AMMI and GGE biplots for G×E analysis of wheat genotypes under rain fed conditions in central zone of India

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Abstract: The highly significant environments, genotypes and G×E interaction observed by AMMI analysis of 17 wheat genotypes evaluated at 8 locations in the central zone of the country. Environments(E), genotypes -environment interaction(GE) and genotypes explained 68.8%, 17.6% and 3.2% of the total sum of squares respectively. First four interaction principal components accounted 33.7%, 30.2%, 14.6% and 12.6% of the G×E interaction variation, respectively. The highest positive IPCA1 score of genotype G_8 followed by G_{11} and G_{10} supported by yield higher than the grand mean 21.8q/ha. Environments E_4 (Jabalpur) and E_8 (Partapgarh) recorded maximum yield 32.6q/ha and 28.4q/ha while lowest yield was realized in E_1 (Arnej). GGE biplot analysis under polygon view indicated that G_{13} was better in E_6 (Sagar), whereas G_1 was better in E_7 (Bilaspur) and E_8 (Partapgarh). The genotype G_1, at the centre of concentric circles, was the ideal genotype in terms of yield performance as compared to the other genotypes. In addition, G_{15} and G_{12}, located on the next consecutive concentric circle, may be regarded as desirable genotypes.

Keywords: AMMI model, AMMI stability value, GGE biplot, Stability index

INTRODUCTION

Analysis of genotype interaction with locations would be necessary to have information on the stable performance of genotypes (Lin and Binns, 1994). This interaction reduces the association between phenotypic and genotypic values and leads to biased estimates (Freeman, 1990). The importance of interaction in cultivar evaluation and breeding programs has been demonstrated in almost all the major crops (Najafian *et al.,* 2010; Zali *et al.,* 2011). Various statistical methods (parametric and non-parametric), concepts, and definitions of stability have been described over the years by number of researchers (Lin *et al.,* 1986; Becker and Léon, 1988; Crossa *et al.,* 1990; Mohammadi and Amri, 2008; Bose *et al.,* 2014).

Single model cannot provide an accurate picture of stability statistics because of the genotype's multivariate response to varying environments (Lin *et al.,* 1986), whereas stability indices are usually based univariate approaches (Gauch 1992; Crossa *et al.,* 1990). AMMI (additive main effects and multiplicative interaction) analysis is widely used a multivariate technique for interaction investigation (Mohammadi *et al.,* 2010). This method has been found effective as it captures a large portion of the interaction sum of squares; at the same time separates main as well as interaction effects (Farshadfar and Sutka, 2006). The meaningful interpretation of data to support a breeding program such as genotype stability is necessary at multi locations trials

(Gauch and Zobel 1996). The AMMI model has been used extensively in recent past to analyze and interpret genotype × environment interactions and results can be displayed graphically (Crossa *et al.,* 1990; Purchase *et al.,* 2000a).

The Indian wheat programme coordinated by the Indian Institute of Wheat and Barley Research, Karnal, Haryana. The wheat genotypes developed by various research centers for the timely sown (irrigated) and timely sown (rain fed) environments. The seventeen wheat genotypes were evaluated under eight locations representing typical rain fed climatic conditions of the central zone. The study based on AMMI and GGE biplot analysis methods to highlight the G × E interaction in MET trials and stratification of genotypes as per their adaptability for rain fed conditions of the central zone. The major objectives of the study were (i) to identify wheat genotypes with high and stable yield across rain fed environments (ii) to study the relationships, similarities, and dissimilarities among yield-stability statistics.

MATERIALS AND METHODS

The materials comprised of seventeen genotypes G_1 (NIAW 1885),G_2(NIAW 2030),G_3(PBW 689),G_4(WH 1142),G_5(HI 8755),G_6(MP 1279),G_7(K 1215),G_8(K 1217),G_9(CG 1010),G_{10}(MACS 3916),G_{11}(MACS 3927), G_{12}(UAS 451),G_{13}(DDW 30),G_{14}(HI 1500),G_{15} (MP 3288),G_{16}(HI 8627) and G_{17}(A 9-30-1) including advanced breeding lines and released checks of wheat

developed at various centers under All India Coordinated Wheat Improvement Programme (AICW&BIP). Field trials were conducted at eight locations namely Arnej(E_1), Dhandhuka(E_2), Tanchha (E_3), Jabalpur(E_4), Indore(E_5), Sagar(E_6), Bilaspur(E_7) and Pratapgarh(E_8) representing different rain fed conditions of the central zone of the country. More details are given in table 1 for ready reference. The data were recorded for all morphological trails but grain yield (q/ha) were subjected to statistical analysis. The AMMI analysis first fits additive effects for the genotypes and environments by the usual additive ANOVA (Analysis of Variance) procedure and then fits multiplicative effects for G×E (genotype × environment) by principal component analysis (PCA). The AMMI analysis was conducted with the Genstat software 17.1. In addition to the above stability parameters, various yield-stability statistics were also calculated.   The AMMI stability value (ASV) described by Purchase *et al.* (2000a) was calculated as follows:

