Electronic Journal of Plant Breeding,
ISSN 0975-928X

DOI:10.5958/0975-928X.2016.00002.8

Yield stability of wheat genotypes for northern western plains zone of India

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(Received: March 2015; Accepted: June 2016)

Abstract

In this investigation 23 genotypes of wheat were tested for stability in 19 locations of North Western plains of the country, Yield data generated from the trials were analysed using AMMI analysis. The distribution of genotype by AMMI revealed that the genotypes 10,13, 20,12,15 and 14 scattered close to the origin, indicating minimal interaction of these genotypes with environments. Studied environments explained 57.2% of the total variation, whereas G and GxE captured 6.2% and 24.3%, respectively. First two principal components (PC1 and PC2) were used to create a 2-dimensional GGE biplot and explained 26.4% and 14.3% of GGE sum of squares (SS), respectively. Environments of Karnal, Ludhiana and Gurdaspur fall in same sector with genotypes 23 & 16. The spearman correlations calculated based on ranks by stability methods varied from positive value 0.97 to negative correlation of 0.759. The cultivar superiority estimate (Pi) maintained negative correlation with other estimates ranking.

Keywords bread wheat, G × E interaction, Bipot analysis, stability

Introduction

Plant breeders pay much attention to understand the relationship between crop performance and environment. Phenotype is an output of genotype (G), environment (E) and their interaction GxE [Eberhart and Russell .1966]. Cross over type genotype environment interaction change genotype ranks in different environments, i.e., different genotypes is better in different environments [Yan and Tinker .2005]. The detection of GxE in multi location trials has led to the development of procedures for stability analyses [Lin et al .1986]. The numerous stability estimates are available to the researchers to deal with interaction effects appropriately. Stability is an important concept for plant breeders interested in analyzing GE data [Becker and Leon .1988].

Many statistical methods have been developed to analyze data from multi environment trials to gain understanding and useful interpretation of GxE interaction, with the ultimate aim of identifying promising cultivars with stability in crop improvement programs. Statistical methods that have recently received attention are pattern analysis [DeLacy et al .1996] and the additive main effects and multiplicative interaction (AMMI) model [Gauch and Zobel .1996]. The AMMI model incorporates both additive and multiplicative components of the two-way structure that can, more effectively, account for the underlying interaction [Shafii and Price.1998].

The extensive usefulness of GGE biplot has been elucidated in recent past [Yan and Kang.2003]. The GGE biplot is a multi-faceted tool in quantitative genetic analyses and plant breeding for GE analysis [Fan et al .2007, Laffont et al .2007].

The objectives of the study were to (1) interpret G main effect and GxE interaction obtained by site regression analysis of yield performances of 23 bread wheat genotypes over 19 environments; (2) application of the GGE biplot technique to examine the possible discrimination of genotypes vis-a-vis environments; (3) visual assessment of yield variation across environments based on the GGE biplot and (4) application of biplot methods to determine discriminating ability and representativeness of the environments.

Materials and Methods

The twenty three genotypes of wheat were planted in research fields in randomized complete block designs with four replications in nineteen locations of North Western Plains zone of country during 2013-14 cropping season. More over the details on the experimental material and environments are given in Table 1. The observations are conducted for important morphological traits further grain yield in all the environments were used for the detailed study. The combined analysis of variance on grain yield was conducted by Genstat 17.1 version software to determine the effect of environment (E), genotype (G) and GxE interaction. Rank correlation coefficients between pairs of stability estimates were computed via SAS 9.3 software. Wricke [1962] proposed the contribution of a genotype to the interaction sum of squares could be used as a measure of its stability and low ecovalence (W^2i) value associated with relative high stability. The environmental variance, S^2x is a stability measure for the static stability concept [Lin et al .1986]. Annicchiarico [2002] suggested a reliable genotype characterized by having consistently high yield across environments. Purchase *et al* [2000] developed the AMMI stability value (ASV) based on the AMMI model's IPC1 and IPC2 scores. The genotypes with the lowest ASV value would be more stable. Superiority index (Pi), determined by utilizing the highest-yielding genotypes within each environment as a reference point. Genotypes with the largest yield difference from the reference genotype will have the highest Pi values [Lin and Binns,1988]. Geometric adaptability index (GAI) was used to evaluate the adaptability of genotypes [Mohammadi and Amri , 2008]. The genotypes with the higher GAI would be desirable. Spearman's rank correlation coefficients were calculated among the ranks given by criterion of stability estimates [Mohammadi et al 2010].

