analytic measures of adaptability ASV and ASV1consider two significant IPCAs of the AMMI analysis for adaptability behaviour.

Table.1

Mohamadi & Amri 2008	**Geometric Adaptability Index**	**GAI =** $\sqrt[n]{\prod_{k=1}^{n} \bar{X}_k}$
Purchase1997	AMMI stability value	ASV = $[(\frac{SSIPC\ 1}{SSIPC\ 2} PCI)^2 + (PC2)^2]^{1/2}$
Zali et al2012	AMMI stability value	ASV1 = $[\frac{SSIPC\ 1}{SSIPC\ 2} (PCI)^2 + (PC2)^2]^{1/2}$
Resende 2004	Harmonic mean of Genetic Values	$MHVG_i$ = Number of environments / $\sum_{i=1}^{k} \frac{1}{X_i}$
Resende&Durate 2007	Relative performance of genotypic values across environments	$PRVG_{ij} = VG_{ij} / VG_i$
Resende&Durate 2007	Harmonic mean of Relative performance of genotypic values	$MHPRVG_{i.}$ = Number of environments / $\sum_{j=1}^{k} \frac{1}{PRVG_{ij}}$

Table.2 Parentage details of barley genotypes and environmental conditions (2018-19)

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	RD 2552	RD2035/DL472	E1	Varanasi	25° 19' N	82° 59' E	81
G2	K1055		E2	Faizabad	26° 46' N	82° 9' E	97
G3	HUB113	KARAN280/C138	E3	Kanpur	26° 26' N	80° 19' E	126
G4	RD2969	RD2552/RD2503//RD 2715	E4	Ranchi	23°20'N	85°18'E	651
G5	DWRB137	DWR28/DWRUB64	E5	Sabour	25°23' N	87°04' E	46
G6	K508	K394/K141					

Table.3 Parentage details of barley genotypes and environmental conditions (2019-20)

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	NDB1748	CEV96060/MSEL//CANELA ACBSSO	E1	Kanpur	26° 26' N	80° 19' E	126
G2	KB1830	RD 2784/Jyoti	E2	Saini	28°12' N	75°40' E	
G3	RD3020	RD 2035/ RD 2624//RD 2715	E3	Varanasi	25° 19' N	82° 59' E	81
G4	DWRB213	CONCHITA/DWRUB64	E4	Faizabad	26° 46' N	82° 9' E	97
G5	Lakhan	K12/IB226	E5	Chianki	23°45'N	85°30'E	215
G6	RD3022	RD 2607 / RD 2651	E6	Ranchi	23°20'N	85°18'E	651
G7	HUB269	31st INBON-04 / RD 2552	E7	Pusa	28°38 ' N	77°09' E	52
G8	PL925	VJM315/BH919	E8	Sabour	25°23' N	87°04' E	46
G9	HUB270	RD-2618 /RD-2660					
G10	KB1815	Ghinneri(smooth_awns)/6/JLB70-01/5/DeirAlla106//DL70/Pyo/3/RM1508 /4/Arizona5908/Aths//Avt/Attiki/3/Ager					
G11	RD3019	RD 2715 / RD 2552					
G12	K 603	K257/C138					
G13	PL918	VMorales/6/LEGACY//PENCO/CHEVRON-BAR/7/LIGNEE527/GERBEL/3/BOYB* 2/ SURB//CI12225.2D/4/GLORIA-BAR/COME					
G14	KB1832	K 603 x RD 2715					
G15	RD3021	DWR 64 / RD 2503					

Table.4 Multi environment trails analysis by AMMI of feed barley genotypes (2018-19)

Source	Degree of freedom	Mean Sum of Squares	Significance level	% contributions of factors
Treatments	29	201.84	.0000000 ***	86.80
Genotypes (G)	5	181.74	.0000000 ***	13.48
Environments (E)	4	462.74	.0000000 ***	27.45
Interactions (GxE)	20	154.68	.0000000 ***	45.88
IPC1	8	218.29	.0000000 ***	
IPC2	6	126.16	.0000000 ***	
IPC3	4	135.42	.0000000 ***	
Residual	2	24.35	.0496326 *	
Error	90	9.89		
Total	119	56.67		

Table.5 Ranking of feed barley genotypes as per descriptive measures (2018-19)

