

STABILITY AND GENOTYPES \times ENVIRONMENT INTERACTION ANALYSIS USING BIPLOTS IN WHEAT GENOTYPES

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Abstract

Highly significant effects due to environments, genotypes and genotype \times environment interaction were observed during evaluation of 12 wheat genotypes across 17 environments in the central zone in India. The environmental effect explained larger proportion (68.5%) of total variation followed by genotype \times environment interaction effect (15.2%) and marginally by genotype effects (2.5%). Interaction effect partitioned into four significant interaction principal components with respective contributions as 33.7, 18.3, 15.2 and 9.6%, respectively. Biplots based on AMMI analysis identified G3(GW 451), G9 (GW 322), G4(HI 8750) and G11 (HI 8498) as the stable genotypes and E12 (Rewa), E11 (Bhopal), E1 (Anand) and E13 (Sagar) environments contributed largest to interaction effects. GGE biplot analysis pointed out G5 (MP 3382) as ideal genotype followed by G3 (GW 451).

Introduction

Genotype \times environment interaction affects the genotypes performances in different environmental conditions (Becker and Leon 1988). Main task of breeders is to develop genotypes either with general adaptability, or specific adaptability i.e. suitable for particular environments (Ebdon and Gauch 2002a). Large number of methods had been observed in literature to study the stable performance of genotypes over environments (Mohammadi and Amri 2008). Mostly used multivariate methods include principal component analysis (PCA) (Gower 1967), cluster analysis (Mungomery *et al.* 1974) and additive main effects and multiplicative interaction models (AMMI) (Gauch and Zobel 1997).

Recently the differences in genotype performance across environments had been assessed by the graphical biplots based on the significant principal component scores (Vita *et al.* 2010). Genotypes (or environments) with greater IPC scores (either positive or negative) had large interactions and vice versa for small interactions (Gauch 2006). GGE biplot, powerful model, had been observed as an effective for identifying the best-performing cultivar across environments (Yan *et al.* 2007). Stable genotype would show shorter projection on the average environment coordinate (AEC) abscissa, irrespective of direction (Yan and Kang 2003). The present study applied AMMI and GGE biplot methods to stratify the wheat genotypes as per environmental conditions for specific recommendations.

Materials and Methods

Twelve advanced wheat genotypes were grown in 17 environmental locations pertaining to the central zone of the country during the crop season 2013-2014. Genotypes were evaluated in field trials by randomized complete block designs with four replications. Moreover, the details of genotypes and environmental conditions were given in Table 1 for ready reference.

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Well established software Genstat version 17.1 had been utilized for analysis and graphical plots. Further three more parameters to identify stable genotypes were derived from AMMI analysis. AMMI distance statistic coefficient (D) (Zhang *et al.* 1998) was calculated as distance of the interaction principal component (IPC) point from the origin for significant IPCs, and γ_{is} is the score of genotype i in IPC. Genotype with the lowest value of D considered as the stable performer.

$$\text{AMMI distance (D}_i\text{)} = \sqrt{\sum_{s=1}^n \gamma_{is}^2} \quad (i = 1, 2, 3, \dots, n) \quad (\text{i})$$

Purchase *et al.* 2000) developed the AMMI stability value (ASV) based on IPC1 and IPC2 scores of genotypes. The genotypes with the lowest ASV value would be more stable.

$$\text{AMMI stability value (ASV)} = \sqrt{\left[\frac{\text{SSIPCA1}}{\text{SSIPCA2}} \right] (\text{IPCA1 score})^2 + \text{IPCA2 score}^2} \quad (\text{ii})$$

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

Mohammadi and Amri (2008) used geometric adaptability index (GAI) to evaluate the adaptability of genotypes. The genotypes with the higher GAI would be desirable.

$$\text{Geometric adaptability index (GAI)} = \sqrt[n]{\prod_{k=1}^n \bar{X}_k} \quad (\text{iii})$$

where $\bar{X}_1, \bar{X}_2, \bar{X}_3, \dots, \bar{X}_m$ are the mean yields of the respective genotypes.

Results and Discussion

Combined analysis of variance showed environments (E), genotypes (G) and genotype \times environment interaction (G \times E) effects were highly significantly ($p < 0.01$). Environment effects explained 68.4% of the treatments sum of squares (Table 2).