AMMI Stability Value (ASV) =

$$\sqrt{[\frac{SSIPCA1}{SSIPCA2} * IPCA1\ score]^2 + IPCA2\ score^2}$$

where SSIPCA1 and SSIPCA2 are sum of squares by the IPCA1, IPCA2 respectively

Geometric Adaptability Index (GAI) =

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

in which $\bar{X}_1, \bar{X}_2, \bar{X}_3, \ldots \bar{X}_m$ are the mean yields of the first, second and mth genotype across environments and n is number of environments.

Results and Discussion

The ANOVA for grain yield in nineteen different environments is presented in Table 2. There were significant differences ($P<0.01$) among the environments (E), genotypes (G) and G×E interaction as also reported by Asrat et al 2009. Significant E, G and G×E interaction explained 57.2%, 6.2% and 24.3% of the total sum of squares respectively. In the site regression analysis the first and second interaction principal component analysis (IPCA1 and IPC2) explained 6.4% and 4.5% of the G×E variation, respectively.

AMMI analysis

According to the AMMI, the genotypes are characterized as adaptable to all environments by means greater than grand mean and the IPCA score nearly zero. However, the genotype with high mean performance and with large value of IPCA score are consider as having specific adaptability to the environments [Asrat et al. 2009]. The IPC1 accounted for a total of 26.3% of the GE interaction. Genotypes G3 and G6 with mean yields greater than the overall mean and low IPC1 scores had a high combination of yield and stability performances (Figure 1). Genotypes G2 and G4 were similar to G3 and G6 in the main effect but tended to contribute more to GE interaction. The two genotypes G9 and G18, with mean yields less than the overall mean and with the highest distance from the IPC1 tended to contribute highly to GE interaction and accordingly can be regarded as the most unstable genotypes.

The IPCA 1 versus IPCA 2 biplot explains the magnitude of interaction of genotype with environment. Genotypes and environments that fall into the same sector interact positively; for negative values fall into opposite sectors [Mahnaz et al, 2013]. A genotype showing high positive interaction in an environment obviously best suited to that environment. AMMI analysis permits estimation of interaction effect of a genotype in each environment and to identify suited genotypes for specific environmental conditions. Furthermore, Purchase et al. [2000] pointed out that for IPCA1 versus IPCA2 plot the more stable genotypes score lie close to the center of the biplot (Figure 2). The IPCA 1 component accounted for 26.3 % of G×E interaction, while IPCA 2 accounted for only 18.4%. Distribution of genotype revealed that the genotypes, 10, 13, 20, 12, 15 and 14 scattered close to the origin, indicating minimal interaction of these genotypes with environments (Figure 2). The remaining genotypes scattered away from the origin were more sensitive to environmental interactive forces. Interaction of genotypes with specific environmental conditions was judged by projection of genotype points on to environment spokes. On this basis, the genotype 19 in Delhi, 6 in Uchani, 1&11 in Gurdaspur 12 & 3 in Bhatinda, hence exhibited specific adaptation with environments.

GGE analysis

The polygon is created by involving the number of genotypes that are further away from the biplot source such that all other genotypes are restricted in the polygon [Yan et al.2003]. The vertex genotype in each sector is the best genotype at environment whose markers fall into the respective sector [Yan et al, 2007]. Environments within the same sector share the same wining genotype and environments in different sector have different winning genotypes. The perpendicular lines between adjacent genotypes divide the biplot into sectors (Figure 3). An interesting feature of this view of a GGE biplot is that the vertex genotypes for each sector has higher (some time the highest) yield than the others in all environments that fall in the sector. Karnal, Ludhiana, Gurdaspur fall in same sector with genotypes 23 & 16. More over Durgapura and Bhatinda have positions together on other sector with genotypes 1 & 11. Whereas the Faridabad center falls in other sector with genotypes 22, 9 and 2 (Figure 3).

An ideal genotype has the highest mean and be absolutely stable [Yan et al.2003]. Such an ideal genotype is having the greatest vector length of the high-yielding genotypes and with zero GE (or highest stability), as represented by the dot with an arrow pointing to it. An ideal genotype 20 is located at the center of the concentric circles in Figure 4. The ideal genotype is stable because its projection on the ATC y-axis is near zero. Other genotypes closer to ideal genotypes are more favorable. The 14 and 13 were near to the ideal genotype. Ranking of other genotypes based on the ideal genotype was 7 > 2 > 3 > 4. In other words, the lower yielding genotypes 18 & 2 were unfavorable because they are far from the ideal genotype.