Genotype	Varanasi	Faizabad	Kanpur	Ranchi	Sabour	MEAN	R_k	GM	R_k	HM	R_k	CV	R_k	Sdev	R_k
RD 2552	28.25	37.15	37.41	41.84	32.95	35.52	5	35.21	5	34.89	5	0.1447	2	5.14	2
K1055	30.09	28.26	52.17	24.34	35.01	33.97	6	32.77	6	31.76	6	0.3200	6	10.87	6
HUB113	33.82	38.96	53.62	41.38	34.16	40.39	2	39.80	2	39.27	2	0.1997	4	8.06	5
RD2969	24.99	33.77	44.11	43.34	36.98	36.64	4	35.90	4	35.11	4	0.2135	5	7.82	4
DWRB137	44.14	39.81	38.59	43.34	43.05	41.78	1	41.73	1	41.67	1	0.0582	1	2.43	1
K508	36.76	46.21	42.39	39.01	31.22	39.11	3	38.78	3	38.43	3	0.1452	3	5.68	3

Table.6 Adaptability measures of feed barley genotypes evaluated under MET (2018-19)

Genotype	IPC1	IPC2	IPC3	ASV1	R_{ASV1}	ASV	R_{ASV}	PRVG	R_{PRVG}	HMPRVG	R_{HMPRVG}
RD 2552	1.529	1.002	-0.098	3.67	4	2.53	4	0.9379	5	0.9311	5
K1055	-3.511	-1.191	-0.504	8.19	6	5.46	6	0.8891	6	0.8555	6
HUB113	-1.176	0.885	1.048	2.85	3	1.99	2	1.0584	2	1.0537	2
RD2969	0.132	2.292	-1.252	2.31	1	2.30	3	0.9605	4	0.9463	4
DWRB137	1.865	-2.139	-1.645	4.81	5	3.55	5	1.1183	1	1.0984	1
K508	1.161	-0.849	2.450	2.81	2	1.96	1	1.0359	3	1.0235	3

Table.7 Loadings of adaptability measures as per Principal Components (2018-19)

Component	PC1	PC2
IPC1	0.2626	0.1279
IPC2	-0.0683	0.4488
IPC3	0.0382	0.2540
ASV1	-0.1916	-0.4106
ASV	-0.1936	-0.4209
Varanasi	0.2299	-0.3324
Faizabad	0.2677	0.1490
Kanpur	-0.1686	-0.0447
Ranchi	0.2569	0.2318
Sabour	0.1138	-0.3683
Average	0.2912	-0.1005
CV	-0.3003	0.0246
Sdev	-0.2818	0.0575
GM	0.3011	-0.0882
HM	0.3060	-0.0855
PRVG	0.2972	-0.1197
HMPRVG	0.3030	-0.0670
% variation	57.35	20.39

Table.8 Multi environment trails analysis by AMMI of barley genotypes (2019-20)

Source	Degree of Freedom	Mean Sum of Squares	Significance level	% contributions of factors
Treatments	119	204.15	***	76.87
Genotypes (G)	14	237.83	***	10.54
Environments (E)	7	1675.30	***	37.11
Interactions (GxE)	98	94.26	***	29.23
IPC1	20	252.63	***	
IPC2	18	80.55	***	
IPC3	16	79.05	*	
IPC4	14	55.16		
IPC5	12	27.75		
IPC6	10	24.29		
Residual	8	15.21		
Error	240	30.45		
Total	359	88.03		

Table.9 Ranking of barley genotypes as per descriptive measures (2019-20)

