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GENOTYPE BY ENVIRONMENT AND GGE-BIPLOT ANALYSES FOR SEED COTTON YIELD IN UPLAND COTTON

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Abstract

Field testing in multiple environments can help in identifying relatively stable genotypes. A total of 28 upland cotton genotypes were tested in the normal cotton growing season during 2012 and 2013 at three locations (Peshawar, D.I.Khan and Faisalabad) of Pakistan. Genotypes (G) across environments (Y-Years, L-Locations) revealed significant ($p<0.01$) differences for seed cotton yield. Genotypes varied significantly ($p<0.01$) for their average mean performance over different years and locations. Moreover, the interaction effects due to G × Y × L were also significant ($p<0.01$). In total sum of squares, the involvement of genotypes, environments (years, locations) and their interactions ranged from 3.01 to 37.90%. Overall, the variation was mainly attributed to environments (years) (37.90%) followed by the G × Y × L (17.94%) and genotypes (15.33%). Analysis of locations revealed that the cotton genotypes showed maximum mean values for seed cotton yield in Peshawar region, Pakistan. Comparative performance of genotypes through genotype by environment interaction (GEI) revealed that genotypes produced maximum seed cotton yield during 2013 at Peshawar followed by NIBGE - Faisalabad, Pakistan. The seed cotton yield was found significantly ($p<0.01$) positively associated with earliness, morphological and yield traits, while the said association was negative with majority of the fiber quality traits. Stability in performance of the 28 genotypes was tested using GGE-biplot approach across six environments. Based on GEI and GG-biplot analysis, genotypes NIBGE-4 and IR-NIBGE-2620 were identified as vertex and ideal cultivars with more stability and seed cotton yield.

Key words: Cotton genotypes-cultivars; Environments; G × E environment interaction; Correlation; GGE-biplot analysis; Stability; *Gossypium hirsutum* L.

Introduction

Cotton (*Gossypium* spp.) is one of the leading natural textile fiber producing crops, and is also a main source of edible oil in Pakistan (Khan *et al*., 2007b; 2009c; 2010a). Cotton germplasm has narrow genetic base and little variation is available for the development of high yielding cotton cultivars (Khan, 2011; Rahman *et al*., 2005, 2011; Abbas *et al*., 2015). The performance of crop depends on genotypes and the prevailing conditions including environment in which the plants are grown, and genotype by environment interaction (Gomez & Gomez, 1984; Gul *et al*., 2014, 2016). Genotypes and some environmental factors (plant population, fertilizer rate and pest control etc.) can be controlled. However, other factors of environment such as rainfall, day length, soil properties and solar radiations are generally fixed and difficult to change, and termed as uncontrollable factors (Gul *et al*., 2014; Khan, 2013). The effects of uncontrollable factors on the performance of crop are as essential as that of controllable factors, and the evaluation and quantification of these effects are very important. Because the fixed factors are expected to change with site and crop season. These effects on genotypes in the form of variations are measurable and can be evaluated (Gul *et al*., 2016). In crops research, it is important to study the response of a genotype by arranging the experiments in several replications in different sites for 2-3 cropping seasons to avoid and or minimize the effects of the uncontrollable environmental conditions.

Genotype by environment interaction (GEI) is of great importance in the study of major crops grown in diverse environments (Blanche *et al*., 2006). Stable expression of different attributes of cotton genotypes in different environments is very difficult to attain (Kerby *et al*., 2000). GEI is a differential genotypes performance at various environments and is important to breeders because the interaction components provide basic information related to the adaptability of a crop cultivar. Significant genotype by environment interaction expresses that phenotypic responses are not similar for all genotypes under varied agro-ecological conditions (Khan *et al*., 2009a; Rahman *et al*., 2002; Iqbal and Rahman, 2017). Importance of G × E interaction was recognized in plant breeding as it reduce the stability of genotype values under different environments. The effect of environment on growth and phenology varies depending on crop species, cultivar and growth stages. The G × E interaction may change performance of a crop; therefore, the extent of environmental effects on a trait determines the importance of screening over locations and years (Gul *et al*., 2016).

Genotypes respond differently in different environment—largely due to their genetic make-up and environment, and some genotypes performed well in few environments than that of the others (Ali *et al*., 2005; Khan & Hassan, 2011). According to previous studies, G × E interactions for complex traits like seed cotton yield can retard the progress for identifying the best genotypes (Gul *et al*., 2016). Genotype × environment interaction for any cultivar reduces usefulness of genotype mean over all locations for selecting and advancing superior genotypes. Stable genotypes have smaller G × E interactions while those with large interactions are unstable. Genotype by environment interactions are major factors for reducing the selection efficiency—thus breeding program is handicapped. However, the G × E interactions are helpful in rating the performance of a genotype in different environments (Baker & Leon, 1988).

A genotype is considered to be stable if its variance among various environments is less. This concept of stability is extremely helpful in studying the quality traits, and response to biotic factors including diseases (Baker & Leon, 1988). A genotype is considered stable when it shows potential of high adaptability in a wide range of environments. Such studies would lead to make selections for candidate varieties which can produce maximum yield in all environments (Cooper & DeLacy, 1994).