Comparison of statistical methods in the ranking of genotypes

The ranks for 23 tested genotypes in 19 environments based on each of the statistical methods mentioned above are given in Table 3. Comparison of the statistical methods based on the ranks showed that the methods generally gave similar results in the ranking of genotypes as reported by Mohammadi *et al*. 2010. For example, the five top-ranked genotypes based on Gm were G20, G12, G13, G16, and G14; based on the ASV were G10 followed by G2, G12, G5, and G15; based on GAI were G20, G12, G13, G16 and G14; and based on the static stability were G10, G2, G5, G14, and G20.

Relationships among the statistical methods

Significant rank correlations were found between ranking of genotypes for stability estimates (Table 4).With respect to yield, the stability estimates were significantly correlated in the ranking of genotypes [Mozaffar et al. 2014]. The correlations varied from positive value 0.97 to negative correlation of 0.759. The cultivar superiority estimate maintained negative correlation with other estimates ranking. Wricke estimate ranking showed direct positive significant correlation between ranks by Gm, ASV and GAI. This indicates that AMMI agreed most closely in ranking genotypes for yield.

Acknowledgements

Authors gratefully acknowledge the support extended by Dr RPS Verma, ICARDA Morocco and Dr Murari Singh, Senior Biometrician, ICARDA Jordan for this study. The multi-environment testing was performed within the All India Coordinated Wheat & Barley Improvement project (AICW&BIP) for the northern western plains zone of the country. The contribution of staff members at the specific centers of AICW&BIP are acknowledged for their hard work to conduct the field trails and data recording for this research.

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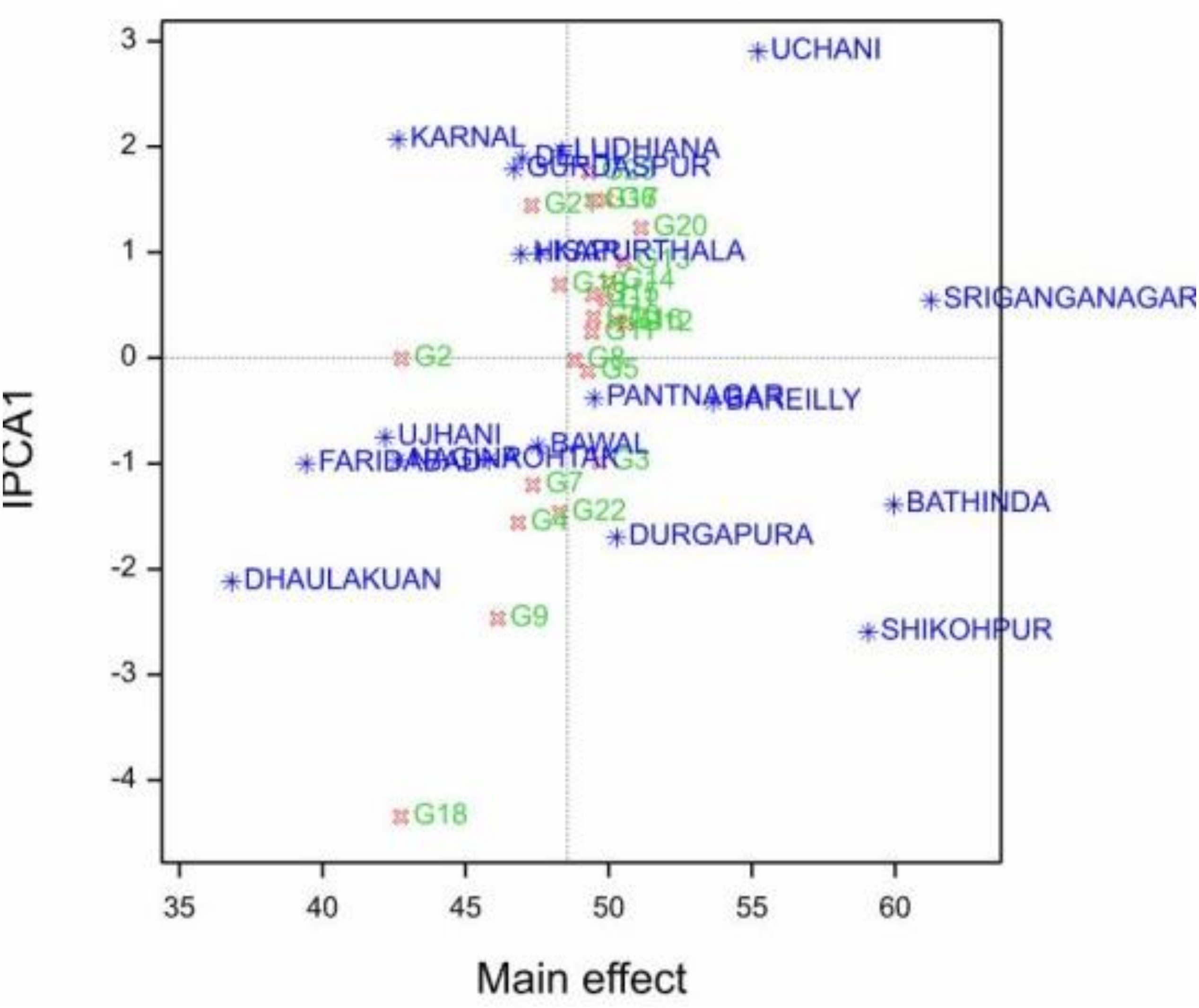
DOI:10.5958/0975-928X.2016.00002.8



