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AMMI ANALYSIS FOR STABILITY, ADAPTABILITY AND GE INTERACTION STUDIES IN COTTON (*GOSSYPIUM HIRSUTUM* L.)

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ABSTRACT

The present study was conducted to determine the yield stability, adaptability and to analyze the GE interaction of 9 cotton genotypes using a randomized complete block design (RCBD) with three replications at six locations in Punjab, Pakistan during the growing season of 2010 and 2011 (twelve environments). Additive main effects and multiplicative interactions (AMMI) analysis revealed that the major contributions to treatment sum of squares were environments (38.51%), GE (35.27%) and genotypes (26.22%), respectively, suggesting that the seed cotton yield of genotypes were under the major environmental effects of GE interactions. The first two principal component axes (PCA 1 and 2) cumulatively contributed to 64.34% of the total GE interaction and were significant ($p \leq 0.01$). The biplot technique was used to identify appropriate genotype to special locations / environments. Results showed that genotypes BH-172, MNH-814 and NIAB-2009 with the lowest interaction, and genotypes FH-4243, FH-113, CIM-496, CIM-573, VH-289 and MNH-886 with the highest interaction were the most stable and unstable genotypes, respectively. Moreover, genotypes NIAB-2009, MNH-814, VH-289, MNH-886, CIM-573 and BH-172 were more suitable for Sahiwal, Vehari and Bahawalpur conditions while genotypes FH-4243, FH-113 and CIM-496 were better suited for Faisalabad conditions.

Key words: AMMI, biplot, stability analysis, GE interaction, seed cotton yield.

INTRODUCTION

Upland cotton (*Gossypium* spp.) is the primary source of natural fiber worldwide. In Pakistan, it is an important cash crop and lifeline of the textile industry. Millions of farmers are directly associated with cultivation and harvesting of cotton crop and sale of lint. Many others are indirectly linked with cotton value chain. Cotton production in Pakistan is low when compared to many other cotton producing countries. The world cotton productivity is 759 kg lint/ha compared to Pakistan's average of 707 kg lint/ha.

Sustainable cotton production requires identification and cultivation of stable cultivars. Several methods of estimating phenotypic stability across environments by determining GE interaction effects are available (Eberhart and Russel, 1966; Crossa, 1990; and Gauch, 1992). Cotton genotypes have been evaluated by many scientists for GE interaction effects for seed cotton yield and CLCuV resistance (Naveed *et al.*, 2006, Naveed *et al.*, 2007 a and b, Khan *et al.*, 2008 a and b). Among the various statistical procedures developed for the study of GE interaction, AMMI model has been revealed to be efficient because it captures a large portion of the GE sum of squares and austerely separates main and interaction effects that present agricultural researchers with different kinds of opportunities, and this model often provides agronomically meaningful interpretation of the data (Ebdon and Gauch, 2002). The results of AMMI analysis are useful in supporting breeding program decisions such as specific adaptations to target (tolerances to disease, heat and drought, cold) and selection of environments or test site locations (Gauch and Zobel, 1997).

The objectives of this study were (i) To identify stable genotypes by determining GE interaction effects obtained by AMMI analysis of seed cotton yield over twelve environments, (ii) To visually assess how to vary yield performances across environments based on the biplot (iii) To determine genotypes with high yields, depending on the differential genotypic responses to environments.

MATERIALS AND METHODS

Plant Material and Site Characteristics: A total of nine genotypes were evaluated at twelve environments (Table-1) for this study carried out during the cropping seasons 2010 and 2011. The genotypes comprised FH-113, BH-172, VH-289, CIM-573, MNH-814, MNH-886, FH-4243, NIAB-2009 and CIM-496.

Experimental Design, Plot Size and Cultural Practices: Layout of all the experiments was randomized complete block design (RCBD) with three replications. For each entry, plot size measured 4.572 m × 6.096 m, comprising six rows set 75 cm apart. Distance between plants within rows was 30 cm. Normal agronomic and cultural practices (irrigation, weeding, hoeing, and fertilizer applications) were adopted as and when required. However, none of plants were sprayed against sucking insects especially white fly.