GGE biplot was recommended as the most appropriate analysis to evaluate the genotype performance under different environments (Yan *et al*., 2007). It has been reported that genotype main effects should be integrated with genotype into environment interaction (GEI) for evaluation of genotypes under different environments using GGE biplot analysis (Yan & Kang, 2003). Environment is evaluated for discrimination ability (ability to differentiate between genotypes), representativeness (ability to represent the target region) and desirability index (distance from ideal location) (Yan, 2001). GGE biplot is also used for evaluation of genotypes for average performance and stability. Therefore, keeping in view the importance of upland cotton, the present research was planned with the aim to study the genotypic response and identify relative well adaptive and stable cultivars across six environments based on genotype by environment interactions and GGE biplot analysis.

Materials and Methods

Breeding material and procedure: A total of 28 upland cotton genotypes developed by Plant Genomics & Molecular Breeding Lab, NIBGE, Faisalabad, and Central Cotton Research Institute, Multan, Pakistan were grown for two years (2012 and 2013) at three different locations i.e., a) The University of Agriculture, Peshawar, b) Cotton Research Station, Dera Ismail Khan, and c) National Institute for Biotechnology and Genetic Engineering (NIBGE), Faisalabad, Pakistan (Table 1). Sowing was undertaken during the mid of May across the six environments. All the experiments were arranged in the randomized complete block (RCB) design with three replications. Each genotype was grown in a sub-plot having four rows of five meters in length. The plant-to-plant distance was 30 cm while rows were 75 cm apart. All standard agronomic practices (recommended by the Agriculture Department of the corresponding province) were applied from sowing till harvesting. Maximum and minimum temperatures at three locations during 2012 and 2013 for the crop seasons are provided in Figure 1. Picking of each plant was undertaken separately in the last week of November.

Table 1. Pedigree of 28 upland cotton genotypes used in the study.

S. No.	Genotypes	Parentage	Breeding centre	Released / under approval
G-1	IR-NIBGE-901	PGMB-33/FH-901	NIBGE, Faisalabad	2011
G-2	IR-NIBGE-1524-4	PGMB-33/NIBGE-2	-do-	2010
G-3	IR-NIBGE-3	PGMB-33/FH-1000	-do-	2012
G-4	IR-NIBGE-4	PGMB-33/CIM-448	-do-	Under approval
G-5	IR-NIBGE-5	PGMB-33/CIM496	-do-	Under approval
G-6	IR-3300-24	PGMB-33/BH-160	-do-	Under approval
G-7	IR-3300-13	PGMB-33/BH-160	-do-	Under approval
G-8	NIBGE-115	S-12/LRA-5166	-do-	2012
G-9	NN-3	S-12/LRA-5166	-do-	Under approval
G-10	NIBGE-2472	S-12/LRA-5166	-do-	Germplasm
G-11	NIBGE-2	LRA-5166/S-12	-do-	2006
G-12	IR-2379	PGMB-33/FH-1000	-do-	Germplasm
G-13	IR-NIBGE-3701-38	PGMB-33/CIM-448	-do-	2010
G-14	IR-1526	PGMB-33/NIBGE-2	-do-	Germplasm
G-15	NIBGE-314	S-12/LRA-5166	-do-	Under approval
G-16	NIBGE-5	S-12/LRA-5166	-do-	Germplasm
G-17	NIBGE-4	S-12/ CIM-448	-do-	Germplasm
G-18	IR NIBGE-2620	IR-901/Rajhans	-do-	Germplasm
G-19	NIBGE 758-8	S-12/ CIM-448	-do-	Germplasm
G-20	IR-NIBGE-3701-33-6	PGMB-33/CIM-448	-do-	2010
G-21	SLH-284	-	CRS, Sahiwal	Under approval
G-22	CIM-446	CP 15/2 × S 12	CCRI, Multan	1998
G-23	CIM-473	CIM-402/LRA-5166	-do-	2002
G-24	CIM-496	CIM-425/755-6/93	-do-	2005
G-25	CIM-499	CIM-433/755-6/93	-do-	2003
G-26	CIM-506	CIM-360/CP-15/2	-do-	2004
G-27	CIM-554	2579-04/97/W-1103	-do-	2009
G-28	CIM-707	CIM-243/738-6/93	-do-	2004

