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GGE BIPLOT ANALYSIS OF ADVANCED BREAD WHEAT LINES ACROSS DIFFERENT SITES OF PAKISTAN

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Abstract

Ten advance bread wheat lines along with local check were evaluated at seven diverse sites. The environment accounted for 79% of total sum of squares while GxE interaction variance was found 8% and for genotypes 2%. Cluster analysis showed that genotypes and environments could be separated into 5 and 4 respectively of different response pattern across environments and across genotypes. The genotypes NR-310 and NR-314 were different from the remaining genotypes in their response across the environments. The genotypes NR-305 and NR-306, being in the bottom right quadrant, gave the highest average yield and were defined as widely adapted for the sites. This study provides valuable information about the performance of elite wheat lines at different sites of the country to be considered potential breeding material.

Introduction

Information in respect of sustainable and sound performance is required for selection of wheat (*Triticum aestivum* L.) genotypes to be advanced for further study. That information is typically generated through a series of test designed to sample the target environments and to predict genotype performance in those environments (Cooper *et al.*, 1993, Johnson, 2004; Roozeboom *et al.*, 2004; Nelson *et al.*, 2005). Efficient testing of genotypes in breeding programs requires a set of complementary location that adequately sample environments with minimum duplication (Hamblin *et al.*, 1980). Only one test would be needed if genotypes performed similarly in all environments. However, genotypic and environmental differences often exist for the same set of genotypes when tested over a range of environments (Hill, 1975; Delacy *et al.*, 1990).

The highly variable wheat growing environments provide ample opportunity for differentiation of target environments and manifestation of genotype environment interactions. The multiplication trials used in plant breeding are subject two main sources of variation genotypes, location and their interaction (Petersen, 1994). When G x E interactions are predictable, they can be exploited by targeting specific genotypes to appropriate sub regions (Cross *et al.*, 2002). The GGE biplots used by Yan *et al.*, (2000) and Yan & Rajan (2002) demonstrated the ability of biplots to display the essential features of a two-way data set. Kempton (1984) applied biplots to the analysis and interpretation of multiplication data. Biplots of GGE facilitate the rapid identification of groups of locations with minimal crossover interactions particularly with the same highest yielding genotype (Yan *et al.*, 2003, Rubio *et al.*, 2004; Ihsan *et al.*, 2007).

Improving the prediction of genotype performance requires a thorough understanding of the interaction between genotype and location as well as objective approach for grouping test locations to maximize their effectiveness. Indemnification of homogenous sub groups should facilitate identification of genotypes for a wide range of growing environments. The current objective was to estimate the relative contribution of genotype and location to yield variability in wheat performance tests conducted in variable environments, and also to identify the area specific lines and study the pattern of G x E interaction for grain yield.

Materials and Methods

The experimental material comprised of 10 advance lines of wheat with local check (Table 1). The study was conducted during 2006-07 at seven sites of Pakistan viz., NARC (Islamabad), AARI (Faisalabad), RARI (Bahawalpur), BARI, (ChakwaI), CCRI (Pirsabak), NIFA, (Peshawar) and ARI, (Quetta) using randomized block design with three replications to identify the area specific lines and to study the pattern of G x E interaction for grain yield. The experimental plots consisted of six rows of five-meter length and inter row spacing of 0.30 m at each site. Similar cultural practices were followed across all the sites. At maturity, data for grain yield were determined by manual harvesting/threshing taking four central rows ($5m^2$ net plot) of each plot in each trial discarding the border ones.

Data for grain yield per plot was converted to kg/ha and analyzed for analysis of variance to examine the partitioning of sum of squares to G, E and GxE interaction. For classification, a hierarchical agglomerative clustering method (Williams, 1976) with incremental sum of squares (Ward, 1963) as the fusion criteria was applied to the matrices of all the studied attributes. Dendogram was constructed on the basis of fusion level to investigate similarities in pattern of performance among genotypes and environments. GGE biplot techniques developed by Gabriel (1971) were used to make possible the display in a single graph of the performance of each genotype at each environment for grain yield. In graphic display each genotype is presented by point, called marker, defined by genotype's scores on all PCs, and each environment is presented by vector defined by environment's scores on all PCs. The primary and secondary effects of genotypes and environments were calculated according to the shifted multiplicative model to search for separability in crop cultivars (Cornelius *et al.*, 1992) GGE Biplot can be multidimensional, two dimensional biplots using only the first and second PCs are most common, both for biological reason as well as for easy comprehension.

Results and Discussion

Analysis of variance indicated that differences among genotypes, locations and genotypes x environments were highly significant (Table 2). The partitioning of the sum of squares indicated that environment accounted for 79% of the total sum of squares. GxE interaction variance was found 8% and for genotype 2% of the total sum of squares (Table 2).