Legends for figure

1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.
G 1	G 2	G 3	G 4	G 5	G 6	G 7	G 8	G 9	G 10	G 11	G 12
PBW 697	TL 2995	DBW 88	WH 1156	PBW 681	DBW 95	HD 2967	HD 3128	WH 1157	WH 1138	PBW 677	HD 3132
13.	14.	15.	16.	17.	18.	19.	20.	21.	22.	23.	
G 13	G 14	G 15	G 16	G 17	G 18	G 19	G 20	G 21	G 22	G 23	
WH 1154	PBW 692	DPW 621-50	HD 3086	PBW 698	HD 3133	HUW 675	WH 1105	K 1204	PBW 695	HUW 666	

Fig. 1 AMMI-1 biplot showing IPCA1 versus means

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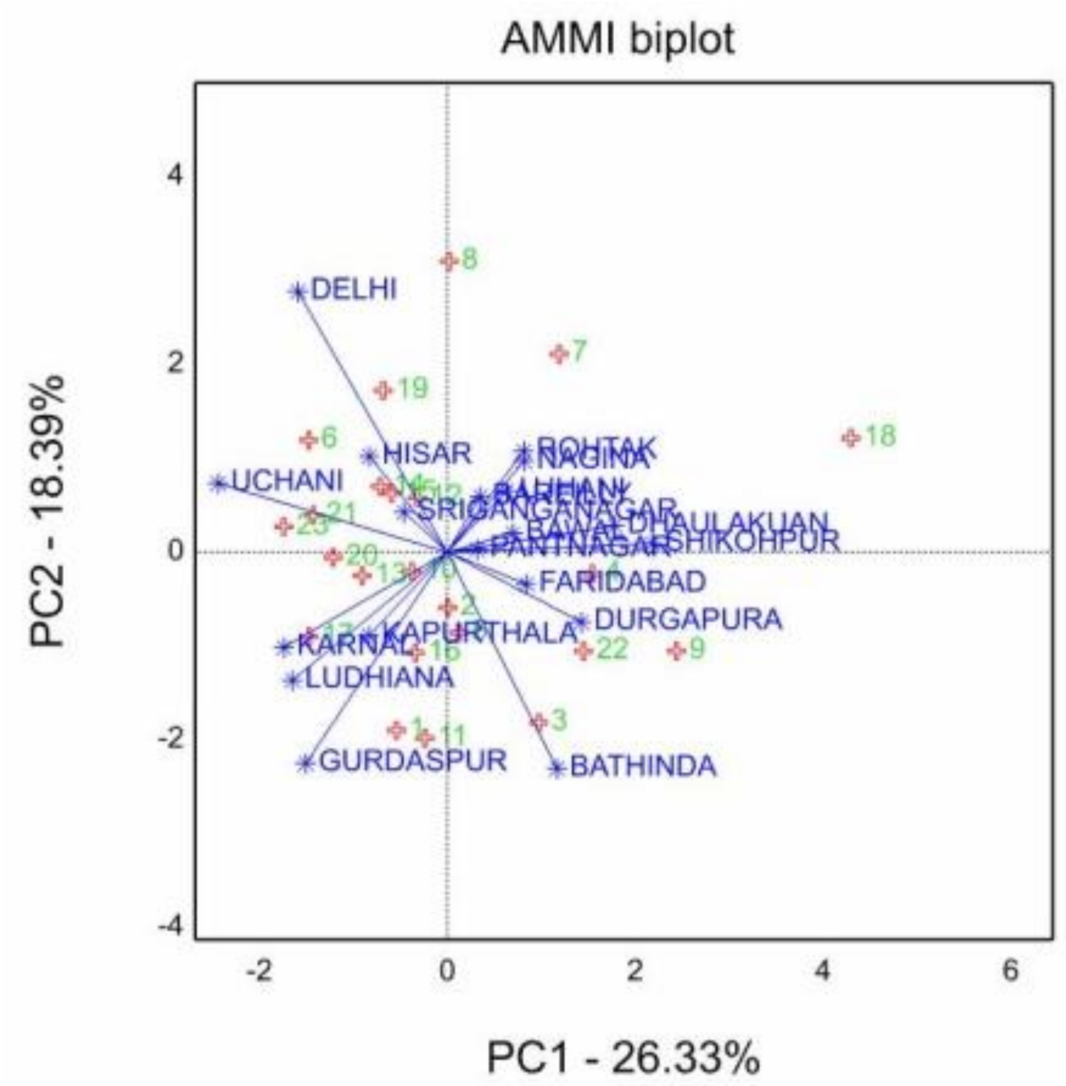