CLCuV Disease Incidence (%) Methodology: CLCuV disease incidence (%) and reaction of the cultivars was determined using the disease scale (Table 1) described by Akhtar and Khan (2002), Akhtar *et al*. 2010 and Farooq *et al*. 2011. Then %age of CLCuV disease incidence was calculated by using the following formula;

$$\text{CLCuV incidence (\%)} = \frac{\text{Sum of all disease ratings}}{\text{total number of plants}} \times 16.16$$

Seed cotton was picked when the crop was mature and recorded as Kg / plot and extrapolated in Kg / hectare.

Statistical Analysis: Yield data of 9 cotton genotypes were subjected to analysis of variance (ANOVA) using the Mstatc package (Russell, D. Freed, Michigan State University, USA). Where the "F" statistics indicated significance, the means were separated using Fisher's protected Least Significance Difference test (LSD) at P = 0.05. To determine the effects of genotype × environment interaction on yields, the data were subjected to Additive Main effects and Multiplicative Interaction (AMMI) analysis using IRRISTAT (10) Version 4.4 computer package. The biplot was drawn by placing the overall mean on the X-axis and respective score (IPCA) on Y-axis. To assess fitting AMMI model, predictive and postdictive approaches offered by Zobel *et al*. (1988) were applied to the data analysis.

The AMMI model is:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \epsilon_{ger}$$

where Y_{ger}= yield of genotype g in environment e for replicate r; μ = grand mean; α_g = mean deviation of the genotype g (genotype mean minus grand mean); and β_e = mean deviation of environmental mean; λ_n = the singular value for IPCA axis n; γ_{gn} = the genotype g eigenvector value for IPCA axis n; δ_{en} = the environment e eigenvector value for IPCA axis n; ρ_{ge} = the residual; and ϵ_{ger} = the error.

Furthermore, AMMI's stability value (ASV) was calculated in order to rank genotypes in terms of stability using the formula suggested by Purchase (1997) as shown below:

$$\text{ASV} = \sqrt{\left[\frac{\text{SS IPCA 1}}{\text{SS IPCA 2}}(\text{IPCA score 1})\right]^2 + [\text{ IPCA score 2}]^2}$$

Where: SS = Sum of squares;
IPCA1 = interaction principal component analysis axis 1;
IPCA2 = interaction principal component analysis axis 2

In general, an absolute AMMI stability value (ASV) was determined using a procedure that combines IPCA1 and IPCA2. NCSS 2000 software (Hintze, 1998) was used in estimating their association. In addition to these, the AMMI adjusted mean seed cotton yield (kg / ha) for each genotype was estimated from untransformed (original) data to demonstrate mean performance.

RESULTS AND DISCUSSION

Genotype × environment interactions (GEI) are of leading concern to plant breeders for developing improved cultivars. For a cultivar to be commercially successful must perform well across the range of environments in which allowed to grow. The presence of GE interactions reduces the correlation between phenotype and genotype, and makes it difficult to judge the genetic potential of a genotype (Sharma *et al*., 1987). Moreover, the stability of a cultivar refers to its consistency in performance across environments and is affected by the presence of GE interactions. In the presence of significant GE interactions, stability parameters are estimated to determine the superiority of individual genotypes across the range of environments.

AMMI ANOVA: The AMMI analysis of variance for seed cotton yield (kg ha^{-1}) of the 9 cotton genotypes tested across 12 environments is presented in Table 3. The AMMI model revealed the presence of significant differences between environments that accounted for 38.51% of the treatment SS. The genotypes and GE interaction also accounted significantly for 26.22 % and 35.27 respectively of the treatment SS. In the present study, the combined analysis of variance for seed cotton yield exhibited that effects due to environment, genotypes and their interaction were highly significant ($P<0.01$) leading to extension of analysis for estimating stability parameters. A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in seed cotton yield. The degree of the GEI sum of squares was larger than that for genotypes, indicating that there were substantial differences in genotypic response across environments. Similarly large contribution of environment was also reported by Naveed *et al*. (2007a) in which they indicated that environments accounted for the largest proportion followed by GEI and genotypes. It also implied that the yield was affected by both the environment and GEI effects (Ntawuruhunga *et al*., 2001).

The first interaction principal component axis (IPCA1) was highly significant, capturing 37.79% of the total variation in the GE interaction SS and 20.45% of the interaction degrees of freedom. The second and third interaction principal component axis (IPCA2 and IPCA3) explained a further 26.55% and 16.40% of sum of squares of this GE interaction. The first six interaction principal component axes (IPCA 1-6) accounted for 99.85% of total GE interaction, leaving 0.16% of the variation in the GE interaction in the residual. The residual in fact accounts for only 0.057% of total SS. In addition, sum of the squares of first three interaction principal component axes (IPCA 1, IPCA 2 and IPCA 3) were higher than the sum of squares of the genotypes.

