

## Malt Barley Genotypes Assessed by Analytic Adaptability Measures for NWPZ of the Country

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### Abstract

Highly significant effects of the environment (E), genotypes (G), and GxE interaction had been observed by AMMI analysis. Environment explained 51.4% whereas GxE interaction accounted for 22.1% of treatment variations in yield during first year. Harmonic Mean of Genotypic Values (HMGV) expressed higher values for DWRB160, DWRB184, and BH902. Ranking of genotype as per IPCA-1 were BH902, DWRB182, DWRB101. While IPCA-2, selected DWRB101, DWRB123, DWRB184 genotypes. Values of ASV1 selected DWRB101, DWRB182, BH902 and ASV identified DWRB101, DWRB123, DWRB182 barley genotypes. Adaptability measures Harmonic Mean of Relative Performance of Genotypic Values (HM-PRVG) and Relative Performance of Genotypic Values (RPGV) identified DWRB160, DWRB184, and BH902 as the genotypes of performance among the locations. Biplot graphical analysis exhibited adaptability measures PRVG, HMPRVG along with IPC3, mean, GM, HM grouped in a cluster. During 2019-20 cropping season Environment effects accounted 79.7% whereas GxE interaction contributed for 7.7% % of treatment variations in yield. HMGV expressed higher values for DWRB196, DWRB123, and RD2849. IPCA-1 scores, desired ranking of genotypes was DWRB182, PL908, RD2849. While IPCA-2 pointed towards PL908, RD2849, DWRB196, as genotypes of choice. Analytic measures ASV and ASV1 selected PL908, RD2849, DWRB123 barley genotypes. HMRPGV along with PRVG settled for DWRB196, DWRB123, and RD2849. Adaptability measures PRVG, HMPRVG clustered with mean, GM, HM and observed in different quadrant of biplot analysis.

**Keywords:** AMMI, ASV, ASV1, HMGV, GAI, HMPRVG, Biplots

### Introduction

Barley (*Hordeum vulgare* L.) described as the most cosmopolitan of the crops as it is grown over the wide range of environmental conditions [1, 2]. Commonly known, as “poor man’s crop” owing to low requirements of input along with better adaptability to harsh conditions [3]. Traditionally the crop cultivated and used as a grain crop for human consumption as well feed for animals [4]. Grains consist of ample quantity of  $\beta$ -glucan beneficial in decreasing the glucose level of diabetic patients and to reduce the cholesterol of heart patients [5]. Malt barley has huge industrial requirements. GxE interaction analysis under multi location trials carried out by AMMI analytic tools [6]. Barley breeders identify malt barley genotypes with stable yield with broad or narrow adaptation performance of the genotypes [1]. Number of adaptability measures based on AMMI stability had observed in literature [7]. Analytic measure of adaptability as the harmonic means of the relative per-

formance of the predicted genotypic values (MHPRVG) utilized productivity, stability, and adaptability simultaneously of genotypes [8]. Comparative performance of AMMI based measures had been studied with relatively new adaptability measures for malt barley genotypes evaluated under North Western Plains Zone of the country.

### Material and methods

Parts of sub-humid Sutlej-Ganga Alluvial Plains and arid western plains, which comprises Punjab, Haryana, Delhi, Rajasthan (except Kota and Udaipur divisions), Western Uttar Pradesh (except Jhansi division and hilly areas), parts of Jammu and Kashmir (Jammu and Kathua districts) and parts of Himachal Pradesh (Pantnagar and Una districts) categorized as the North Western Plain Zone of India. Eight promising genotypes in advanced trials evaluated at six one major locations of the zone and nine geno-

types at eight locations 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.

**Table 1: Parentage details of barley genotypes and locations of the zone (2018-19)**

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	DWRB184	DWRUB52/DWR81	E1	Bawal	28 o 10'N	76 o 50'E	266
G2	DWRB182	DWRUB52/DWRB78	E2	Durgapura	26 o 51'N	75 o 47'E	390
G3	DWRB160	DWRB62/DWRB73	E3	Hisar	29 o 10' N	75 o 46'E	229
G4	RD2849	DWRUB52/PL705	E4	Ludhiana	30 o 54' N	75 o 48 'E	247
G5	DWRB137	DWR28/DWRUB64	E5	Pantnagar	29 o 02'N	79 o 48'E	243.8
G6	DWRB123	DWRUB54/DWR51	E6	Karnal	29 o 43' N	70 o 58'E	245
G7	DWRB101	DWR28/BH581					
G8	BH902	BH495/RD2552					