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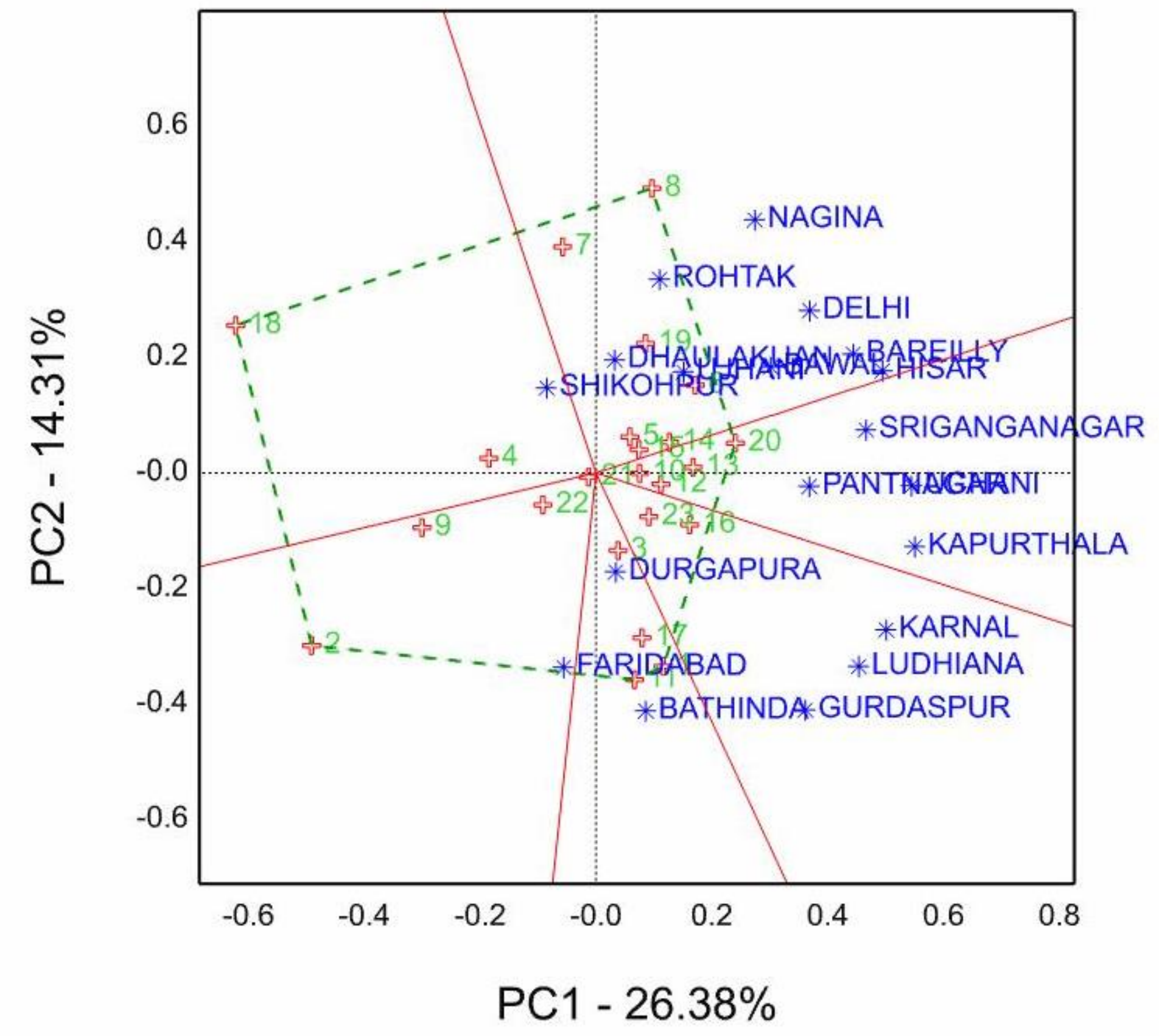
1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.
G 1	G 2	G 3	G 4	G 5	G 6	G 7	G 8	G 9	G 10	G 11	G 12
PBW 697	TL 2995	DBW 88	WH 1156	PBW 681	DBW 95	HD 2967	HD 3128	WH 1157	WH 1138	PBW 677	HD 3132
13.	14.	15.	16.	17.	18.	19.	20.	21.	22.	23.	
G 13	G 14	G 15	G 16	G 17	G 18	G 19	G 20	G 21	G 22	G 23	
WH 1154	PBW 692	DPW 621-50	HD 3086	PBW 698	HD 3133	HUW 675	WH 1105	K 1204	PBW 695	HUW 666	