Diversity of environments justified as yield varied from 25.3 at E3 (Bardoli) to 70.2 q/ha at E10 (Powerkheda) (Table 3). Genotype average yield ranged from 47.7 (G12) to 54.3 (G8) (Table 3). G \times E interaction sum of squares was about 7 times as compared to genotypes, indicated sizeable differences in genotypes across environments (Sadeghi *et al.* 2011). The differential ranking of genotypes across environments confirmed crossover type G \times E interaction effects (Table 2). Genotypes G8(HD 4728) and G3(GW 451) were the top yielders at four environments while G5 (MP 3382) at three environments (E9 (Jabalpur), E10 (Powarkheda) and E13 (Sagar)). Genotype G8 (HD 4728) recorded the top yield 75.0 at the highest yielding environment E4 (Banswara).

Further partitioning of G \times E interaction by AMMI analysis revealed four significant principal components scores (Table 2). More than half of G \times E interaction accounted by first two principal components with individual contribution as 33.7 and 18.3%, respectively. This suggested the first and second principal component terms was adequate for cross-validation by graphical biplots.

AMMI1 (IPCA1 vs means) and AMMI2 (IPCA2 vs IPCA1) biplots were generated to illustrate the effects of genotype and environment simultaneously. In Fig. 1, the x-coordinate indicates the main effects (means) and the y-coordinate indicates the effects of the interaction (IPCA1). The horizontal dotted line showed the interaction score of zero and the vertical dotted lines indicated the grand mean yield. Displacement along the vertical axis indicated interaction effects and displacement along the horizontal axis indicated main effects (Ebdon *et al.* 2002a).

Table 1. Details of wheat genotypes, parentage and environmental locations.

Code	Genotypes	Parentage	Code	Environments	Latitude	Longitude
G1	HI 8737	HI8177/HI8158//HI8498	E1	Anand	22° 35' N	72° 55' E
G2	HD 4730	ALTAR84/STINT//SILVER45	E2	Amreli	21°35' N	71°12' E
G3	GW 451	GW324/4/CROC-1/A.SQURRO SA(205)//JUP/BJY/3/./5/GW399	E3	Bardoli	21° 07' N	73° 06' E
G4	HI 8750	HG822/HI8498	E4	Junagarh	21° 31' N	70° 33' E
G5	MP 3382	CHOIX/STAR/3/HE1/3*CNO79/ /2*SERI/4/GW273	E5	SK Nagar	24° 19' N	72° 19' E
G6	HI 8736	HI8416/SARANGPUR LOCAL/HD4672	E6	Vijapur	23°35' N	72°55' E
G7	MACS 6604	WAXWING/4/SNI/TRAP#1/3/K AUZ*2/TRAP//KAUZ	E7	Gwalior	26° 13' N	78° 14' E
G8	HD 4728	ALTAR84/STINT//SILVER_45/ 3/SOMAT_3.1/4/GREEN_ 14//YAV_10/AUK	E8	Indore	22°37'N	75°50' E
G9	GW 322	PBW173/GW196	E9	Jabalpur	23°90' N	79°58' E
G10	HI 1544	HINDI62/BOBWHITE/CPAN20 99	E10	Powarkheda	22° 44'N	77° 42' E
G11	HI 8498	RAJ6070/RAJ911	E11	Bhopal	23°25'99 "N	77°41'26" E
G12	MPO 1215	GW1113/GW1114//HI8381	E12	Rewa	24° 31' N	81° 15' E
			E13	Sagar	24° 27' N	78° 21' E
			E14	Banswara	23°33'N	74°27'E
			E15	Udaipur	24° 34' N	70°42'E
			E16	Bilaspur	22° 9' N	82° 12' E
			E17	Raipur	21°16' N	81°36' E

Table 2. AMMI analysis for 12 wheat genotypes in 17 environments in central zone.

Source	Degree of freedom	Sum of squares	Mean sum of squares	Variance ratio	Probability value	% TSS	% G × E
Treatments	203	88202	434.5	20.93	<0.001		
Genotypes	11	2537	230.6	11.11	<0.001	2.48	
Environments	16	70074	4379.6	89.17	<0.001	68.46	
Block	51	2505	49.1	2.37	<0.001	2.45	
Interactions	176	15592	88.6	4.27	<0.001	15.23	
IPCA 1	26	5252	202.0	9.73	<0.001	5.13	33.68
IPCA 2	24	2858	119.1	5.74	<0.001	2.79	18.33
IPCA 3	22	2371	107.8	5.19	<0.001	2.32	15.21
IPCA 4	20	1492	74.6	3.59	<0.001	1.46	9.57
Residuals	84	3618	43.1	2.07	<0.001		
Error	561	11646	20.8				
Total	815	102353	125.6				

%TSS, percentage of total sum of squares, % G × E, percentage of G × E total sum of squares.