**Table 2: Parentage details of barley genotypes and locations of the zone (2019-20)**

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	DWRB 196	DWRUB52/ DWR81	E1	Karnal	29 o 43' N	70 o 58'E	245
G2	RD2849	DWRUB52/PL705	E2	Hisar	29 o 10' N	75 o 46'E	229
G3	PL908	RD2740/RD2743	E3	Modipuram	29 o 05' N	77 o 70'E	226
G4	DWRB 101	DWR28/BH581	E4	Durgapura	26 o 51'N	75 o 47'E	390
G5	DWRB160	DWRB62/ DWRB73	E5	Pantnagar	29 o 02'N	79 o 48'E	243.8
G6	DWRB182	DWRUB52/ DWRB78	E6	Bathinda	30 o 09' N	74 o 55 'E	211
G7	DWRB123	DWRUB54/ DWR51	E7	Bawal	28 o 10'N	76 o 50'E	266
G8	BH902	BH495/RD2552	E8	Ludhiana	30 o 54' N	75 o 48 'E	247
G9	DWRB 197	DWRUB52/ DWR84					

Mohamadi & Amri 2008

Geometric Adaptability Index

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

Purchase1997

AMMI stability value

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

Zali et al 2012

AMMI stability value

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

Resende & Durate 2007

Harmonic mean of Genetic Values

$$MHVG_i = \text{Number of environments} / \sum_{i=1}^k \frac{1}{X_i}$$

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

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

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 [9]. Highly significant effects of the environment (E), genotypes (G), and GxE interaction had been observed by AMMI analysis [Table 3]. Environment explained about significantly 51.4% of the total sum of squares due to treatments indicating that diverse environments caused most of the variations in genotypes yield. Genotypes explained only 6.8% of a total sum of squares, whereas GxE interaction accounted for 22.1% of treatment variations in yield. Partitioning of GxE interaction revealed that only first two out of four multiplicative terms were significant and explained of interaction sum of squares and the remaining was discarded [10].

**Table 3: Multi environment trials analysis by AMMI of barley genotypes (2018-19)**

Source	Degree of freedom	Mean Sum of Squares	Significance level	% contributions of factors
Treatments	47	221.05	.0000000 ***	80.24
Genotypes (G)	7	124.90	.0000003 ***	6.75
Environments (E)	5	1330.11	.0000000 ***	51.37
Interactions (GxE)	35	81.84	.0000000 ***	22.12
IPC1	11	156.37	.0000000 ***	
IPC2	9	94.57	.0001604 ***	
IPC3	7	22.05		
IPC4	5	23.23		
Residual	3	7.63		
Error	144	17.76		
Total	191	67.79		

#### 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 79.7% of the total sum of squares due to treatments indicating that diverse environments caused most of the variations in genotypes yield. Genotypes explained only 5.0% of a total sum of squares, whereas GxE interaction accounted for 7.7% of treatment variations in yield. Partitioning of GxE interaction revealed that only first two out of six multiplicative terms were significant and explained of interaction sum of squares and the remaining was discarded.

#### Ranking of Genotypes as Per Descriptive Measures

##### First year of study 2018-19

An average yield of genotypes selected DWRB160, DWRB184, BH902 genotypes [Table 4]. This measure though simple to calculate, but unable to exploit full information contained in the dataset. Geometric mean is used to evaluate the adaptability of genotypes. Geometric mean observed DWRB160, DWRB184, BH902 were top-ranked genotypes. Harmonic Mean of Genotypic Values of yield expressed higher values for DWRB160, DWRB184, BH902 genotypes.

**Table 4: Ranking of barley genotypes as per descriptive measures (2018-19)**

Genotype	Bawal	Durgapura	Hisar	Ludhiana	Pantnagar	Karnal	MEAN	Rk	GM	Rk	HM	Rk	CV	Rk	Sdev	Rk
DWRB184	56.58	64.58	48.18	54.27	50.88	65.07	56.59	2	56.24	2	55.88	2	0.1236	4	6.99	5
DWRB182	56.21	53.01	41.85	48.23	49.09	56.10	50.75	8	50.49	8	50.22	8	0.1086	3	5.51	3
DWRB160	56.88	57.64	48.09	60.31	53.49	63.52	56.65	1	56.43	1	56.21	1	0.0950	1	5.38	2
RD2849	70.56	61.11	43.52	52.34	59.59	51.14	56.37	4	55.72	4	55.07	4	0.1669	7	9.41	7
DWRB137	54.68	71.53	37.84	56.20	47.97	63.97	55.36	5	54.26	5	53.11	6	0.2134	8	11.82	8
DWRB123	58.89	59.95	45.40	52.09	54.85	54.83	54.33	6	54.11	6	53.88	5	0.0966	2	5.25	1
DWRB101	53.77	60.88	40.96	50.54	49.10	57.08	52.05	7	51.65	7	51.23	7	0.1332	5	6.93	4
BH902	61.11	68.52	44.82	56.97	53.18	54.25	56.47	3	56.00	3	55.52	3	0.1413	6	7.98	6