Fig, 2 : AMMI2 biplot depicts the first two principal axes of interactions



Legends for figure

1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.
G 1 PBW 697	G 2 TL 2995	G 3 DBW 88	G 4 WH 1156	G 5 PBW 681	G 6 DBW 95	G 7 HD 2967	G 8 HD 3128	G 9 WH 1157	G 10 WH 1138	G 11 PBW 677	G 12 HD 3132
13.	14.	15.	16.	17.	18.	19.	20.	21.	22.	23.	
G 13 WH 1154	G 14 PBW 692	G 15 DPW 621-50	G 16 HD 3086	G 17 PBW 698	G 18 HD 3133	G 19 HUW 675	G 20 WH 1105	G 21 K 1204	G 22 PBW 695	G 23 HUW 666	

Fig. 3 GGE polygon view of genotype – environment interaction

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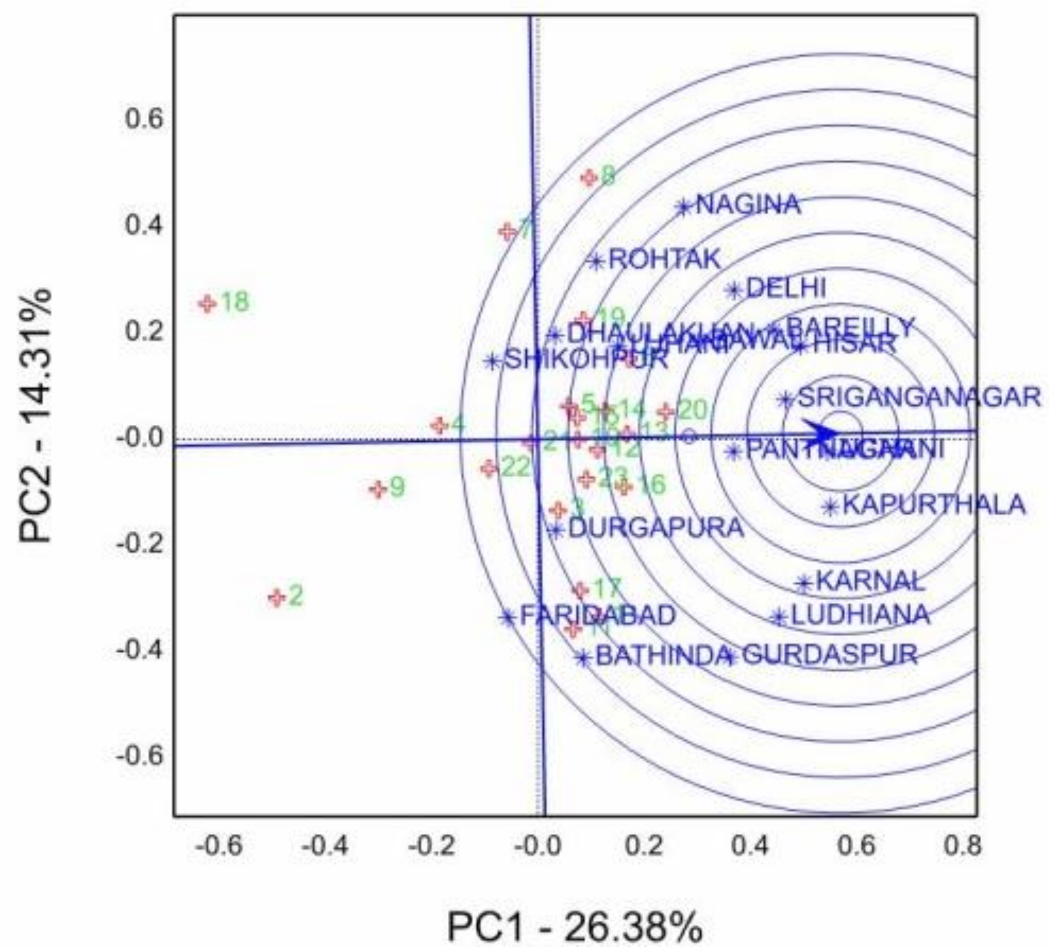