Genotype	Kanpur	Saini	Varanasi	Faizabad	Chianki	Ranchi	Pusa	Sabour	Mean	R_k	GM	R_k	HM	R_k	CV	R_k	Sdev	R_k
NDB1748	38.05	18.84	30.09	28.99	27.13	36.96	28.26	19.68	28.50	9	27.72	8	26.915	8	0.2440	5	6.95	3
KB1830	40.58	31.52	21.07	28.69	45.00	48.91	27.18	23.08	33.25	4	31.88	5	30.593	5	0.3112	9	10.35	11
RD3020	51.18	34.42	30.00	27.72	38.23	31.52	25.73	20.39	32.40	6	31.32	6	30.327	6	0.2876	7	9.32	8
DWRB213	50.00	33.52	29.78	28.87	32.89	36.96	28.26	31.06	33.92	2	33.37	2	32.907	2	0.2091	2	7.09	4
Lakhan	35.96	25.36	41.07	29.59	41.29	35.87	30.80	31.58	33.94	1	33.53	1	33.109	1	0.1654	1	5.61	1
RD3022	45.02	38.04	19.42	28.08	25.64	34.24	14.49	24.37	28.66	8	27.08	10	25.489	10	0.3491	10	10.00	9
HUB69	35.14	26.09	33.35	29.77	30.38	48.37	32.43	24.78	32.54	5	31.91	4	31.354	3	0.2241	4	7.29	5
PL925	38.77	19.93	11.29	24.16	21.61	30.43	22.10	18.83	23.39	15	22.14	13	20.862	11	0.3507	11	8.20	7
HUB270	24.46	21.74	36.25	26.87	34.92	25.54	34.06	20.38	28.03	10	27.43	9	26.854	9	0.2214	3	6.21	2
KB1815	40.13	33.33	6.79	27.78	36.57	36.41	12.32	19.92	26.65	11	23.15	11	18.847	13	0.4631	13	12.34	13
RD3019	42.21	30.07	23.10	22.95	30.12	32.61	16.30	7.55	25.61	12	23.11	12	19.926	12	0.4150	12	10.63	12
K 603	26.81	18.48	43.71	27.78	28.74	34.78	23.92	28.70	29.11	7	28.31	7	27.538	7	0.2572	6	7.49	6
PL918	52.08	35.33	9.61	28.02	19.27	31.96	13.77	9.17	24.90	14	21.05	15	17.691	15	0.5965	15	14.85	15
KB1832	51.63	32.61	22.45	29.89	32.93	46.20	30.07	23.31	33.64	3	32.37	3	31.225	4	0.3060	8	10.29	10
RD3021	41.30	44.20	15.15	27.72	20.30	29.89	12.50	8.36	24.93	13	21.67	14	18.548	14	0.5292	14	13.19	14

Table.10 Adaptability measures of barley genotypes evaluated under MET (2019-20)

Genotype	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	ASV1	R_{ASV1}	ASV	R_{ASV}	PRVG	R_{PRVG}	HMPRVG	R_{HMPRVG}
NDB1748	1.457	-0.125	-1.585	-0.836	0.011	0.339	5.08	9	2.72	9	0.9841	9	0.9487	7
KB1830	-0.423	1.863	-0.079	-1.169	-0.186	0.384	2.38	4	2.02	6	1.1270	5	1.0984	4
RD3020	-1.026	1.442	0.478	0.278	0.099	1.209	3.86	8	2.40	8	1.1008	6	1.0849	6
DWRB213	-0.309	-1.165	1.681	-1.208	-0.987	1.093	1.59	2	1.30	3	1.1725	2	1.1570	1
Lakhan	-0.431	-2.034	-0.740	0.568	-0.030	0.619	2.53	6	2.19	7	1.2018	1	1.1392	2
RD3022	1.626	-0.562	0.905	0.395	1.440	1.060	5.69	11	3.09	11	0.9685	10	0.9207	9
HUB69	0.680	-0.413	0.643	1.143	0.873	-0.423	2.41	5	1.34	4	1.1315	4	1.0955	5
PL925	-2.291	-2.023	-0.400	0.632	0.418	-1.043	8.24	13	4.73	13	0.7920	15	0.7494	12
HUB270	1.438	1.446	-1.990	-0.232	1.115	-0.465	5.21	10	3.05	10	1.0032	8	0.9134	10
KB1815	-0.138	-0.259	-1.955	0.175	-0.844	0.258	0.55	1	0.36	1	0.8820	11	0.7044	13
RD3019	0.863	-0.006	-0.651	0.597	-1.961	-0.446	3.01	7	1.61	5	0.8423	12	0.7574	11
K 603	3.408	0.652	1.828	1.217	-0.628	-0.871	11.89	15	6.40	15	1.0414	7	0.9396	8
PL918	-3.236	1.344	0.308	1.704	0.097	0.184	11.36	14	6.19	14	0.8000	14	0.6718	15
KB1832	-1.997	0.906	1.065	-1.411	0.033	-1.288	7.02	12	3.84	12	1.1366	3	1.1223	3
RD3021	0.378	-1.064	0.494	-1.855	0.549	-0.610	1.69	3	1.28	2	0.8164	13	0.7019	14