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

Where, SSIPCA1/SSIPCA2 is the weight given to the IPCA1 value. The higher the IPCA score, either negative or positive, the more specifically adapted a genotype is to certain environments. Lower ASV scores indicate a more stable genotype across environments. This ASV is comparable with the methods used by Shukla, Eberhart and Russell for genotype stability (Purchase *et al.,* 2000b). 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.

Geometric Adaptability Index (GAI) = $\sqrt[n]{\prod_{k=1}^{n} \bar{X}_k}$

in which $\bar{X_1}, \bar{X_2,}\bar{X_3}..........\bar{X}_m$ are the mean yields of the first, second and mth genotype across environments and n is number of environments.

RESULTS AND DISCUSSION

Yield adaptation across environments: Combined ANOVA analysis showed highly significant differences (P< 0.001) of 17 genotypes under rainfed conditions (Table 2). The significant interaction suggests that yield of genotypes varied across rainfed conditions of the central zone. The mean grain yield of studied genotypes varied from 18.57 to 24.1 q/ha under rain locations of the zone. Genotype HI8627 recorded highest grain yield (24.1 q/ha) over all environments and followed by MP1279 and A9-30-1 (Table 3). Jabalpur showed maximum average yield of genotypes followed by Pratapgarh and Tancha though large variation observed among centers as ranged from 12.5 to 32.3 q/ha. Not a single genotypes exhibited superiority over more than one location. This justified the interaction among genotype and environment. The magnitude of the G×E

sum of squares 17.6 was about six times larger than that for genotypes sum of squares 3.2, indicating sizeable differences in genotypic response across environments. This suggests the possible existence of different genotype groups (Mohammadi *et al.,* 2011).

AMMI analysis: Highly significant environments, genotypes and G×E interaction explained 68.8%, 3.2% and 17.6% of the total sum of squares, respectively (Table 2). The first four interaction principal component analysis (IPCA1, IPCA2, IPCA3 and IPCA4) explained 33.7%, 30.2%, 14.6% and 12.6% of the G×E interaction variation, respectively.

Biplot graphical analysis for IPCA 1 against the environment means (Fig. 2) revealed that genotype G_8 had the highest positive IPCA score followed by G_{11} and G_{10}. The grain yield of G_8, G_{10}, G_{11} and G_{15} genotypes is higher than the grand mean. Genotypes G_1, G_6 and G_{17} had high grain yield but negative IPCA 1 score. G_4 had low grain yield and negative IPCA 1 score. The maximum grain yield was recorded in E_4 (Jabalpur) environment followed by E_8 (Pratapgarh) location. The lowest grain yield was recorded in E_1 (Arnej) environment. The highest positive IPCA score was shown by E_6 (Sagar) followed by E_4 (Jabalpur). E_8 (Pratapgarh) had positive interaction with genotypes G_{15}, G_{12} and G_{11} and negative interaction with G_6 and G_{17}. On the contrary, E_2 (Dhandhuka) had highest negative IPCA 1 score and negative interaction with G_{14}, G_3 and G_{16} and positive interaction with G_4. Genotypes G_1 and G_6 had IPCA score near zero and grain yield near to the grand mean and hence, can be considered as stable. Genotypes G_1, G_6 and G_{17} were adapted to E_3 (Tancha) environment, where as genotypes G_9, G_{13}, G_7 were adapted to E_7 (Bilaspur) and E_5 (Indore) locations.

Classification of environments: The AMMI IPCA 1 divided studied 8 environments into four groups: Group I comprised E_6 (Sagar), E_4 (Jabalpur), E_8 (Pratapgarh) with maximum positive IPCA1 value and genotypes had maximum yield over the average value. Group II comprised E_3 (Tancha) with negative IPCA1 score. This environment characterized by maximum rainfall and at minimum height from mean sea level (msl). In group III, E_1 (Arnej) was placed along with E_2 (Dhandhuka) showing negative IPCA1 values with lowest yield. This group was characterized by marginal differences for rainfall and msl values. Last group IV had E_5 (Indore) with E_7 (Bilaspur) as also supported by latitude marks.