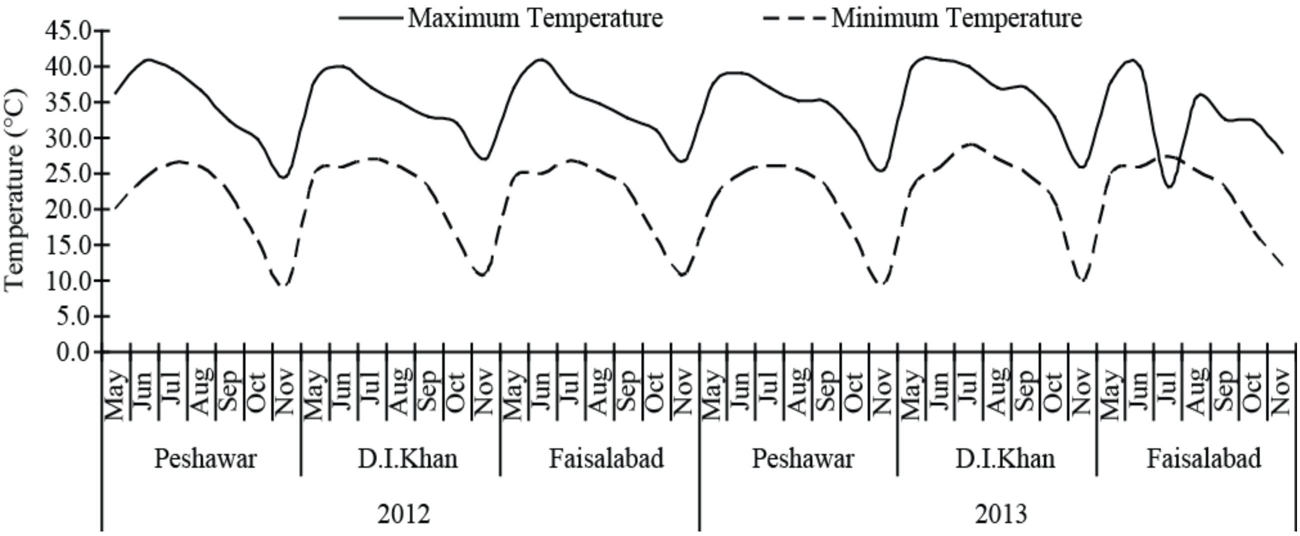

Fig. 1. Maximum and minimum temperatures during 2012 and 2013 at three locations.

Trait measurement and analysis: In central two rows, ten plants were randomly selected in each sub-plot/replication to record the data pertaining to seed cotton yield of each plant. The seed cotton yield was measured using a balance and was analyzed using the analysis of variance to test the null hypothesis of no differences among various genotypes, years/seasons, locations/sites and their interactions (Hicks, 1982; Gomez & Gomez, 1984). The least significant differences (LSD) test among the various traits were also calculated for the genotypes-cultivars, seasons-years, locations-sites and their interaction means. The data were also analyzed by deploying GGE biplot assay to explain G × E interactions (Yan, 2001).

Results

Genotype by environment study: Genotype by environment study was carried out for 28 upland genotypes by growing in two consecutive normal cotton growing seasons (2012-2013) at three different locations. Combined analysis of variance revealed that years-seasons and locations-sites exhibited nonsignificant differences for seed cotton yield plant^{-1} (Table 2). Overall, the genotypes exhibited highly significant differences for seed cotton yield. The interaction of year × location for seed cotton yield was found nonsignificant. While the other three interactions (genotype × year, genotype × location and genotype × year × location) showed significant ($p<0.01$) differences for seed cotton yield.

The component share of the genotypes, environments (years and locations) and their interaction have been formulated as variation attributed to each component. In the present investigation, the input to sum of squares for years, locations, and year × location ranged from 3.01 to 37.90%, and for genotypes, genotype × year, genotype × location and genotype × year × location ranged from 4.46 to 17.94% (Table 2). Overall, the variation was mainly attributed to environment - years (37.90%) followed G × Y × L (17.94%) and genotypes (15.33%). In mean performance of the genotypes during both growing seasons at three locations, on average the genotypes revealed maximum seed cotton yield per plant grown during 2013 (171.95 g) and minimum in 2012 (118.92 g) which also confirmed the major share of variation by cropping seasons.

For seed cotton yield per plant, on average the genotype means over years and locations ranged from 122.79 to 197.82 g (Table 3). Maximum seed cotton yield was observed in genotype NIBGE-4 (197.82 g) and it was found similar in performance with IR-NIBGE-2620 (182.89 g), which might be due to their genetic potential and the environment in which grown (Fig. 1). However, minimum seed cotton yield was observed for cultivar CIM-707 (122.79 g) and it was found same in performance with ten other genotypes ranging from 124.28 to 136.42 g. For year means, on average the genotypes observed with maximum seed cotton yield grown during 2013 (171.95 g) and minimum in 2012 (118.92 g). For locations, overall the genotypes grown at Peshawar produced maximum seed cotton yield per plant (160.34 g) while minimum at D.I.Khan (131.40 g). For genotype × year × location interactions, seed cotton yield mean values ranged from 56.27 to 248.39 g. Maximum seed cotton yield was observed by same genotype NIBGE-4 (248.39 g) grown during 2013 at D.I.Khan and it was found at par with IR-NIBGE-2620, NIBGE-5 and 10 other genotypes ranging 205.87 to 246.08 g grown at three locations during 2013. However, least seed cotton yield was observed for IR-NIBGE-5 (56.27 g) during 2012 at D.I.Khan. Overall, through G × E analysis, genotype NIBGE-4 followed by IR-NIBGE-2620 produced maximum seed cotton yield per plant.