AMMI analysis revealed that mean squares for the PCA 1 and PCA 2 were significant at P = 0.01 and cumulatively contributed to 64.34% of the total GEI. Therefore, the postdictive evaluation using an F-test at $P \leq 0.01$ suggested that two principal component axes of the interaction were significant for the model with 34 degrees of freedom. However, the prediction assessment indicated that AMMI with only two interaction principal component axes was the best predictive model (Zobel *et al*., 1988). Conversely, Sivapalan *et al*. (2000) recommended a predictive AMMI model with the first four PCAs. This model (AMMI 1 and AMMI 2) had 34 degrees of freedom. Further interaction principal component axes captured mostly noise and therefore did not help to predict validation observations. According to Gauch and Zobel, (1996) and, Yan and Rajcan, (2002), the most accurate model for AMMI can be predicted by using the first two PCAs. These results indicate that the number of the terms to be included in an AMMI model cannot be specified prior to trying AMMI predictive assessment. In general, factors like type of crop, diversity of the germplasm and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa *et al*., 1990b). Thus, results indicate that the AMMI model fits the data well, and justifies the use of AMMI 2. So the interaction of the 9 cotton genotypes with twelve environments was best predicted by the first two principal components of genotypes and environments.

Mean seed cotton yield (kg ha^{-1}) at 12 environments, their ranking orders and IPCA 1 and 2 are presented in Table 4. Mean yields ranged from 1138 kg ha^{-1} for 'E10' to 2622 kg ha^{-1} for 'E9'. With regard to IPCA 1 score, E5 and E6 gave the lowest scores respectively while E7 attained highest IPCA 1 score. The AMMI model 2 biplot was generated by plotting IPCA 1 scores against genotype and environmental means of 9 cotton genotypes and 12 environments was demonstrated in Figure 1. Displacement along the abscissa reflected differences in main effects, whereas displacement along the ordinate exhibited differences in interaction effects. Genotypes and environments on the same parallel line, relative to the ordinate, have similar yields, and a genotype or environment on the right side of the midpoint of this axis has higher yields than those on the left hand side. Regardless of IPCA 1 scores direction, environments such as E3, E7, E6, E8, E11 and E9 were on the right hand side of the midpoint of the main effect axis, seemed to be favorable environments for seed cotton yield among the genotypes evaluated. E4, E5 and E2 were moderately favorable while E1, E12 and E10 were less favorable environments. The environments showed much variability in both main effects and interactions. However, the high potential environments were found in quadrant II (E3, E6, E8, E11 and E9) with positive IPCA values and quadrant III (E7) with negative IPCA values, while the lower potential environments were sparsely distributed in quadrant I (E2, E5 and E4) with positive IPCA values and quadrant IV (E10, E1 and E12) with negative IPCA1 values. Among the High Potential Environments (HPE), E6 exhibited minimum interaction effect. This biplot also indicated E9 as the highest yielding environment. Whatever the direction is, the greater the IPCA scores, the more specifically adapted these genotypes were to certain environments (Zobel *et al*., 1988; Crossa *et al*., 1990a, 1997). Genotypes with IPCA1 scores near zero (either positive or negative) had little interaction across environments and, *vice versa* for environments (Crossa *et al*., 1991). Genotype and environment mean combinations with IPCA1 scores of the same sign produced positive specific interaction effects, whereas combinations of opposite sign had negative specific interactions. Among the HPE environments, E6 exhibited lowest IPCA 1 score and recorded as the most stable environment despite ranked 4th with respect to yield. Although environments E9, E11 and E8 were ranked 1st, 2nd and 3rd with respect to seed cotton yield but attained greater IPCA 1 scores.