Table 3. Stability estimates and mean yield (q/ha) of wheat genotypes across environments.

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	E13	E14	E15	E16	E17	Gm	D _i	ASV	GAI
G1	48.4	51.6	17.0	59.7	44.4	56.7	46.5	50.0	53.8	68.1	52.4	56.2	39.3	52.5	58.8	43.5	47.5	49.8	2.66	1.159	48.13
G2	47.1	56.2	22.9	54.2	42.8	55.7	55.4	57.0	57.7	77.3	56.1	53.5	37.8	67.5	61.9	49.1	48.9	53.0	3.02	4.466	51.48
G3	52.5	54.5	31.5	59.7	59.9	66.1	49.3	50.5	57.4	72.8	56.8	57.1	38.8	55.0	48.7	52.2	49.4	53.6	2.36	3.006	52.78
G4	42.8	49.4	27.9	54.0	42.3	61.1	57.0	52.2	53.8	75.8	50.1	54.8	40.9	57.5	49.6	46.6	49.0	50.9	2.39	2.122	49.87
G5	51.0	44.1	28.9	52.7	45.6	60.3	45.1	48.2	58.6	79.4	45.8	61.2	45.6	62.5	45.4	47.9	52.6	51.5	3.43	3.089	50.39
G6	48.7	57.4	22.0	61.9	40.3	61.1	42.7	55.2	57.3	65.3	54.0	56.1	37.6	67.5	51.1	44.0	48.9	51.2	2.39	3.100	49.73
G7	55.7	51.5	29.1	58.1	57.0	62.5	47.9	49.9	40.8	64.6	45.5	58.2	43.5	57.5	53.9	44.7	57.5	51.6	3.53	5.986	50.79
G8	50.7	54.1	26.6	63.6	45.9	63.0	56.0	57.6	55.3	68.8	57.5	54.8	38.8	75.0	57.6	45.7	52.9	54.3	3.18	3.204	53.05
G9	56.3	53.6	28.6	57.5	59.8	61.6	49.9	53.9	56.5	58.4	54.6	57.5	43.1	65.0	45.1	43.2	49.5	52.6	3.76	3.723	51.76
G10	56.5	50.2	29.6	53.5	54.0	63.7	43.7	51.0	44.5	72.1	48.0	56.3	38.8	57.5	57.9	50.5	55.4	51.9	3.12	4.383	51.02
G11	43.6	51.5	20.1	56.6	41.2	59.2	44.7	47.7	57.2	64.9	50.2	54.2	45.4	60.0	57.7	49.1	43.0	49.8	2.25	2.488	48.44
G12	34.6	50.5	19.0	52.6	48.0	55.8	38.5	48.3	54.4	74.6	51.1	57.8	39.9	61.8	46.2	37.9	39.5	47.7	3.19	3.139	45.88
Mean	49.0	52.0	25.3	57.0	48.4	60.6	48.1	51.8	53.9	70.2	51.9	56.5	40.8	61.6	52.8	46.2	49.5				

Gm - genotype mean yield, D_i - AMMI distance, ASV-AMMI stability value, GAI - geometric adaptability index.