Legends for figure

1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.
G 1 PBW 697	G 2 TL 2995	G 3 DBW 88	G 4 WH 1156	G 5 PBW 681	G 6 DBW 95	G 7 HD 2967	G 8 HD 3128	G 9 WH 1157	G 10 WH 1138	G 11 PBW 677	G 12 HD 3132
13.	14.	15.	16.	17.	18.	19.	20.	21.	22.	23.	
G 13 WH 1154	G 14 PBW 692	G 15 DPW 621-50	G 16 HD 3086	G 17 PBW 698	G 18 HD 3133	G 19 HUW 675	G 20 WH 1105	G 21 K 1204	G 22 PBW 695	G 23 HUW 666	

Fig. 4 Ranking of genotypes relative to ideal genotype

Table 1: Details of genotypes, parentage and environments

	Code	Entry	Parentage	Environments	Latitude	Longitude
1.	G 1	PBW 697	DBW18/3/WL711-AE.OVATA/CS(S)//WL711 NN/4/DBW18	Delhi	28^{o}35’N	77^{o}12’E
2.	G 2	TL 2995	TL2608/JNIT141//JNIT128	Hisar	29º10’N	75º 46’E
3.	G 3	DBW 88	KAUZ// ALTAR84/AOS/3/MILAN/KAUZ/4/H U ITES	Bawal	28^{o}97’47’’N	76^{o}58’92’’E
4.	G 4	WH 1156	TILHI/PASTOR	Rohtak	28^{o}89’90’’N	76^{o}57’96’’E
5.	G 5	PBW 681	UP2338/KALYANSONA	Faridabad	28^{o}40’89’’N	77^{o}31’77’’ E
6.	G 6	DBW 95	K9908/PBW534	Uchani	29^{o} 43' N	76^{o} 58'E
7.	G 7	HD 2967	ALD/CU C//U R E S/H D 21 60M / HD227 8	DWR-Karnal	29^{o}43’N	76^{o}58’E
8.	G 8	HD 3128	VL849/HW5015	Shikohpur	27^{o} 39' N	76^{o} 39'E
9.	G 9	WH 1157	MUNIA/CHTO//AMSEL	Dhaulakuan	30^{o} 04' N	77o 5'E
10.	G 10	WH 1138	PBW65*2/PASTOR	Ludhiana	30^{o}54’ N	75^{o}52’ E
11.	G 11	PBW 677	PFAU/MILAN/5/CHEN/A.SQUARROSA//BCN/3/VEE#7/BOW/4/PASTOR	Bathinda	30^{o}21’99’’N	74^{o}94’54’’ E
12.	G 12	HD 3132	WH542/UP2425	Gurdaspur	32^{0}03’N	75^{0}24’E
13.	G 13	WH 1154	WH337/HD2255//RAJ3077	Kapurthala	31^{o}38’N	75^{o}38’ E
14.	G 14	PBW 692	INQUALAB91*3/TUKURU//DBW1B	Durgapura	26^{o}51’N	75^{o}47’ E
15.	G 15	DPW 621-50	KAUZ// ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES	Sriganganagar	29^{o}66’ N	73^{o}53’ E
16.	G 16	HD 3086	DBW14/HD2733//HUW468	Nagina	29^{o}0 28’N	78^{o} 32’E
17.	G 17	PBW 698	BW9250*3/YR10/6*AVOCET/3/BW9250*3//YR15/6*AVOCET	Bareilly	28^{o}22’N	79^{o}24’ E
18.	G 18	HD 3133	MILAN/S.87230//BABAX	Ujhani	28^{o}32’N	79^{o}51’68’’ E
19.	G 19	HUW 675	ALTAR84/K AUZ// MILAN/HUW510	Pantnagar	29^{o}N	79^{o} 30´E
20.	G 20	WH 1105	MILAN/S87230//BABAX			
21.	G 21	K 1204	K8434/PBW343			
22.	G 22	PBW 695	PSN/BOW//MILAN/3/2*BERKUT			
23.	G 23	HUW 666	HUW206/ALTAR84//VE E/MILAN			