Consistent yield performance judged by lower values of Coefficient of Variation and genotypes DWRB160, DWRB123, DWRB182 would be suitable for considered locations of this zone of the country. Minimum values of standard deviation of yield values selected DWRB123, DWRB160, DWRB182 barley genotypes. 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 DWRB196, DWRB123, RD2849 genotypes [Table 5]. Geometric mean observed DWRB196, DWRB123, RD2849 were top-ranked genotypes. Harmonic mean of genetic values (HMGV) expressed higher values for DWRB196 DWRB123, RD2849 genotypes. Consistent yield performance of DWRB196, RD2849, DWRB160 judged by lower values of Coefficient of Variation. Minimum values of standard deviation of yield values selected DWRB196, DWRB160, RD2849 barley genotypes.

**Table 5: Adaptability measures of barley genotypes evaluated under MET (2018-19)**

Genotype	IPC1	IPC2	IPC3	IPC4	ASV1	RASV1	ASV	RASV	PRVG	RPRVG	HM-PRVG	RHM-PRVG
DWRB184	1.365	0.758	-0.814	-1.128	2.86	6	2.08	5	1.0337	2	1.030	2
DWRB182	-0.519	1.382	-0.961	0.220	1.74	2	1.57	3	0.9275	8	0.926	8
DWRB160	0.629	2.146	1.300	1.078	2.49	5	2.32	6	1.0381	1	1.033	1
RD2849	-3.245	-0.950	-0.579	0.735	6.63	8	4.71	8	1.0284	4	1.017	4
DWRB137	2.503	-1.979	-0.453	1.015	5.43	7	4.07	7	1.0012	5	0.991	6
DWRB123	-0.966	0.331	0.266	-0.808	1.98	4	1.41	2	0.9939	6	0.992	5
DWRB101	0.594	-0.087	-0.260	-0.377	1.20	1	0.85	1	0.9482	7	0.948	7
BH902	-0.360	-1.600	1.502	-0.736	1.76	3	1.68	4	1.0291	3	1.026	3

### 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. The IPCA scores of genotypes in the AMMI analysis are an indication of stability or adaptability over environments [11]. The ranking of genotype as per absolute IPCA-1 scores were BH902, DWRB182, DWRB101 [Table 6]. While for IPCA-2, genotypes DWRB101, DWRB123, DWRB184 would be of choice. Values of IPCA-3 favored DWRB101, DWRB123, DWRB137 barley genotypes. As per IPCA-4, DWRB182, DWRB101, RD2849 genotypes would be of stable performance.

Analytic measures of adaptability ASV and ASV1 consider two significant IPCAs of the AMMI analysis for adaptability behaviour. Values of ASV1 selected DWRB101, DWRB182, BH902 and ASV identified DWRB101, DWRB123, DWRB182 barley genotypes. 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 DWRB160, DWRB184, and BH902 as 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) overcrop years. Relative Performance of Genotypic Values had settled for DWRB160, DWRB184, BH902 genotypes.

**Table 6: Loadings of adaptability measures as per Principal Components (2018-19)**

Component	PC1	PC2
IPC1	0.0328	-0.0645
IPC2	0.1264	0.3294
IPC3	-0.1515	0.2229
IPC4	-0.0700	-0.1899
ASV1	-0.2143	-0.2893
ASV	-0.2287	-0.2758
CV	-0.1246	-0.4162
Sdev	-0.1629	-0.3954
Bawal	-0.1974	-0.0299
Durgapura	-0.2044	-0.2208
Hisar	-0.1354	0.4003
Ludhiana	-0.2754	0.0973
Pantnagar	-0.2067	0.1125
Karnal	-0.0484	0.0207
MEAN	-0.3553	0.0638
GM	-0.3464	0.1203
HM	-0.3304	0.1780
PRVG	-0.3505	0.1030
HMPRVG	-0.3414	0.1375
% variation	40.02	25.97

### Second Year 2019-20

The ranking of genotype as per absolute IPCA-1 scores were DWRB182, PL908, RD2849 [Table 7]. While for IPCA-2, genotypes PL908, RD2849, DWRB196, would be of choice. Values of IPCA-3 favored RD2849, BH902, DWRB 197 barley geno-

types. As per IPCA-4, DWRB196, DWRB197, RD2849 genotypes would be of stable performance. Genotypes DWRB 196, BH902, DWRB123 as per IPCA-6 measure while IPCA-5 settled for DWRB160, RD2849, DWRB123 barley genotypes.