Mean performance of 9 genotypes over the environments, IPCA and ASV scores for the seed cotton yield is presented in Table 5. MNH-886, NIAB-2009 and MNH-814 gave the highest seed cotton yields averaging 2403, 2334 and 2244 kg/ha, respectively. Genotypes, VH-289, BH-172 and FH-113 produced above average seed cotton yield of 2068, 1967 and 1936 kg/ha, respectively, and performed better to the check variety, CIM-496 which attained the lowest yield level averaging 1164 kg/ha. Figure 1 exhibited three groups of genotypes. Group one includes genotypes MNH-814 and NIAB-2009 that attained above average seed cotton yield coupled with interaction scores close to zero. Furthermore, these genotypes also performed well across all the environments. Group 2 includes genotypes BH-172, VH-289 and MNH-886 that produced above average seed cotton yield along with positive interaction scores where they interacted positively with favored environments E3, E6, E8, E9 and E11. Similarly despite producing below average seed cotton yield, genotype CIM-573 interacted positively with the environments E2, E4 and E5 because all their interaction scores had similar signs (Zobel *et al*., 1988; Crossa *et al*., 1997). These results suggest the specific adaptation of these genotypes to certain environments (Zobel *et al*., 1988; Crossa *et al*., 1990a, 1997). The high interaction of above and below average producing seed cotton yield genotypes with environments was also confirmed by high ASV (Table 5) suggesting erratic yield across environments. In fact, ASV is the distance from zero in a two dimensional scatter gram of IPCA1 scores against IPCA2 scores. Since the IPCA1 score contributes more to GE sum of scores, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to total GE sum of squares. The distance from zero is then determined using the theorem of Pythagoras (Purchase *et al*., 2000). The larger the ASV value, the more specifically adapted a genotype is to certain environments and vice versa. Genotype MNH-886 produced highest mean yield along with highest IPCA 1 score suggesting greater interaction. This was further confirmed by highest ASV of MNH-886 implying its unstable yield performance across environments and suggesting specified adaptation to certain environments such as E9, E8 and E2 having higher positive IPCA values. Group 3 include genotypes having negative interaction scores which allowed them to perform well in environments with negative interaction values. In this group, genotype FH-113 produced above average seed cotton yield while genotypes FH-4243, CIM-573 and CIM-496 exhibited below average seed cotton yield. In the biplot showing mean yield against IPCA 1 scores, NIAB-2009 and MNH-814 appeared to be the best in terms of mean yield as well as in minimum GEI. However, for the AMMI 2 model, IPCA 2 scores was considered in interpreting GEI that captured 26.55% of the interaction sum of squares as suggested by Gauch and Zobel (1996). A biplot is generated using genotypic and environmental scores of the first two AMMI components (Vargas and Crossa, 2000). Furthermore, Purchase (1997) pointed out that the closer the genotypes score to the center of the biplot, the more stable they are. When IPCA1 was plotted against IPCA2 (Figure 2), genotypes; BH-172, VH-289, MNH-814 and NIAB-2009 were found closer or at a lesser distance from the center of the biplot when compared with other genotypes. Although MNH-886 achieved the highest and better mean yield performance when compared with NIAB-2009 yet it exhibited the highest interaction with the environments (IPCA 1 score), sinking the reliability of its performance. On the other hand, NIAB-2009 exhibited almost no interaction with the environments (IPCA 1 score), convincing the reliability of its performance. FH-4243, FH-113, MNH-886, CIM-573 and CIM-496 remained in their previous positions, and were unstable in performance, as indicated in both biplots. The best genotypes with respect to environments E2, E8 and E9 were VH-289, MNH-814, NIAB-2009 and MNH-886. Genotypes BH-172 and CIM-573 were best for environments E3, E4, E5, E6 and E11; genotypes FH-4243 and FH-113 were best for environments E7, E10 and E12; and for E1 the best genotype was CIM-496. Thus, based on Figure 2 and ASV ranking as well as in mean yield (Table 5), BH-172 and MNH-814 were identified to be superior followed by NIAB-2009 in yield stability.

Reaction of cotton leaf curl virus (CLCuV) to various environments is presented in Table 4. CLCuV disease index ranged from 0.6% for E1 to 6.0% for E10. Ten (E2, E3, E4, E5, E6, E7, E8, E9, E11 and E12) out of twelve environments showed resistance to CLCuV while E1 proved highly resistant and E10 as moderate resistant. No environment proved immune to CLCuV. Keeping in view the IPCA 1 score and mean yield performance in environments, CLCuV disease incidence in E6 was lesser as compared to E9, E11 and E8 environments and could be the reason along with other prevailing biotic and abiotic stresses for stability in field performance (Cock, 1985). Although E9 attained the highest mean yield yet IPCA 1 score was on higher side when compared to E6. Mean CLCuV disease index in different genotypes (Table 5) ranged from 2.2% (VH-289, MNH-814, MNH-886 and NIAB-2009) to 3.2% (CIM-496) followed by 3.1% in FH-4243 and 2.8% in FH-113. Genotype BH-172 attained 2.6% CLCuV disease index. All the genotypes evaluated for yield stability proved disease resistant.