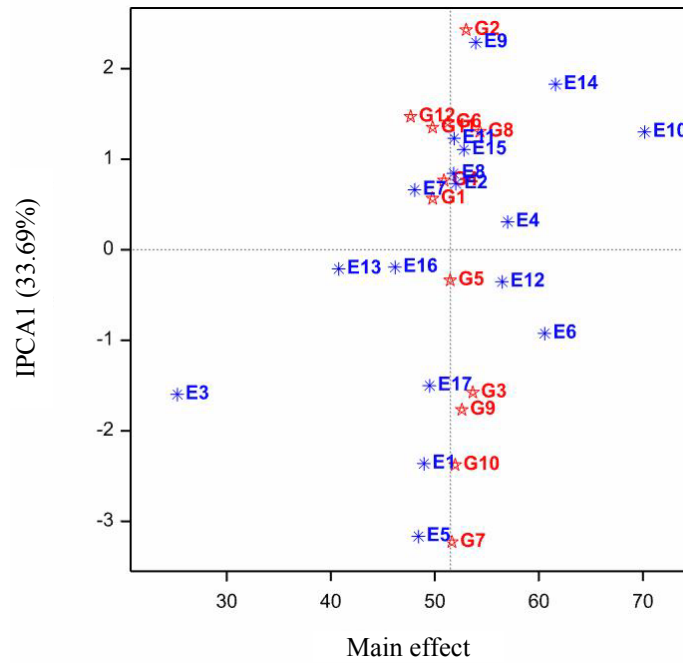


Fig. 1. AMMI-1 biplot of first IPCA scores against genotypes and environmental means.

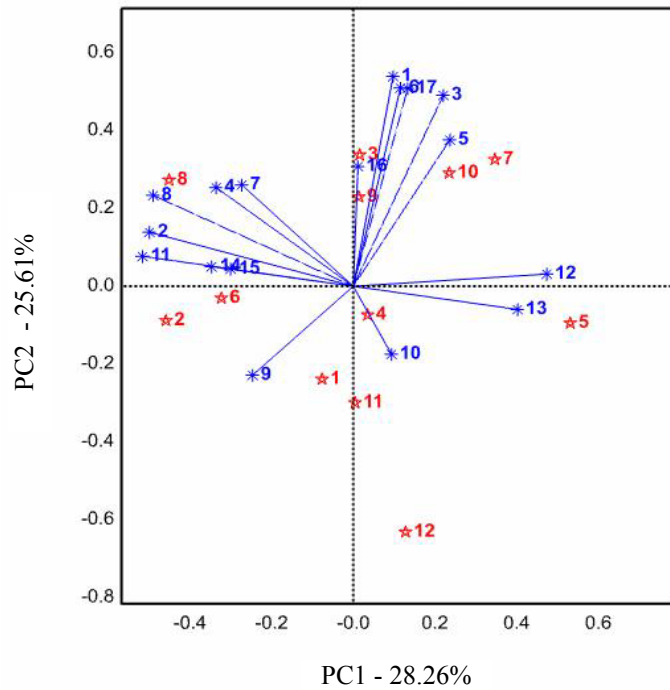


Fig. 2. Biplot depicts the relationship among test environments.

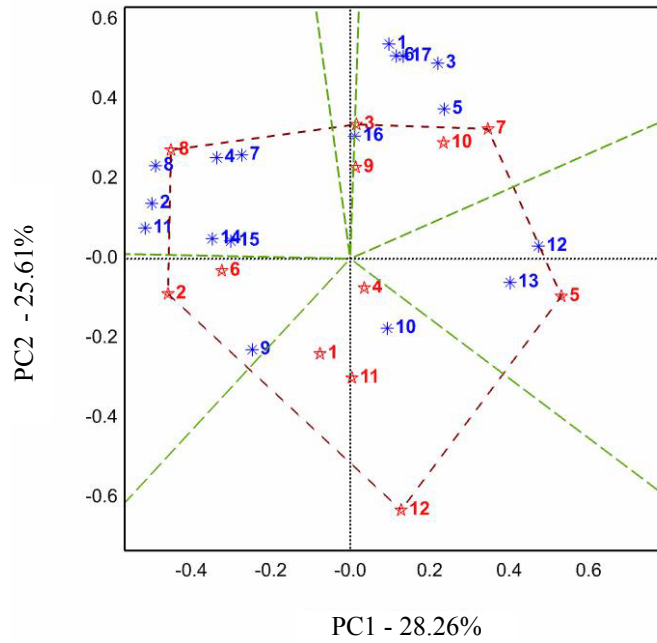


Fig. 3. Polygon view of GGE biplot analysis.