**Table 7: 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	71	383.19	***	92.47
Genotypes (G)	8	184.72	***	5.02
Environments (E)	7	3351.68	***	79.74
Interactions (GxE)	56	40.48	***	7.71
IPC1	14	80.36	***	
IPC2	12	60.40	**	
IPC3	10	26.62		
IPC4	8	10.41		
IPC5	6	5.79		
IPC6	4	5.91		
Residual	2	4.64		
Error	144	15.38		
Total	215	136.84		

Two significant IPCAs of the AMMI analysis considered by ASV and ASV1 for adaptability behaviour. Values of ASV1 selected PL908, RD2849, DWRB123 and ASV identified PL908, RD2849, DWRB123 barley genotypes. Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) ranked DWRB196, DWRB123, and RD2849 as 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) overcrop years. Relative Performance of Genotypic Values had settled for DWRB196, DWRB123, RD2849 genotypes.

### Biplot Analysis First year of study 2018-19

First two highly significant Interaction Principal Components used

for the graphical Biplot analysis to understand the association if any among adaptability measures. First two significant interaction principal components accounted total for 65.9% with 40% & 25.9% with respective share % of total GxE interaction sum of squares [Figure 1]. Loadings of adaptability measures based on two interaction principal components had mentioned in table 6. Measure CV along with Sdev clustered with ASV, ASV1 and IPC4 measure in one quadrant and adaptability measures PRVG, HMPRVG along with IPC3, mean, GM, HM grouped in nearby cluster. Measure's IPC2, and IPC1 were observed as outliers and placed in different quadrants. 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

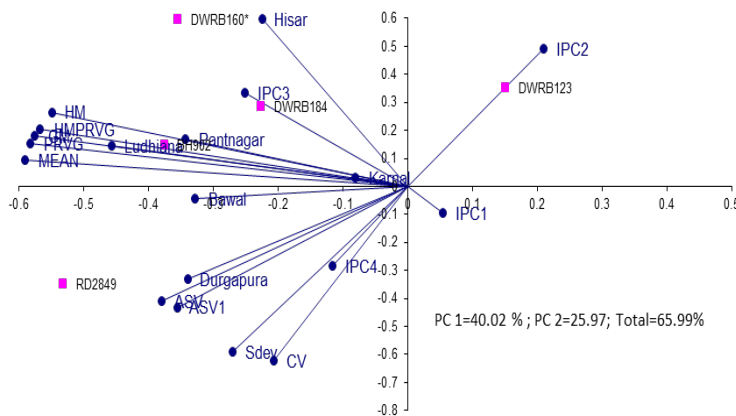


Figure 1: Biplot analysis of adaptability measures for barley genotypes (2018-19)

### Second Year 2019-20

First two significant interaction principal components accounted total for 58.1% with respective share of 40.7% & 17.4% of total GxE interaction sum of squares [Figure 2]. Loadings of adaptability measures based on two interaction principal components had mentioned in table 6. Measure CV along with Sdev clustered with IPC2, IPC4 and IPC5 measure in one quadrant and adaptability

measures PRVG, HMPRVG along with, mean, GM, HM grouped in nearby cluster. Measure's ASV, ASV1 and IPC6 were observed 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 [12-15].