Ward's fusion strategy of hierarchical clustering was used on G x E data of yield (kg ha^{-1}). Cluster analysis showed that genotypes (10) and environments (7) could be separated into 5 and 4 groups respectively for response pattern across the environments and across genotypes (Tables 3 & 4). It clearly indicated that genotypes NR-310 and NR-314 are different from the remaining genotypes in their response over the environments in this study. Also group clusters labeled as five groups (I, II, III, IV and V) has significant different response in terms of grain yield over all seven environments. While within group-III comprising of four lines viz., NR-317, NR-318, NR-319 and local check produced grain yield kg ha^{-1} in same pattern (Fig. 1). As regards the cluster analysis of environments E1 (Islamabad), E4 (Chakwal) and E4 (Peshawar) are grouped in a same group and considered as one mega environment (group-I). Similarly environment clusters has four groups (I, II, III, and IV), which are different to each other. Group-III contains two environments viz: Bhawalpur and Quetta and are similar response to each other. Faisalabad and Pirsabak fall in separate groups and considered as different to each other (Fig. 2).

Table 1. Advance wheat lines evaluated at seven sites of Pakistan during 2007-08.

Entry#	Parentage	Pedigree	Source
G1	PFAU/WEAVER*2//KIRITATI	CGSS01B00076T-099Y-099M-099B-40Y-0B-0ID	NR-301
G2	WBLL4/KUKUNA//WBLL1	CGSS00B00175T-099TOPY-099M-099Y-099M-099M-16Y-0B-0ID	NR-305
G3	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HU	CMSS97M03912T-040Y-020Y-030M-020Y-040M-4Y-2M-0Y-0ID	NR-306
G4	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR	CMSS98Y01814M-040M-0100M-040Y-040M-030Y-20M-2Y-0M-0ID	NR-310
G5	PBW65/2*PASTOR	CGSS97Y00036M-099TOPB-067Y-099M-099Y-099B-5Y-0B-0ID	NR-314
G6	CMH82A.1294/2*KAUZ//BAV92/3/PASTOR	CMSS97Y05714T-040M-3Y-010M-010Y-010M-3Y-2M-0Y	NR-317
G7	KAMERESTI/LOCAL WHITE//INQ 91	NRBW98069-0K-050ID-0K-050ID-12ID-0ID	NR-318
G8	MGR/SUJATA	CMSS99M00952S-0ID-030ID-0K-050ID-1ID-0ID	NR-319
G9	MGR/SUJATA	CMSS99M00952S-0ID-030ID-0K-050ID-11ID-0ID	NR-320
G10	Local Check	GA 2002	Local check

Table 2. Analyses of variance for grain yield of advance lines grown in seven different environments of Pakistan.

Source	df	Sum of squares	F-value	% of total sum of squares
Location	6	295042553.8	74.93**	79
Error1	14	9187410		2
Genotypes	9	7701410.5	3.94**	2
Genotypes x Environments	54	32971980.6	2.81**	8
Error2	126	27338229.7		7
Total	**209**	**372241584.7**		

Table 3. The groups of genotypes having similar response pattern over all the environments for yield (kg ha^{-1}).

Groups	No.	Group members
I	2	NR-301and NR-320
II	2	NR-305 and NR-306
III	4	NR-317, NR-318, NR-319 and Local check
IV	1	NR-310
V	1	NR-314

Table 4. The groups of similar environments over all genotypes for yield (kg ha^{-1}).

Groups	No.	Group members
I	3	E1 (Islamabad), E3 (Chakwal) and E5 (Peshawar)
II	1	E4 (Faisalabad)
III	2	E6 (Bhawalpur) and E7 (Quetta)
IV	1	E2 (Pirsabak)

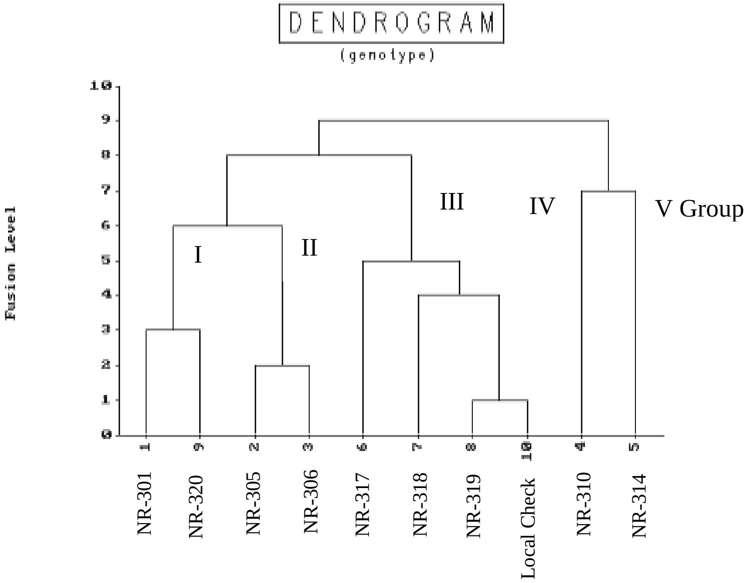

Fig. 1. Dendogram for the classification of 10 advance lines tested in seven environments on the basis of grain yield kgha^{-1}.