Table 2: Combined analysis of variance for AMMI model

Source	Degree of freedom.	Sum of Squares	Mean Sum of squares	Variance ratio	Probability	% TSS
Treatments	436	116369	266.9	24.33	<0.001	
Genotypes	22	8222	373.7	34.07	<0.001	6.20
Environments	18	75929	4218.3	94.52	<0.001	57.23
Block	57	2544	44.6	4.07	<0.001	
Interactions	396	32218	81.4	7.42	<0.001	24.28
IPCA 1	39	8484	217.5	19.83	<0.001	6.39
IPCA 2	37	5924	160.1	14.60	<0.001	4.47
Residuals	320	17810	55.7	5.07	<0.001	
Error	1254	13754	11.0			
Total	1747	132667	75.9			

%TSS, percentage of total sum of squares

Table 3. Ranking of 23 Genotypes based on Stability estimates

Code	Genotype yield	Rk	ASV	Rk	GAI	Rk	Wricke's ecovalence	Rk	Cultivar superiority	Rk	Static stability	Rk
G1	49.91	6	2.070	12	48.99	8	452.0	19	28.68	15	96.33	22
G2	42.76	22	0.594	2	42.31	22	521.2	22	104.21	1	39.11	2
G3	49.67	8	2.314	15	48.91	9	333.0	12	29.49	13	81.20	21
G4	46.83	20	2.248	14	46.20	20	240.7	7	52.50	4	68.33	15
G5	49.28	14	0.883	4	48.81	10	270.6	10	32.88	9	49.66	3
G6	49.90	7	2.455	18	49.12	7	370.9	16	28.95	14	75.93	20
G7	47.35	18	2.746	20	46.67	18	382.7	17	52.96	3	63.07	10
G8	48.81	15	3.135	21	48.23	15	516.3	21	42.66	7	58.66	7
G9	46.12	21	3.692	22	45.43	21	467.0	20	67.26	2	71.58	18
G10	49.47	9	0.583	1	49.15	6	241.7	8	30.62	12	32.41	1
G11	49.41	11	2.033	11	48.71	14	342.6	14	32.29	10	70.50	17
G12	50.61	2	0.750	3	50.11	2	206.5	4	19.05	21	57.14	6
G13	50.52	3	1.338	8	49.92	3	168.0	2	18.30	22	63.18	11
G14	50.00	5	1.254	7	49.53	5	233.1	5	26.93	16	51.11	4
G15	49.43	10	1.068	5	48.75	12	145.4	1	26.35	17	71.99	19
G16	50.25	4	1.188	6	49.59	4	252.7	9	24.07	19	69.47	16
G17	49.41	11	2.319	16	48.77	11	307.8	11	26.31	18	66.49	14
G18	42.74	23	6.343	23	41.61	23	1072.1	23	22.96	20	104.97	23
G19	48.28	16	2.006	10	47.66	17	337.1	13	41.71	8	64.86	12
G20	51.12	1	1.760	9	50.56	1	240.5	6	18.28	23	56.74	5
G21	47.31	19	2.104	13	46.67	18	197.0	3	43.89	5	61.80	8
G22	48.28	16	2.354	17	47.67	16	407.0	18	42.69	6	65.36	13
G23	49.31	13	2.538	19	48.75	12	348.6	15	31.97	11	62.15	9

Gm-Genotype mean yield, GAI- Geometric Adaptability Index, ASV-AMMI stability value, Rk-Ranks based on criteria

Table 4. Spearman correlation coefficient values among stability estimates

	Gm	ASV	GAI	Wricke's ecovalence	Cultivar superiority	Static stability
Gm	0.000	0.455*	0.977**	0.551*	-0.759**	0.076
ASV		0.000	0.498*	0.583**	-0.254	0.517*
GAI			0.000	0.579**	-0.729**	0.211
Wricke's ecovalence				0.000	-0.444	0.268
Cultivar superiority					0.000	0.154
Static stability						0.000

*& ** significant at P<0.05 and P<0.01