In case of correlation of seed cotton yield with various earliness, morphological, yield and fiber quality traits (Table 4) i.e., the positive association of seed cotton yield was highly significant ($p\leq0.01$) with days to first flower opening, height of the plant, number of monopodia and sympodia per plant, number of bolls per sympodia and per plant, boll weight, seeds per boll, seed index and lint index. In case of fiber quantity traits, positive correlation of seed cotton yield was highly signifcant ($p\leq0.01$) with short fiber index and fiber colour, merely significant ($p\leq0.05$) positive with lint % and fiber length. However, the said correlation was negative ($p\leq0.01$) with fiber strength, fiber elongation and nonsignificant negative with fiber maturity.

Table 2. Sum of squares, mean squares and total variation (%) of genotypes across six environments for seed cotton yield in upland cotton.

Sources of variation	d.f.	Sum of squares (S.S)	Mean squares (M.S)	Total variation (%)
Years (Y)	1	354326	354326**	37.90
Locations (L)	2	70555	35278**	7.55
Year × Location	2	28128	14064	3.01
Error (Y × L × Rep.)	12	57604	4800	-
Genotypes (G)	27	143372	5310**	15.33
G × Y	27	41661	1543**	4.46
G × L	54	129228	2393**	13.82
G × Y × L	54	167709	3106**	17.94
Error (G × Y × L × Rep.)	324	242455	748	-

CV (Y × L × Reps. = 47.64); CV (G × Y × L × Rep.) = 18.81

Table 3. Mean performance of upland cotton genotypes for seed cotton yield per plant across G × Y × L interactions.

S.No.	Genotypes	2012			2013			Means (g)
		Peshawar	D.I. Khan	Faisalabad	Peshawar	D.I. Khan	Faisalabad	
G-1	IR-NIBGE-901	171.20	101.79	87.30	167.99	177.02	191.37	149.44
G-2	IR-NIBGE-1524-4	121.02	86.67	98.65	212.70	206.85	133.76	143.27
G-3	IR-NIBGE-3	141.66	92.31	93.80	189.84	184.42	191.97	149.00
G-4	IR-NIBGE-4	138.99	95.46	87.96	128.39	159.75	205.98	136.09
G-5	IR-NIBGE-5	137.57	56.27	87.98	135.33	184.71	210.87	135.45
G-6	IR-3300-24	108.83	88.52	94.58	111.62	183.39	180.99	127.99
G-7	IR-3300-13	137.57	97.70	88.39	127.18	202.37	92.40	124.27
G-8	NIBGE-115	127.68	73.86	147.86	180.83	197.05	153.55	146.81
G-9	NN-3	148.13	97.15	119.10	165.38	236.27	161.06	154.52
G-10	NIBGE-2472	145.43	87.03	121.71	177.02	167.94	152.70	141.97
G-11	NIBGE-2	146.39	79.35	104.63	206.85	177.19	164.36	146.46
G-12	IR-2379	153.80	111.50	128.71	184.42	111.62	164.01	142.34
G-13	IR-NIBGE-3701-38	142.14	89.39	141.79	164.84	196.58	175.00	151.62
G-14	IR-1526	130.99	101.84	132.46	165.43	172.55	199.45	150.45
G-15	NIBGE-314	177.52	117.48	165.12	178.62	160.89	185.70	164.22
G-16	NIBGE-5	186.37	102.30	144.85	240.52	146.75	190.21	168.50
G-17	NIBGE-4	145.78	193.20	152.75	205.87	248.39	240.93	197.82
G-18	IR-NIBGE-2620	178.60	134.90	164.81	246.08	190.74	182.23	182.89
G-19	NIBGE-758-8	160.75	95.55	89.80	180.41	170.72	163.37	143.43
G-20	IR-NIBGE-3701-33-6	151.92	123.31	68.60	199.14	180.12	181.09	150.70
G-21	SLH-284	162.56	117.83	83.95	163.44	163.42	220.82	152.00
G-22	CIM-446	108.28	114.83	61.34	199.99	98.52	180.22	127.20
G-23	CIM-473	110.58	120.21	79.21	201.74	105.34	179.45	132.75
G-24	CIM-496	126.04	103.07	92.92	182.54	87.47	170.14	127.03
G-25	CIM-499	134.07	131.64	98.04	179.56	96.09	163.66	133.84
G-26	CIM-506	146.19	112.39	87.52	169.07	83.91	199.01	133.01
G-27	CIM-554	150.21	87.56	135.73	144.97	79.70	220.34	136.42
G-28	CIM-707	129.76	85.75	111.25	149.00	89.65	171.32	122.79
Year means (g)		118.92			171.95			
Location means (g)		160.34	131.40	144.59				
LSD0.05 Genotypes				17.939				
LSD0.05 Years				13.448				
LSD0.05 Locations				16.471				
LSD0.05 G × Y × L				44.842				

Table 4. Correlation of seed cotton yield with various traits.