The biplot graphical analysis for IPCA 2 (Fig. 2) showed that genotypes G_{12} followed by and G_{15} had the highest positive IPCA 2 score with mean grain yield more than grand mean. Besides, genotypes G_{17}, G_6, and G_8 had positive IPCA 2 score and higher grain yield. Genotypes G_2 and G_{14} had high positive IPCA 2 score and grain yield less than the grand mean. Environments E_8 (Pratapgarh), and E_7 (Bilaspur) had high positive IPCA scores where as E_2 (Dhandhuka)

Table 1. Details of wheat genotypes, parentage and environments.

Code	Geno-types	Parentage	Code	Environ-ments	Latitude	Longitude	Total rainfall (mm)	Mean sea level (m)
G1	NIAW 1885	ALTAR84/A, SQUARROSA/TAUS// OPATA/3/ATTILA	E1	Arnej	21°45' N	71°15' E	280.0	31.8
G2	NIAW 2030	LOK45/NIAW34	E2	Dhandhuka	22°5'N/S	72°05'E/W	348.7	39.78
G3	PBW 689	PBW442/WH576//DWR232	E3	Tanchha	21° N	72° E	978.5	15.64
G4	WH 1142	OEN/Ae.Sq.(TAUS)/ FCT/3/2*WEAVER	E4	Jabalpur	23°90' N	79°58' E	359.2	394
G5	HI 8755	IND92-9/WH899//HD4644//HI498	E5	Indore	22° 37'N	75°50' E	288.2	557
G6	MP 1279	GW322/HW2451	E6	Sagar	24° 27' N	78° 21' E	185.2	530
G7	K 1215	UP2338/CPAN3004	E7	Bilaspur	22° 9' N	82° 12' E	223.5	292.3
G8	K 1217	HUW468/NW2036	E8	Pratapgarh	24°03'16''N	74°77'87'' E		
G9	CG 1010	KYZ0144|KYZ283						
G10	MACS 3916	MACS2846/T.CARTHLICUM						
G11	MACS 3927	MACS2846/NIDW15						
G12	UAS 451	LHNKE/HCN//PATA_2						
G13	DDW 30	DBP01-01/PDW233						
G14	HI 1500	HW 2002*2//STREMPALLI /PNC5						
G15	MP 3288	DOVE/BUC/DL788-2						
G16	HI 8627	HD4672|PDW233						
G17	A 9-30-1	A206/GAZA						

Table 2. AMMI analysis of wheat genotypes over locations.

| Source	Degree of freedom	Sum of squares	Mean sum of squares	Variance ratio	Probability	% TSS	% GxE
Treatments	135	37457	277.5	26.49	<0.001	89.56	
Genotypes	16	1331	83.2	7.94	<0.001	3.18	
Environments	7	28780	4111.5	284.33	<0.001	68.81	
Block	24	347	14.5	1.38	0.1109		
Interactions	112	7345	65.6	6.26	<0.001	17.56	
IPCA 1	22	2477	112.6	10.75	<0.001		33.72
IPCA 2	20	2215	110.8	10.58	<0.001		30.16
IPCA 3	18	1073	59.6	5.69	<0.001		14.61
IPCA 4	16	925	57.8	5.52	<0.001		12.59
Residuals	36	654	18.2	1.74	0.0066		
Error	384	4022	10.5				
Total	543	41825	77.0				
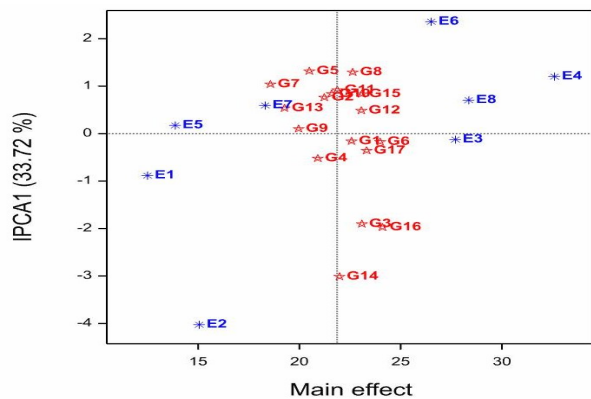
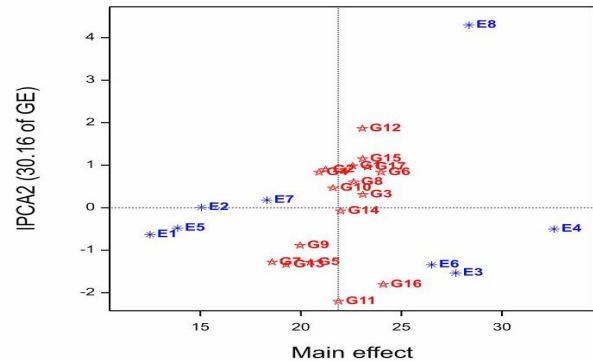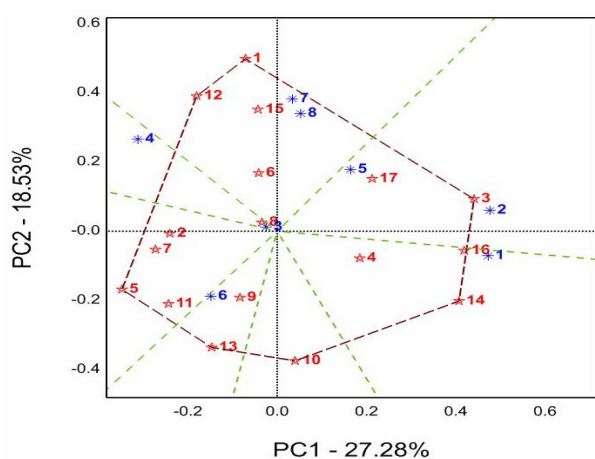**Fig. 1.** *AMMI biplot graph for IPCA 1 and grain yield.*