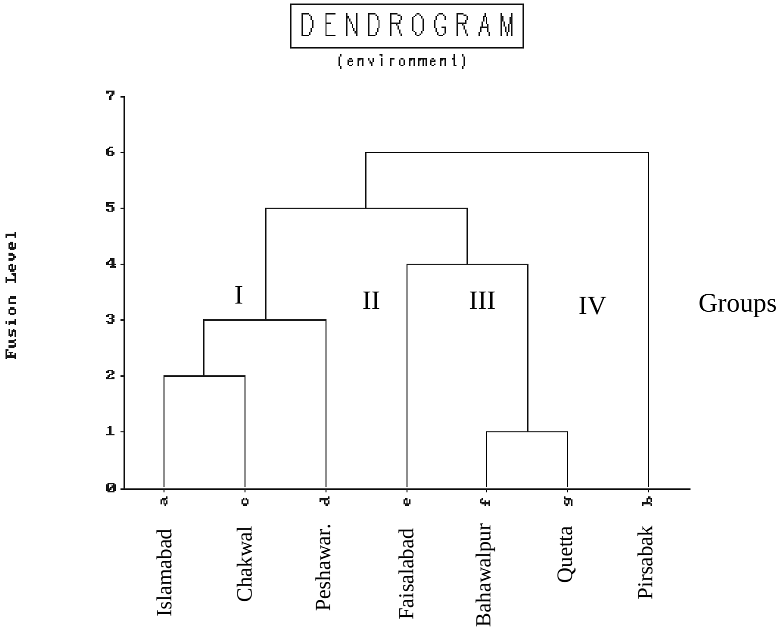

Fig. 2. Dendogram for the classification of seven environments on the basis of grain yield kgha^{-1}.

Performance plots are used to illustrate each genotype group performance in a series of environment groups based on cluster analysis (Fig. 3). Genotype NR-301 showed average performance at all seven environments, whereas, NR-320 shows good to poor performance. Genotype NR-305 and NR-306 showed good performance at three environments Islamabad, Chakwal and Peshawar. Genotype NR-310 and NR-314 was unstable showing good and bad performance.

The coordination analysis is presented in biplot (Fig. 4). The GGE biplot is constructed by plotting the primary effect scores of each genotype and each environment against their respective secondary scores. Biplot can be used to evaluate specific cultivars at specific environments; the environment centered the yield approximated by the product of the genotypic PC1 score by the environment PC1 score, plus the product of the genotypic PC2 score by the environment PC2 score. Geometrically, this is the length of the environment vector (the absolute distance from the plot origin to the marker of the environment multiplied by the length of the genotype distance (the absolute distance from the plot origin to the marker of the genotypes) and by the cosine of the angle between them (Kroonenberg, 1995). This property allows the following information to be visualized (i) the similarity and difference among the environment in their differentiation of the genotypes. (ii) The similarity and difference among the genotypes in their response to the environments and (iii) the nature (positive vs. negative) and magnitude of the interaction between any genotypes.

Therefore, simply the length of their projections can compare the relative yield of the genotype. In the Fig. 4, numbers are representing genotypes and vectors generating from the origin for environments. The genotype G5 (NR-314) had the highest grain yield closer to one mega environment comprising of three vector environments E1 (Islamabad, E4 (Peshawar) and E3 (Chakwal) followed by genotype G3 (NR-306). The genotypes NR-310, NR-317, and NR-318 produced grain yield above average, as has positive magnitude of interaction. Entries that are closer together are similar in performance across environments while adjacent environments are similar in the way they discriminate among genotypes. High yielding and stable genotypes (NR-320 and local check) usually tended to be on the bottom right quadrant of the joint plot.

The genotypes NR-305 and NR-306 being in the bottom right quadrant (Fig. 4) gave the highest average yield and were defined as widely adapted over the sites as described by Vega *et al*., (2001). Genotype NR-310 having a large distance from origin has a large genotype and plus interaction effect. Entries NR-318 and NR-319 had the yield, which were below the average and were highly unstable. Genotype NR-314 gave higher grain yield than average but was not very stable due to its large secondary effects as is evident from Fig.4.