Table 1. Rating scale for cotton leaf curl virus (CLCuV) symptoms

Symptoms	**Disease rating** [y]	**Disease index (%)** [z]	**Disease reaction**
Absence of symptoms.	0	0	Immune
Thickening of a few small veins or the presence of leaf enations on 10 or fewer leaves of a plant.	1	0.1- 1	Highly resistant
Thickening of a small group of veins.	2	1.1- 5	Resistant
Thickening of all veins but no leaf curling.	3	5.1-10	Moderately resistant
Severe vein thickening and leaf curling on the top third of the plant.	4	10.1 – 15	Moderately susceptible
Severe vein thickening and leaf curling on the half of the plant.	5	15.1 – 20	Susceptible
Severe vein thickening, leaf curling, and stunting of the plant with reduced fruit production.	6	>20	Highly susceptible

[y] Disease ratings that include enations are marked with an "E". [z] The percentage disease index was calculated as follows:

$$\text{CLCuV incidence (\%)} = \frac{\text{Sum of all disease ratings}}{\text{total number of plants}} \times 16.16$$

Table 2: AMMI analysis for seed cotton yield of 9 genotypes evaluated across 12 environments

Location	Altitude (meters)	Latitude / Longitude	Average Rainfall (mm)	Year	Milieu	Year	Milieu
Cotton Research Institute, Faisalabad.	184	31° 21′ 52″ N 72° 59′ 40″ E	300	2010	E1	2011	E7
Cotton Research Station, Sahiwal.	172	30° 39′ 52″ N 73° 6′ 30″ E	2000	2010	E2	2011	E8
Cotton Research Station, Vehari.	135	29° 23′ 44″ N 71° 41′ 1″ E	127	2010	E3	2011	E9
Cotton Research Station, Multan.	125	30° 11′ 52″ N 71° 28′ 11″ E	127	2010	E4	2011	E10
Cotton Research Station, Bahawalpur	116	29° 23′ 44″ N 71° 41′ 1″ E	250	2010	E5	2011	E11
Cotton Research Institute, Rahim Yar Khan.	200	28° 25′ 12″ N 70° 18′ 0″ E	100	2010	E6	2011	E12

Table 3. AMMI analysis for seed cotton yield of 9 genotypes evaluated across 12 environments

SOV	df	SS	MS	% SS
Treatments	107	191904880	1793504^a	
Genotypes (G)	8	50318072	6289759^a	26.22
Environments (E)	11	73903104	6718464^a	38.51
GE Interaction	88	67683704	769133^a	35.27
IPCA$_1$	18	25575933	1420885^a	37.79
IPCA$_2$	16	17967418	1122964^a	26.55
IPCA$_3$	14	11101258	792947^a	16.40
IPCA$_4$	12	6198720	516560^a	9.16
IPCA$_5$	10	4254298	425430^a	6.29
IPCA$_6$	8	2476891	322111^a	3.65
IPCA$_{\text{Residual}}$	10	109186	10919^b	0.16
Pooled Error	216	1875096	8681	
Total	323	193779976		
CV		4.88 %		

^{a} Significant at $P<0.01$ level, ^{b} Non-significant at $P<0.05$ level

Table 4: Mean of seed cotton yield (kg ha^{-1}) at 12 environments, their ranking orders, IPCA 1 and 2, mean CLCuV disease index (%) and disease ratings

Environments	Mean Yield Kg / ha	Rank	IPCA1*	IPCA2**	Mean CLCuV Disease Index (%)	Disease Rating
E1	1338	10	-15.76	-14.27	0.6	1
E2	1545	9	18.05	5.3	3.0	2
E3	2114	6	24.11	-10.23	2.6	2
E4	1788	7	9.25	-9.24	4.6	2
E5	1736	8	0.92	-13.23	2.2	2
E6	2363	4	1.07	-14.42	1.5	2
E7	2148	5	-32.76	0.7	1.3	2
E8	2404	3	3.86	30.7	3.0	2
E9	2622	1	10.47	21.84	2.5	2
E10	1138	12	-1.52	0.73	6.0	3
E11	2407	2	3.81	-9.42	1.6	2
E12	1330	11	-21.51	11.54	2.2	2
Overall Average	**1911**					

*, ** are 1st and 2nd interactive principal component analysis axis for environments, respectively.