Fig. 2. *AMMI biplot graph for IPCA 2 and grain yield. Genotypes (G1-G17) are depicted as stars and rain fed environments (E1-E8) are marked as asterisk).*

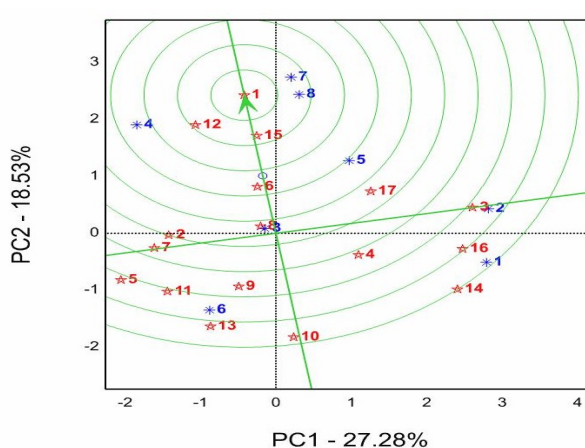**Table 3.** Stability estimates of yield for wheat genotypes tested across 08 environments.

	Arnej	Dhandhuka	Tanchha	Jabalpur	Indore	Sagar	Bilaspur	Pratapgarh	Gm	Rk	GAI	Rk	ASV	Rk
NIAW 1885	1.14	15.73	25.88	**36.42**	16.45	1.25	21.90	31.83	22.58	8	21.16	6	0.998	3
NIAW 2030	1.13	11.60	27.50	34.50	8.81	6.50	17.10	32.70	21.23	12	18.86	13	1.235	7
PBW 689	6.23	23.75	26.33	30.47	15.98	2.88	20.20	28.85	23.09	4	22.51	2	2.155	14
WH 1142	2.64	15.75	24.20	28.15	13.87	3.63	18.78	30.25	20.91	13	19.97	10	1.018	4
HI 8755	8.90	8.45	29.75	34.36	15.46	9.38	14.65	22.98	20.49	14	18.15	15	1.954	13
MP 1279	1.19	19.28	31.63	33.89	13.32	8.88	18.80	34.93	23.99	2	22.17	4	0.855	1
K 1215	1.61	6.30	23.83	33.45	8.20	3.75	**23.18**	18.25	18.57	17	16.23	17	1.73	11
K 1217	2.71	10.83	25.75	32.08	**17.17**	1.63	17.98	32.93	22.64	7	20.91	7	1.567	10
CG 1010	1.34	11.35	30.05	30.86	11.76	3.75	17.68	22.90	19.96	15	18.46	14	0.895	2
MACS 3916	3.88	13.48	23.13	29.39	11.52	4.50	15.43	31.45	21.60	11	19.89	11	1.044	6
MACS 3927	9.85	11.63	**35.13**	33.55	16.38	2.00	15.65	20.78	21.87	10	19.74	12	2.433	15
UAS 451	8.94	12.58	34.25	33.54	13.66	2.25	20.20	**39.05**	23.06	6	20.48	9	1.938	12
DDW 30	2.53	10.45	23.50	33.51	12.86	7.25	14.08	19.95	19.27	16	17.82	16	1.466	8
HI 1500	5.81	**27.38**	29.25	31.64	12.77	**9.50**	12.75	26.75	21.98	9	20.72	8	3.376	17
MP 3288	3.66	13.63	21.63	35.88	15.45	8.63	22.03	33.73	23.08	4	21.61	5	1.48	9
HI 8627	**6.88**	25.75	33.13	31.16	15.73	7.88	20.88	21.38	24.10	1	23.33	1	2.857	16
A 9-30-1	4.16	18.13	26.00	31.25	16.46	7.00	20.10	33.45	23.32	3	22.35	3	1.04	5
Mean	12.51	15.06	27.70	**32.59**	13.87	26.51	18.32	28.36	21.87					