Variables	Correlation of seed cotton yield with various traits	Probability ($p \leq 0.05$)
Days to first flowering	0.133**	0.003
Plant height	0.208**	0.000
Monopodia per plant	0.292**	0.000
Sympodia per plant	0.295**	0.000
Bolls per sympodia	0.738**	0.000
Bolls per plant	0.867**	0.000
Boll weight	0.332**	0.000
Seeds per boll	0.230**	0.000
Seed index	0.181**	0.000
Lint index	0.303**	0.000
Lint %	0.110*	0.014
Fiber length	0.088*	0.049
Micronaire	0.398**	0.000
Fiber strength	-0.138**	0.002
Fiber uniformity index	$0.068^{N.S.}$	0.182
Fiber elongation	$-0.035^{N.S.}$	0.437
Short fiber index	0.117**	0.009
Fiber maturity	$-0.039^{N.S}$	0.378
Fiber colour	0.185**	0.000

GGE biplot analysis (Polygon view): Following the 'which wins where' rule, a total of nine sectors were resulted on the biplot with genotypes i.e., G-9 (NN-3), G-17 (NIBGE-4), G-18 (IR-NIBGE-2620), G-16 (NIBGE-5), G-26 (CIM-506), G-28 (CIM-707) and G-7 (IR-3300-13) vertex genotypes (Fig. 2). Environment E5 (D.I.Khan, 2013) fell into the sector in which G-9 (NN-3) was the vertex cultivar. This means that G-9 (NN-3) was the best cultivar in environment E5 (D.I.Khan, 2013). The four other environments E1 (Peshawar 2012), E2 (D.I.Khan 2012), E3 (NIBGE 2012) and E4 (Peshawar 2013) fell into the sector in which G-17 (NIBGE-4) and G-18 (IR-NIBGE-2620) were the vertex cultivars. This clarified that both G-17 (NIBGE-4) and G-18 (IR-NIBGE-2620) out yielded all other cultivars by producing maximum seed yield in these four environments. Environment E6 (NIBGE 2013) fell into the sector where G-16 (NIBGE-5) was the corner cultivar confirming that this environment was best suited for G-16 (NIBGE-5). No environment fell into sectors where G-26 (CIM-506), G-28 (CIM-707), G-6 (IR-3300-24) and G-7 (IR-3300-13) were placed on the vertices. This demonstrated that these cultivars did not perform well in any of the environments. In other words, these genotypes were identified as poor performing cultivars in some or all of the environments. Moreover, G-20 (IR-NIBGE-3701-33-6) and G-14 (IR-1526) located near to the origin were found less responsive to the environment compared to those located on the vertices far away from the origin.

Average yield and stability of the cultivars: Average seed cotton yield and stability in performance of the different cultivars has been shown in Fig. 3. The cultivar G-17 (NIBGE-4) produced the highest average seed cotton yield per plant followed by G-18 (IR-NIBGE-2620) being placed far away from the origin in positive direction. However, G-28 (CIM-707) followed by G-6 (IR-3300-24) were identified as low yielding genotypes being placed in the negative direction. Similarly, stability and suitability is estimated through the projection of the corresponding cultivar along the ATC Y-axis. Stability of a cultivar is described by the absolute length of the projection. Lower value is desirable—revealed stability. Thus, G-17 (NIBGE-4) followed by G-15 (NIBGE-314) were identified as the most stable whereas G-7 (IR-3300-13) was found as least stable cultivar.

The representative and discriminating ability of environments: In the present study, more vector length was observed in environment E5 (D.I. Khan, 2013), thus demonstrated that genotypes variation was high in this environment. Moreover, the angle between the vectors of this environment was high as compared with the vectors of the other environments which clarified that relationship between E5 (D.I. Khan, 2013) and other environments was relatively less. Remaining five environments showed a close angle among their vectors and thus depicted a close relationship with one another. Regarding seed cotton yield and stability performance, all the six environments were clustered as one mega environment (Figs. 4 and 5).

Evaluation of ideal genotypes and ideal environments: The ideal genotype (IR-NIBGE-2620) is located in the first concentric circle of the biplot. The genotypes which were located close to the ideal genotype were desirable. In this study, G-17 (NIBGE-4) was close to the ideal genotype and located in the second concentric circle after G-18 (IR-NIBGE-2620)--located in the first circle (Fig. 6). Genotypes G-6 (IR-3300-24), G-7 (IR-3300-13) and G-28 (CIM-707) were undesirable genotypes because they were at distant from the first concentric circle. The environment located in the first concentric circle in the biplot termed as ideal environment and environments located close to the ideal environment considered desirable environments. In present study, E3 (NIBGE 2012) is located in first concentric circle followed by E4 (Peshawar 2013) and those environments which are close to the ideal environments are desirable environments (Fig. 7).

Discussion

Significant values of the mean squares due to G, E and G × E interaction revealed greater genetic variability among the cotton genotypes. One the plausible reasons is the diverse genetic background. Secondly, different environmental conditions (tested for performance) may also contribute towards genetic variability. In previous studies, upland cotton genotypes grown under diverse environments depicted significant effects for genotype × year and genotype × year × location for various morphological and yield traits (Machado *et al*., 2002; Ullah *et al*., 2008; Rahman *et al*., 2008; Iqbal and Rahman, 2017). Similarly, across various environments, genotypes performed differently and revealed significant G × E interactions among the upland cotton genotypes (Satish *et al*., 2009; Unay *et al*., 2004; Iqbal and Rahman, 2017). For various agronomic traits in *G. hirsutum* L., significant genotype and environment main effects and G × E interaction effects were reported (Gul *et al*., 2014, 2016). Such commonalities are reported in numerous studies conducted on *G. arb*oreum L. (Iqbal *et al*., 2015).