Table.11 Loadings of adaptability measures as per Principal Components (2019-20)

Component	PC1	PC2
IPC1	-0.0829	-0.2306
IPC2	-0.0117	0.0393
IPC3	-0.0654	0.0965
IPC4	0.0636	-0.2449
IPC5	-0.0247	-0.0673
IPC6	-0.0854	0.2336
ASV1	0.0824	-0.2879
ASV	0.0671	-0.2812
Kanpur	0.0584	0.3973
Saini	0.1043	0.4279
Varanasi	-0.2454	-0.2399
Faizabad	-0.1959	0.1738
Chianki	-0.2239	0.1219
Ranchi	-0.1670	0.1957
Pusa	-0.2724	-0.1400
Sabour	-0.2740	-0.0596
Mean	-0.2976	0.1661
CV	0.2929	0.1651
Sdev	0.2441	0.2705
PRVG	-0.3131	0.0814
MHPRVG	-0.3095	0.0834
GM	-0.3131	0.0865
HM	-0.3154	0.0304
% variation	42.21	16.61

Fig.1 Biplot analysis of adaptability measures for barley genotypes (2018-19)

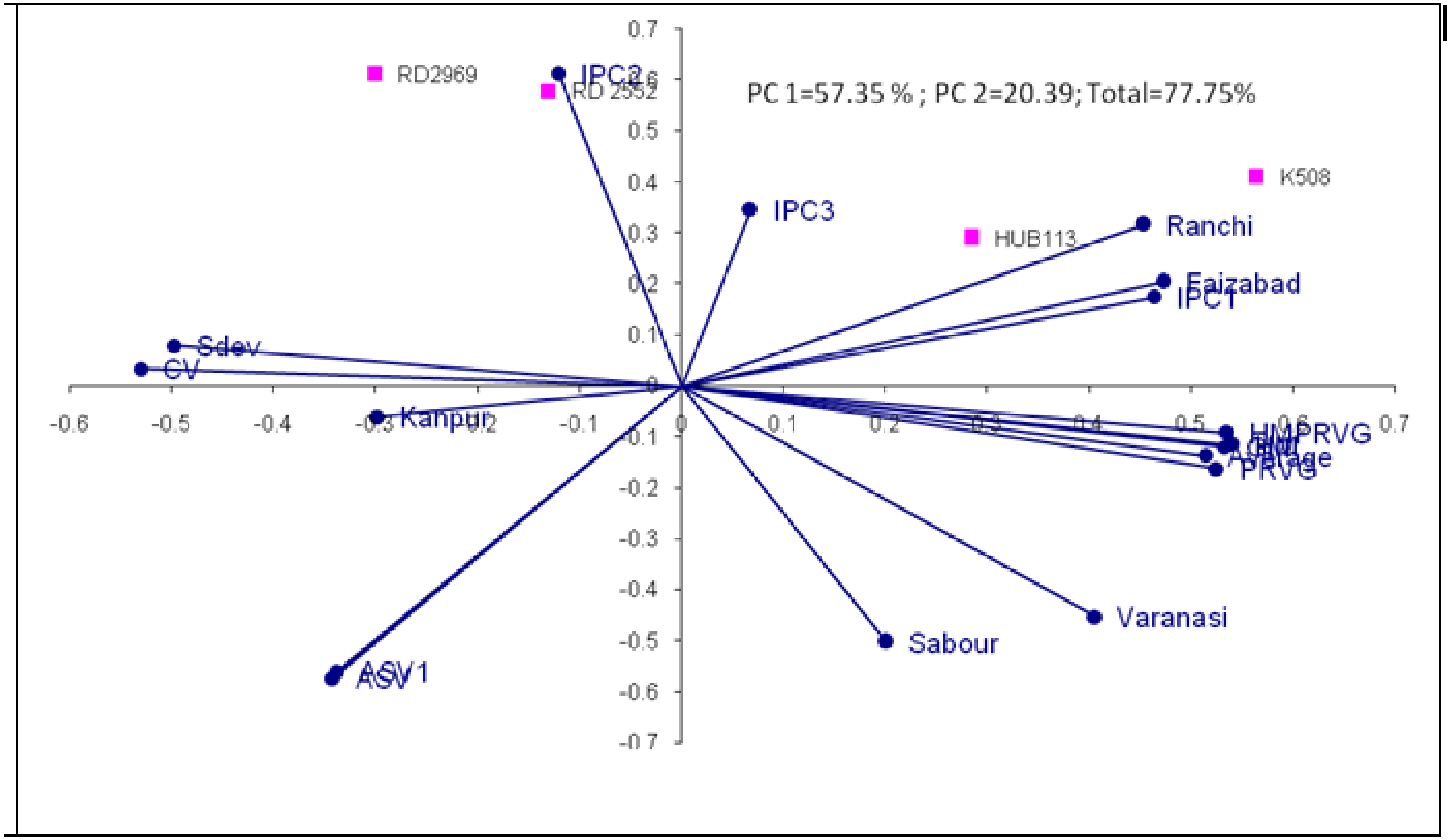
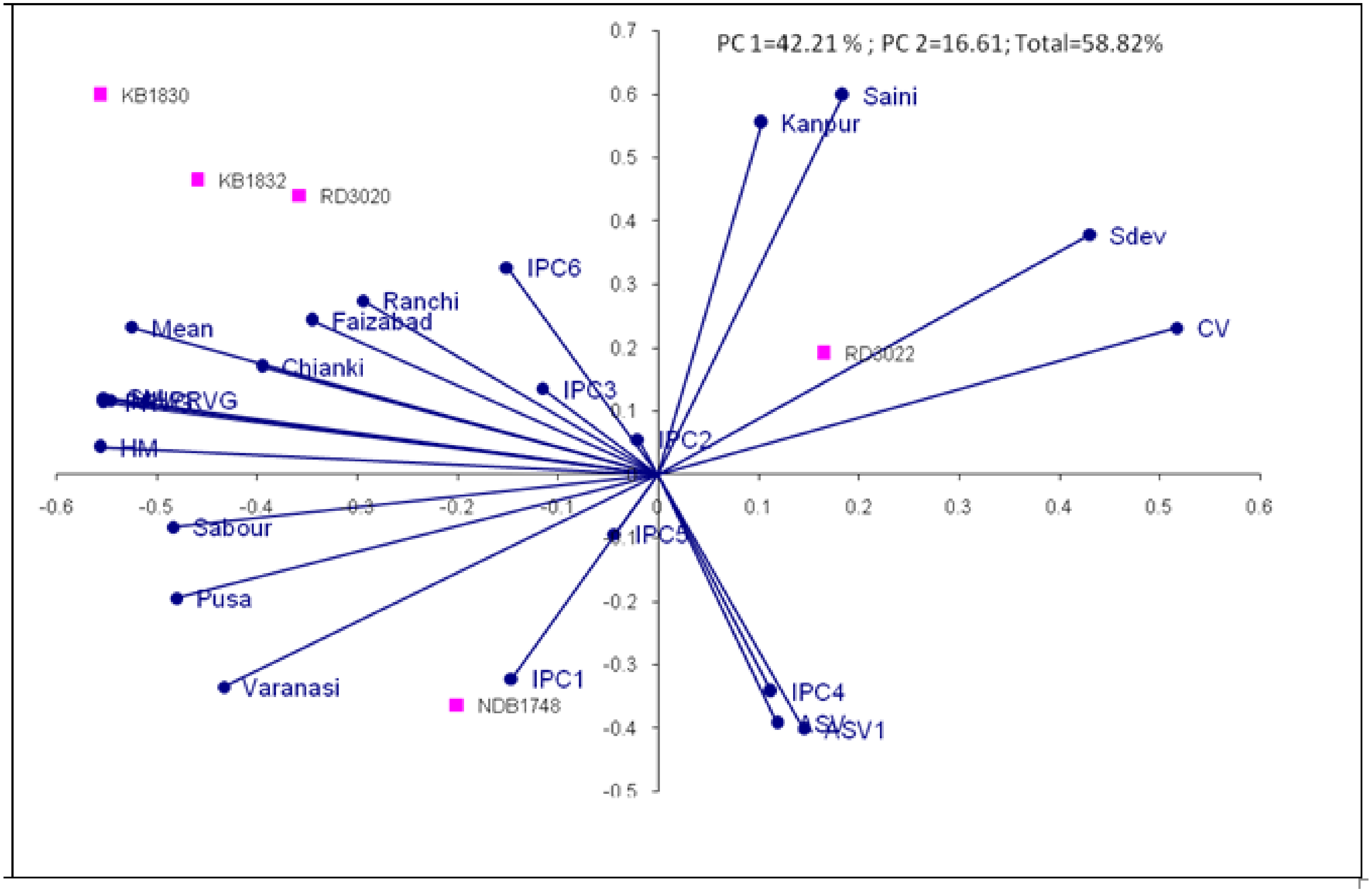