The maximum angle among the vectors of these environments is less than $90^{0.}$ This suggested that these environments were similar in the manner that they discriminate among genotypes as reported by Kroonenberg (1995). These environments had large primary effects and would thus facilitate identification of genotypes with better general adaptation. Therefore from the perspective of selection for high yielding and stable genotypes as is evident from the finding of Yan *et al*., (2001), the best environments should have large primary effect scores but near zero secondary effects. So in the above mentioned environments, E1 (Islamabad), E4 (Chakwal) and E6 (Peshawar) can be termed best for selecting varieties. Environment E2 (Pirsabak) have angle above 180^0 suggesting that it had large interactions with genotypes as reported by de la Vega (2001).

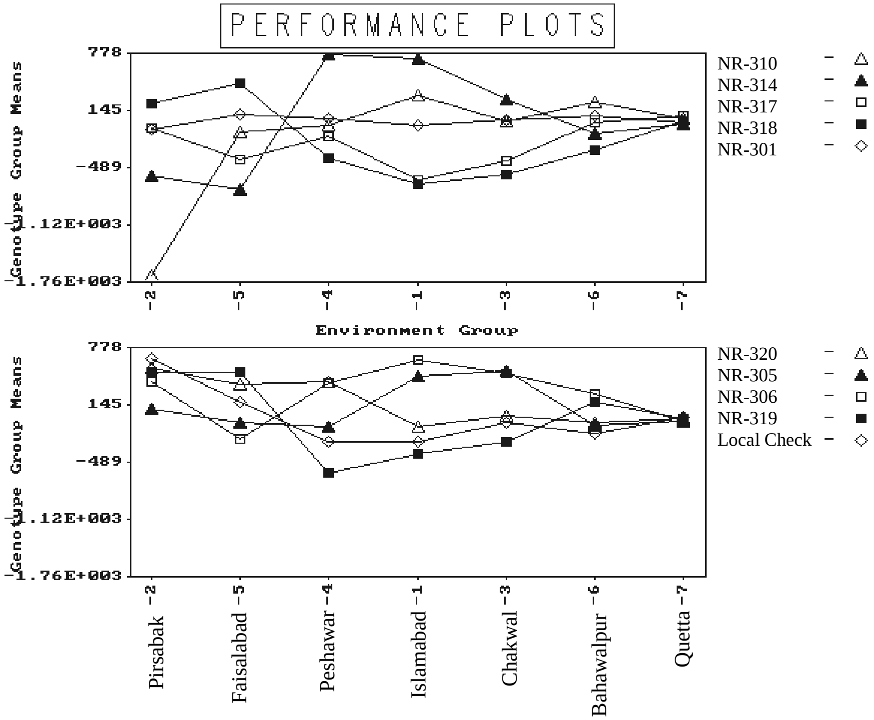

Fig. 3. Performance plots of genotype groups vs. environment groups

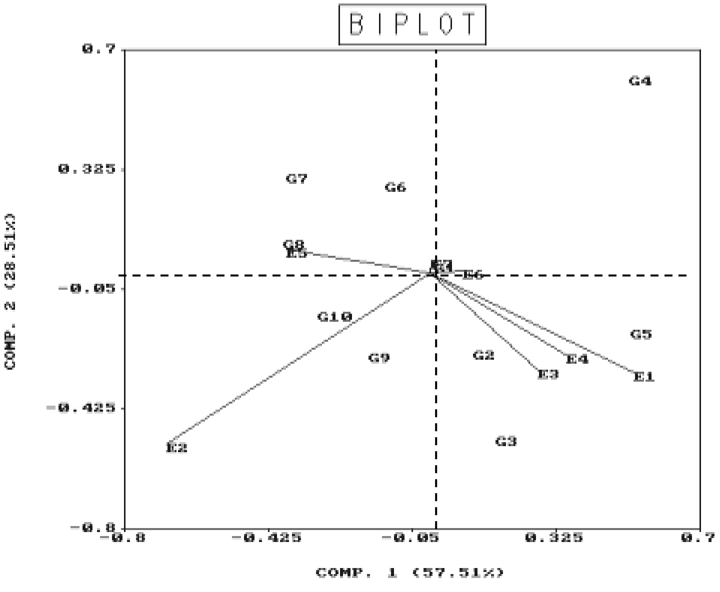

Fig. 4. Biplot of the 1st and 2nd principal components of ten advance lines tested in seven environments. Genotypes are represented by numbers and environment by vectors.

Conclusions

It may be concluded from the research study that response of NR-310 and NR-314 was different from the rest of genotypes over the seven locations. The genotypes NR-305 and NR-306 gave highest average grain yield as compare to other genotypes. So these genotypes are widely adapted over the set of locations/environments and can be used as source of genetic variability in the future wheat breeding program. In terms of environments, Islamabad, Chakwal and Peshawar seemed to be the best for selecting desirable genotypes.

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