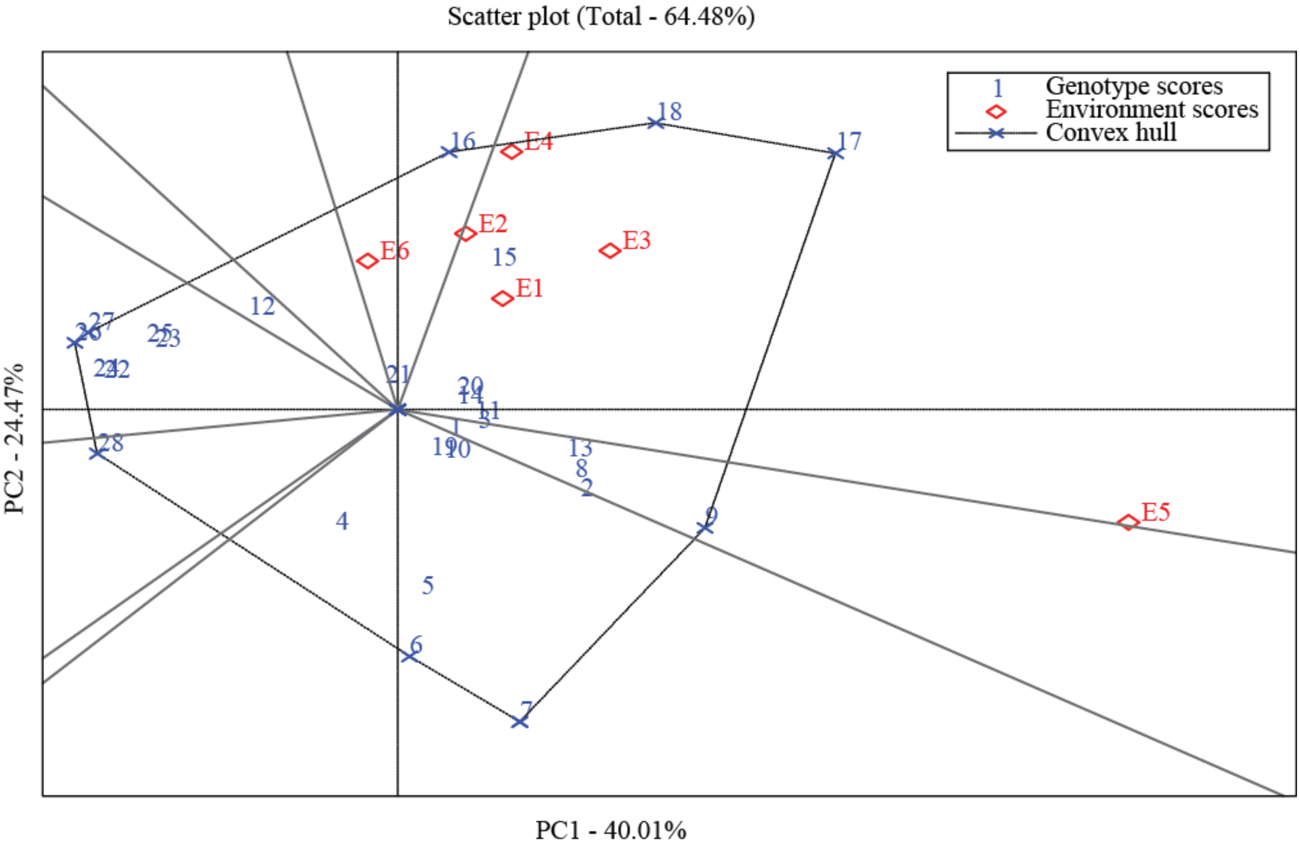

Fig. 2. Polygon view of GGE biplot based on environmental scaling for the 'which-won-where' pattern of genotypes and environments.