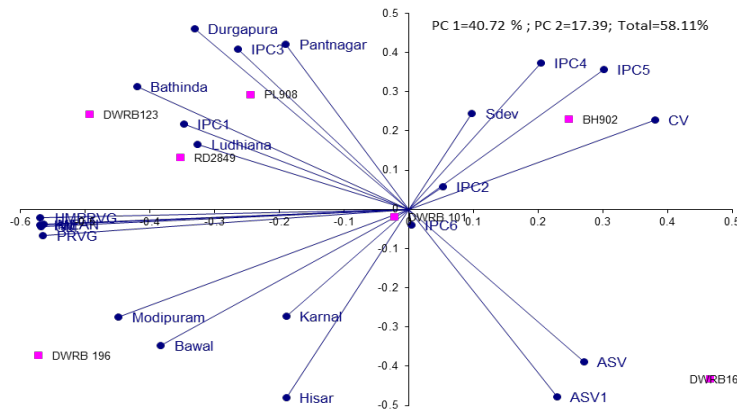


Figure 2: Biplot analysis of adaptability measures for barley genotypes (2019-20)

**Table 8: Ranking of barley genotypes as per descriptive measures (2019-20)**

Genotype	Karnal	Hisar	Modipuram	Durgapura	Pantnagar	Bathinda	Bawal	Ludhiana	Mean	Rk	GM	Rk	HM	Rk	CV	Rk	Sdev	Rk
DWRB 196	37.42	50.74	62.49	66.42	44.21	59.26	62.33	43.64	53.31	1	52.32	1	51.30	1	0.2016	1	10.75	1
RD2849	38.79	43.95	59.92	66.25	50.99	58.82	58.52	36.16	51.67	3	50.60	3	49.48	3	0.2127	2	10.99	3
PL908	32.17	46.14	56.76	67.22	42.77	60.79	61.30	41.71	51.11	4	49.77	4	48.38	4	0.2374	5	12.13	6
DWRB 101	44.49	38.00	62.15	68.84	45.95	57.71	61.18	30.13	51.05	5	49.38	5	47.61	5	0.2632	9	13.44	9
DWRB160	34.64	47.97	57.19	56.33	44.53	53.68	56.25	28.76	47.42	8	46.18	8	44.79	8	0.2272	3	10.77	2
DWRB182	32.71	31.42	49.75	66.18	44.80	53.78	51.82	37.08	45.94	9	44.60	9	43.29	9	0.2583	7	11.87	4
DWRB123	46.16	38.30	60.54	70.99	49.93	60.42	60.30	37.06	52.96	2	51.72	2	50.47	2	0.2274	4	12.04	5
BH902	29.39	45.25	57.44	65.85	48.22	61.04	52.05	33.82	49.13	6	47.53	6	45.81	7	0.2596	8	12.76	8
DWRB 197	46.69	46.85	57.05	61.48	29.31	53.57	62.42	34.29	48.96	7	47.47	7	45.84	6	0.2485	6	12.16	7

**Table 9: Adaptability measures of barley genotypes evaluated under MET (2019-20)**

Genotype	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	ASV1	RASV1	ASV	RASV	PRVG	RPRVG	HM-PRVG	RHM-PRVG
DWRB 196	2.111	0.221	-0.965	0.150	-1.245	0.004	3.28	6	2.64	5	1.0689	1	1.0632	1
RD2849	0.355	-0.126	0.511	-0.479	-0.112	-0.929	0.56	2	0.46	2	1.0317	3	1.0300	3
PL908	0.252	-0.115	0.963	0.766	-0.348	0.850	0.41	1	0.33	1	1.0179	4	1.0100	4
DWRB 101	2.040	-1.193	-0.974	-0.825	0.963	0.226	3.38	8	2.81	7	1.0111	5	1.0009	5
DWRB160	-2.081	0.927	-0.984	-0.652	0.053	0.812	3.36	7	2.75	6	0.9450	8	0.9369	8
DWRB182	0.131	2.074	-0.612	1.343	0.748	-0.406	2.08	4	2.08	4	0.9141	9	0.9032	9
DWRB123	0.380	1.256	2.097	-0.788	0.141	0.051	1.39	3	1.34	3	1.0574	2	1.0502	2
BH902	-0.889	-2.678	0.535	0.867	0.208	-0.022	3.01	5	2.90	9	0.9736	7	0.9630	6
DWRB 197	-2.298	-0.366	-0.571	-0.382	-0.407	-0.586	3.59	9	2.89	8	0.9804	6	0.9525	7

**Table 10: Loadings of adaptability measures as per Principal Components (2019-20)**

Component	PC1	PC2
IPC1	-0.1982	0.1532
IPC2	0.0302	0.0407
IPC3	-0.1507	0.2888
IPC4	0.1170	0.2640
IPC5	0.1722	0.2522
IPC6	0.0022	-0.0281
ASV1	0.1312	-0.3381
ASV	0.1544	-0.2746
CV	0.2175	0.1614
Sdev	0.0559	0.1725
Karnal	-0.1082	-0.1927
Hisar	-0.1081	-0.3388