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

Fig. 3. *Polygon view of GGE based on environment scaling.*

Fig. 4. *Ideal genotype by GGE based on genotype scaling. Genotypes (1-17) are depicted as stars and rain fed environments (1-8) are marked as asterisk.*

showed zero IPCA2 value. These environments had positive interaction with most of the genotypes G_{12}, G_{15}, G_{17}, G_6, G_8, G_{10}, G_3 and G_2. Environments E_5 (Indore) and E1 (Arnej) had negative IPCA 2 scores with G_{16}, G_9 and G_7. Genotype G_{14} had near zero value and mean equal to the grand mean where as genotype G_3 had mean grain yield greater than grand mean and hence, may be considered as stable.

Genotype and genotype environment analysis (GGE analysis): GGE biplot based on environment focused scaling, was used to estimate the pattern of environments (Fig. 3). Environment PC1 score had both negative and positive scores indicating a difference in the yield of genotypes across environments leading to cross-over G ×E interactions. The polygon is formed by connecting the markers of the genotypes

that are further away from the origin in a way that all other genotypes are contained in the polygon (Yan and Kang, 2003). Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more locations as the longest distance mapped by them from the origin. The perpendicular lines are equality lines between adjacent genotypes on the polygon, which facilitate visual comparison of them (Yan and Tinker, 2005). For example, the equality line between G_5 and G_{13} indicates that G_{13} was better in E6, whereas G_1 was better in E_7 and E_8. The vertex genotype (s) for each sector has higher (sometimes the highest) yield than the others in all environments that fall in the sector (Gauch *et al.,* 2008; Yan and Hunt, 2001). These eight equality lines divide the biplot into

eight sectors, and the environments fall into five of them (Fig. 3).

A small circle in the center of a biplot indicates the average environment coordinate (AEC) as the average of the environmental PC1 and PC2 scores (Yan and Kang, 2003). The single-arrowed line passing through the small circle and the biplot origin (0, 0) is called the AEC abscissa with its arrow pointing towards the increasing yield. The AEC ordinate (line perpendicular to the AEC abscissa passing through the origin) indicates stability/instability. The genotypes are ranked along the AEC abscissa and their stability is projected as a vertical line from the AEC abscissa.

An ideal genotype should have the highest mean performance and be absolutely stable (that is, performs the best in all environments). Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes and with zero GEI, as represented by an arrow pointing to it (Fig. 4). A genotype is more desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the centre, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype (Yan and Tinker, 2005). The ranking based on the genotype-focused scaling assumes that stability and mean yield are equally important (Farshadfar *et al.,* 2012; Yan and Hunt, 2001). Fig. 4 revealed that G_1, which fell into the centre of concentric circles, was the ideal genotype in terms of higher yielding ability and stability, compared with the rest of the genotypes. In addition, G_{15} and G_{12}, located on the next consecutive concentric circle, may be regarded as desirable genotypes.

Conclusion

The magnitude of the interaction sum of squares was six times larger than that for genotypes sum of squares, indicating sizeable differences in genotypic response across environments. AMMI analysis showed first two principal components accounted for sizeable interactions sum of squares. Few genotypes showed the higher positive IPCA1 score along with the yields higher than the overall grand mean. Genotypes also showed the higher positive IPCA 2 score with yield more than grand mean. The polygon view by GGE biplot indicated that specificity of genotypes to particular environments. The AMMI based indexes and graphical classification of genotypes vis a vis environments proved more suitable for discriminating genotypes among studied environments. More over the graphical interpretation by GGE biplot analysis is more extensive with wider applicability than the conventional statistical methods.

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