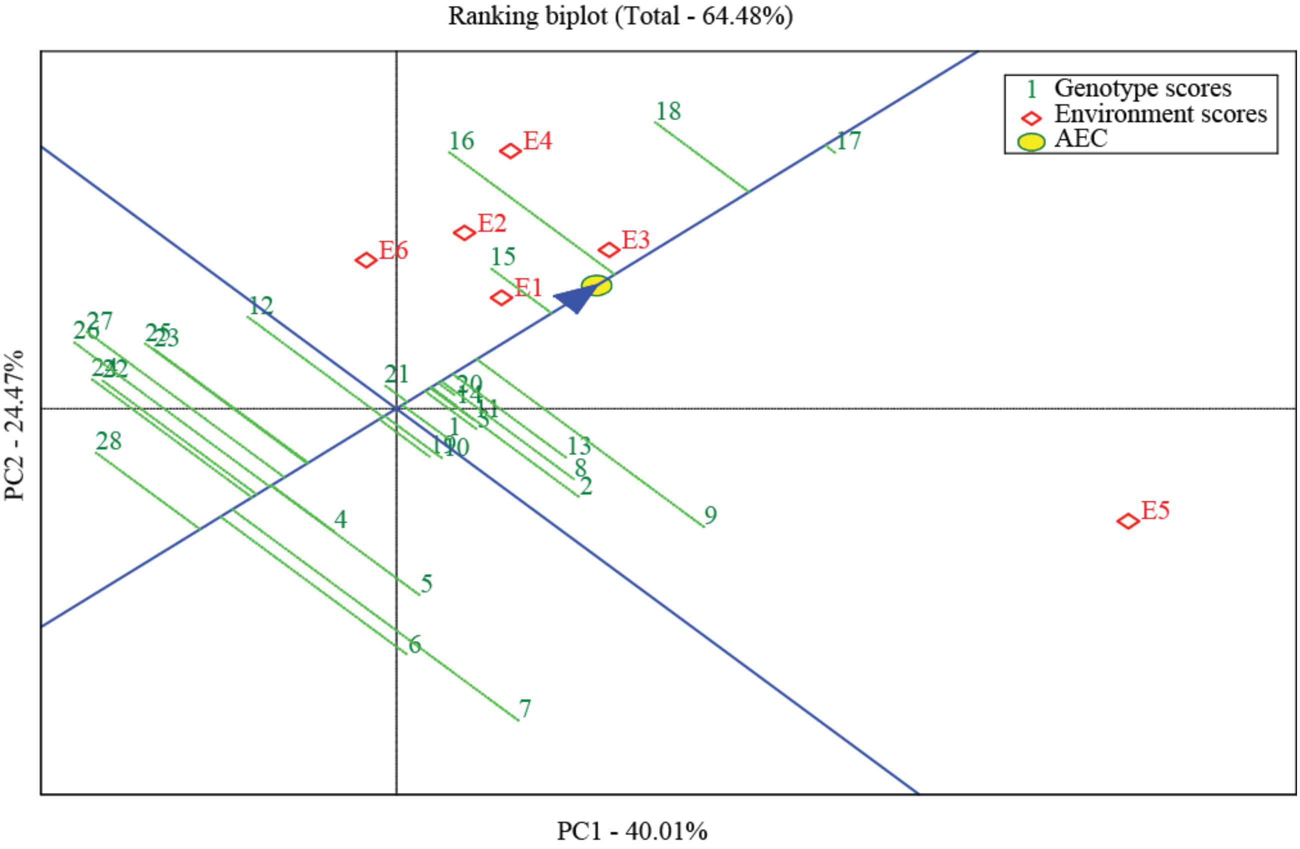

Fig. 3. Average environment coordination (AEC) views of the GGE biplot based on genotype focused scaling for the means performance ranking and stability of genotypes.