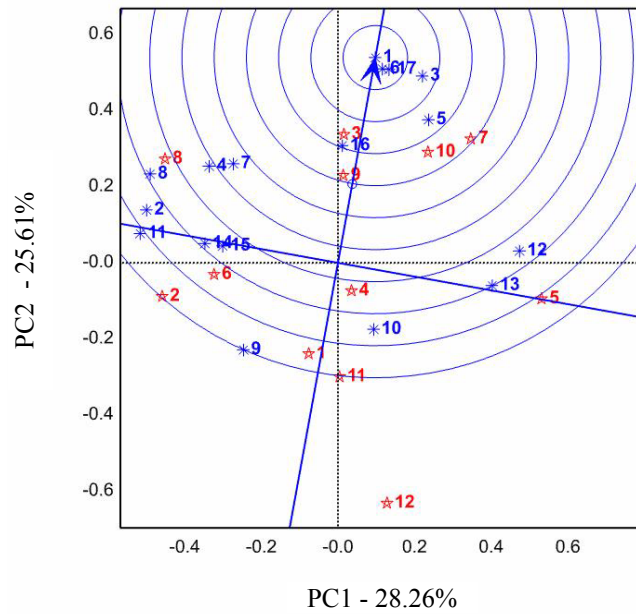


Fig. 4. Evaluation of genotypes relative to an ideal genotype.

Values closer to the origin of the axis (IPCA1) provide a smaller contribution to the interaction effect than in comparison to fur away genotypes. Genotypes G1(HI 8737), G4(HI 8750) and G5 (MP 3382) showed greater stability as lied close to origin. However, averages yields

were on lower sides therefore should not be recommended. While G2 (HD 4730) appeared most unstable, with averages close to the overall average (Ebdon *et al.* 2002b). Genotype G7(MACS 6604) had the lowest yield and stable as compared to G5(MP 3382), widely grown genotypes throughout central zone. Some of the environments stood out with a small contribution to the interaction (E13 (Sagar) and E16 (Bilaspur)); with an intermediate contribution (E4 (Junagarh), and E12 (Rewa)); and with a high contribution (E3 (Bardoli) and E10 (Powarkheda)). Environments E10 (Powarkheda), E14 (Banswara), E6 (Vijapur) and E4 (Junagarh) were recorded yield above the overall average indicated favourable environments to obtain high yields.

Genotypes lied close to the center of the biplot were stable in graph of IPCA1 vs IPCA2 (Purchase *et al.* (2000). G3(GW 451), G9(GW 322), G4(HI 8750) and G11 (HI 8498) were the most stable genotypes; with the genotype G6 (Fig. 2). On the other hand, genotypes G7 (MACS 6604), G5 (MP 3382), and G12(MPO 1215) were the most unstable; i.e. showed specific adaptations, as were distant from the origin. Environment E16 (Bilaspur) was the largest contributor to the phenotypic stability of these genotypes (Fig. 2). E12 (Rewa), E11(Bhopal), E1(Anand), E9 (Jabalpur) and E13 (Sagar) environments contributed mostly to the $G \times E$ interaction.

GGE biplot analysis

Polygon view constructed by joining distant genotypes markers such that all others were placed in the polygon. The perpendicular lines were equality lines between adjacent genotypes depicted on polygon for visual comparison among them (Yan and Tinker 2006). These lines divided polygon into six sectors. Distances from the origin exhibited amount of interaction by genotypes either over environments or by environments over genotypes (Yan and Kang 2003). Genotypes G12(MPO 1215), G5(MP 3382), G7(MACS 6604), G3(GW 451), G8(HD 4728) and G2(HD 4730) expressed interaction on higher side (positively or negatively), whereas E16 (Bilaspur) showed low interaction. Extreme genotypes, G3(GW 451) and G7 (MACS 6604) were located in pairs indicating their similar response pattern. Genotypes at vertex were the winners in the locations included in that sector (Yan and Tinker 2006). Six sectors were observed and G5(MP 3382) clustered with environments E12 (Rewa) and E13 (Sagar) indicated repeatable performance of the genotype. G9(GW 322) was relatively closer to biplot origin and could be good enough for E16 (Bilaspur) location with average adaptation.

An ideal genotype characterized by highest yield along with large stable value (Yan and Kang 2003). GGE biplot defined such a genotype with the greatest vector length of high-yielding and with zero $G \times E$ (or highest stable), as represented by the dot with an arrow as displaced in Fig. 4 (Yan *et al.* 2007). Ideal genotype G9(GW 322) was stable as its projection on the ATC was near to zero. Other favorable genotypes placed close to the ideal genotype. G3(GW 451) was observed near to the ideal genotype. Relative ranking of other genotypes was G10(HI 1544) > G7(MACS 6604). Lower yielding genotypes (G11(HI 8498), G12(MPO 1215), G5(MP 3382)) were seen far from the ideal genotype.

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