Modipuram	-0.2563	-0.1939
Durgapura	-0.1890	0.3255
Pantnagar	-0.1087	0.2974
Bathinda	-0.2398	0.2215
Bawal	-0.2193	-0.2454
Ludhiana	-0.1863	0.1170
MEAN	-0.3222	-0.0265
GM	-0.3248	-0.0316
HM	-0.3253	-0.0284
PRVG	-0.3231	-0.0468
HMPRVG	-0.3252	-0.0154
% variation	40.72	17.39

## Conclusions

Researchers concentrate on genotypes with high productive potential that respond to favorable environments. Often the occurrence of complex type GxE interaction leads to uncertainty in the identification of promising genotype; in this case, techniques exploit adaptability and stability can provide precise information about genotypes performance. The identification of stable and highly productive genotypes between different environments remains a constant challenge for breeders of various crop species around the world. Selection of barley genotypes by the harmonic mean of genotypic values allow to identify the stable and productive genotypes.

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## Conflict of interest

No conflict of interest

## References

- Bocianowski J, Warzecha T, Nowosad K and Bathelt R (2019). Genotype by environment interaction using AMMI model and estimation of additive and epistasis gene effects for 1000-kernel weight in spring barley (*Hordeum vulgare* L.). *Journal of Applied Genetics*, 60: 127-135.
- Kharub Ajit Singh, Kumar D, Kumar Vishnu, Malik Rekha and Verma Ramesh Pal, et al. (2017). Barley research in India: challenges and opportunities. Haryana, India: Indian Council of Agricultural Research, Indian Institute of Wheat and Barley Research (ICAR-IIWBR).
- Kendel M, Dhama NB and Shrestha J (2019). Performance evaluation of barley (*Hordeum vulgare* L.) genotypes in Dolakha, Nepal: from yielding perspective. *Journal of Agriculture and Natural Resources* 2: 322-337.
- Karkee A, Ghimire K H and Joshi BK (2020). Evaluation on naked barley landraces for agro-morphological traits. *Journal of Nepal Agricultural Research Council*. 6:34-43.
- Shimizu C, Kihara M, Aoe S, Araki A and Ito K, et al. (2008). Effect of high  $\beta$ -glucan barley on serum cholesterol concentrations and visceral fat area in Japanese men- A randomized, double-blinded, placebo-controlled trial. *Plant Food Human Nutrition* 63: 21-25
- Agahi K, Jafar Ahmadi, Hassan Amiri Oghan, Mohammad Hossein Fotokian and Sedigheh Fabriki Orang (2020). Analysis of genotype  $\times$  environment interaction for seed yield in spring oilseed rape using the AMMI model. *Crop Breeding and Applied Biotechnology* 20(1): e26502012.
- Tekdal S and Kendal E (2018) AMMI Model to Assess Durum Wheat Genotypes in Multi-Environment Trials. *J Agr Sci Tech*. 20: 153-166.
- Resende MDV de and Duarte JB. 2007. Precision and quality control in variety trials. *Pesquisa Agropecuaria Tropical*. 37(3): 182-194.
- Gauch HG (2013). A Simple Protocol for AMMI Analysis of Yield Trials. *Crop Science* 53:1860-1869.
- Oyekunle M, A Menkir, H Mani, G. Olaoye and IS Usman, et al. (2017). Stability analysis of maize cultivars adapted to tropical environments using AMMI analysis. *Cereal Res. Commun.* 45: 336-345.
- Kendal E and Tekdal S (2016). Application of AMMI Model for Evolution Spring Barley Genotypes in Multi-Environment Trials. *Bangladesh J. Bot.* 45: 613-620.
- Mohammadi R and Amri A (2008). Comparison of parametric and non-parametric methods for selecting stable and adapted durum wheat genotypes in variable environments. *Euphytica* 159: 419-432.
- Purchase JL (1997). Parametric analysis to describe G  $\times$  E interaction and yield stability in winter wheat. Ph.D. thesis. Dep. of Agronomy, Faculty of Agriculture, Univ. of the Orange Free State, Bloemfontein, South Africa.
- Rao AR and Prabhakaran VT (2005). Use of AMMI in simultaneous selection of genotypes for yield and stability. *Journal of the Indian Society of Agricultural Statistics* 59: 76-82.
- Zali H, Farshadfar E, Sabaghpour SH and Karimizadeh R



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(2012). Evaluation of genotype  $\times$  environment interaction in chickpea using measures of stability from AMMI model. *Annals of Biological Research* 3: 3126-3136.

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