Fig.2 Biplot analysis of adaptability measures for barley genotypes (2019-20)



Values of ASV1 selected RD2969, K508 and ASV identified K508, HUB113 barley genotypes (Ajay *et al.,* 2019). Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) method, the genotypes can be simultaneously sorted by genotypic values (yield) and stability using the harmonic means of the yield so that the smaller the standard deviation of genotypic performance among the locations.

Values of HMRPGV ranked DWRB137, HUB113as the performance of the genotypes among the locations. When considering the yield and adaptability simultaneously, the recommended approach is the relative performance of genetic values (RPGV) over crop years. Relative Performance of Genotypic Values had settled for DWRB137, HUB113 genotypes.

Second year 2019-20

KB1815, DWRB213, RD3021 were the top ranked genotype as per absolute IPCA-1 scores (Table 8). While for IPCA-2 identified RD3019, NDB1748, KB1815 genotypes would be of choice. Values of IPCA-3 favoredKB1830, PL918, PL925 barley genotypes. As per IPCA-4, KB1815, HUB270, RD3020 genotypes would be of stable performance. IPCA-5 settled for NDB1748, Lakhan, KB1832 barley genotypes. PL918, KB1815, NDB1748 as per IPCA-6 measure. Two significant IPCAs of the AMMI analysis considered by ASV and ASV1 for adaptability behaviour. Values of ASV1 selected KB1815, DWRB213, RD3021 and ASV identified KB1815, RD3021, DWRB213 barley genotypes. Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) values ranked DWRB213, Lakhan, KB1832 as of stable performance among the locations. Relative Performance of Genotypic Values (RPGV) had settled for Lakhan, DWRB213, KB1832 genotypes.

Biplot analysis

First year of study 2018-19

Biplot analysis based on first two highly significant Interaction Principal Components exploited to understand the association if any among adaptability measures.

First two significant interaction principal components contribute to the tune of 57.3&20.4 to the total for 77.8 % of total GxE interaction sum of squares (Figure 1). Loadings of adaptability measures based on two interaction principal components had mentioned in table 6. CV clustered with Sdev and IPC2 measure in one quadrant and adaptability measures PRVG, HMPRVG along with mean, GM, HM grouped in nearby cluster. Measure’s IPC1, and IPC3 joined hands to form another cluster. Clustering of analytic measures ASV and ASV1 observed where close proximity of average yield among adaptability measures of genotypes was of more concern.

Second year 2019-20

Total contributions to the tune of 58.8% with respective % share of 42.2&16.6 towards the total GxE interaction sum of squares accounted by first two significant interaction principal components (Figure 2). Loadings of adaptability measures based on two interaction principal components had mentioned in table 10. Measure CV clustered with Sdev one quadrant while ASV, ASV1 and IPC4 were grouped together. Measures IPC2, IPC3 and IPC6 clustered with adaptability measures PRVG, HMPRVG, mean, GM, HM in nearby quadrant. Measure’s IPC1, IPC5 were observed as outliers in different quadrant. Clustering of analytic measures expressed close proximity among themselves; this implies mean yield of genotypes would be suitable to express adaptability of genotypes as far this zone is concerned. High production potential of promising genotypes that respond to favourable environments emphasized by researchers around the country. The presence of complex type GxE interaction leads to uncertainty in the identification process. More importance had laid to recent techniques to understand the adaptability and stability more precisely. Selection of barley genotypes by the harmonic mean of genotypic values allow the breeders of various crop species around the world to identify the stable and productive genotypes.

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