Table 5. AMMI adjusted mean seed cotton yield (kg/ha) based on untransformed data, AMMI stability values (ASV), ranking orders and mean CLCuV disease index (%) of the 9 genotypes tested across 12 environments.

Genotype	Mean Yield	Rank	IPCA 1	IPCA 2	ASV		Mean CLCuV	Disease
	Kg/ha				Value	Rank	Disease Index (%)	Rating
FH-113	1936	6	-22.67	3.18	32.42	6	2.8	2
BH-172	1967	5	13.68	-3.42	19.76	1	2.6	2
VH-289	2068	4	20.31	0.62	28.91	5	2.2	2
CIM-573	1481	8	2.51	-32.63	32.82	7	2.8	2
MNH-814	2244	3	-0.01	20.60	20.60	2	2.2	2
MNH-886	2403	1	28.71	1.30	40.87	9	2.2	2
FH-4243	1603	7	-27.11	5.15	38.92	8	3.1	2
NIAB-2009	2334	2	0.11	23.74	23.74	3	2.2	2
CIM-496 (C)	1164	9	-15.52	-18.54	28.84	4	3.2	2
Overall Average	**1911**							

IPCA = Interactive principal component analysis axis for genotypes.

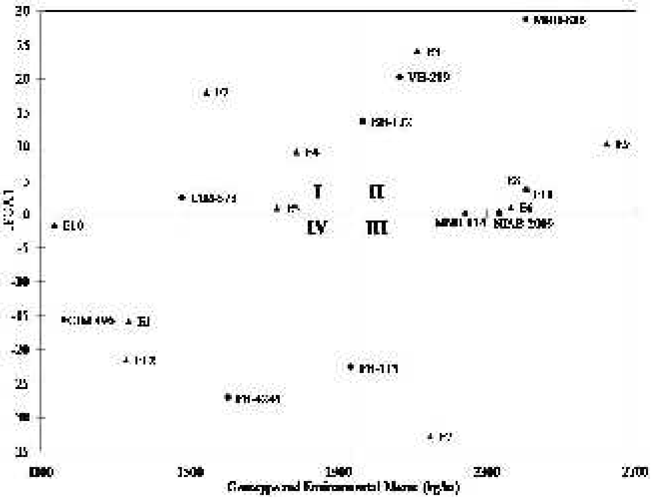

Figure 1. AMMI model 2 biplot of the 9 cotton genetypes (*) evalated in 12 environmnents (▽)

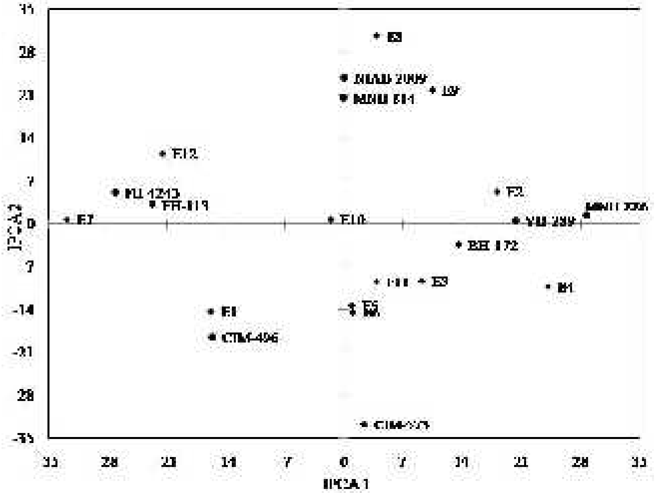

Figure 2. Biplot of 9 genotypes and 12 environments for seed cotton yield using genotypic and environmental scores.

Conclusion: The study indicated that the genotypes responded differently to variable environments. Three high yielding and CLCuV resistant cotton genotypes BH-172, MNH-814 and NIAB-2009 were found as stable and thus may be used to improve seed cotton yield in Punjab, Pakistan. Therefore, their possible national release should be sought for.

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