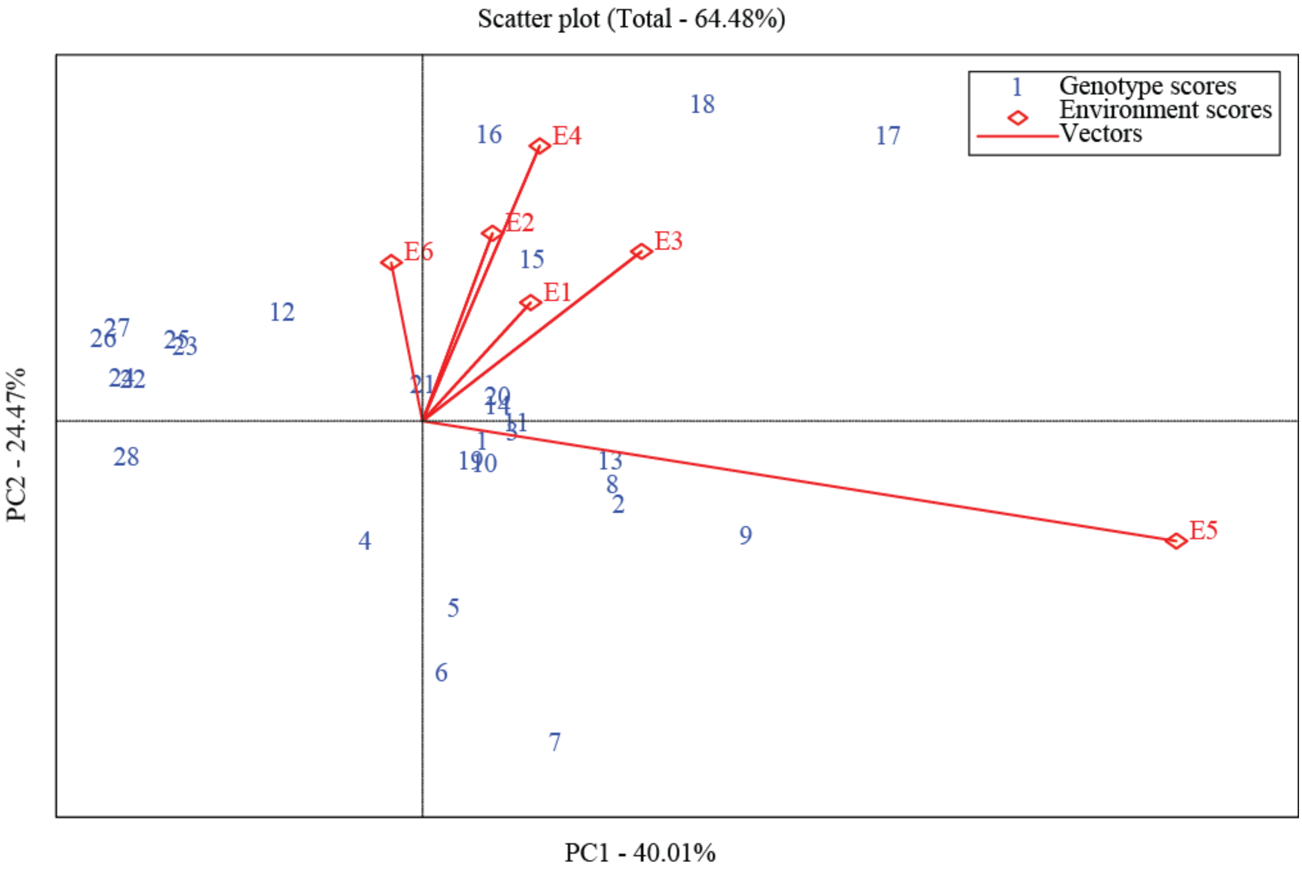

Fig. 4. GGE biplot for the evaluation of the relationships among the six environments.

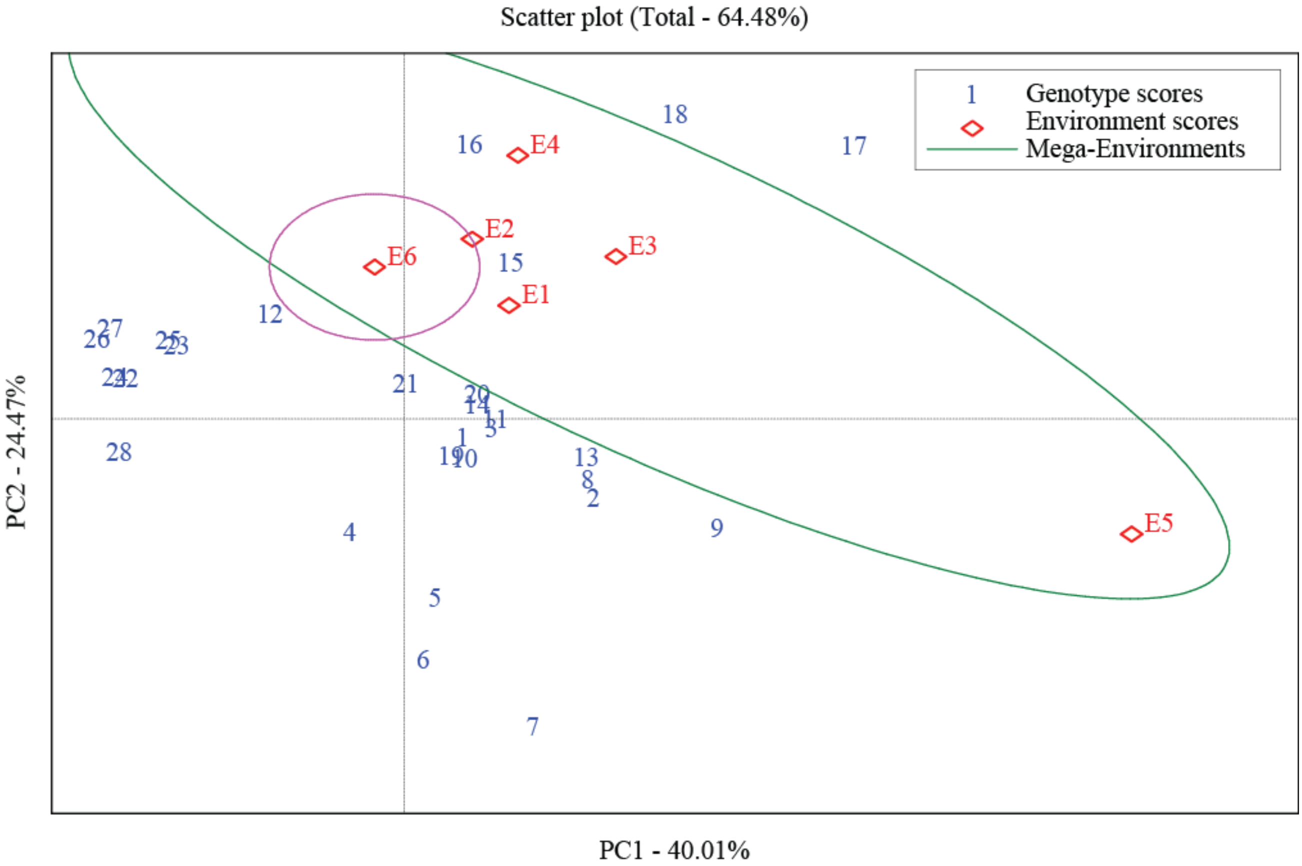

Fig. 5. GGE biplot for the evaluation of the mega environments among the six environments.

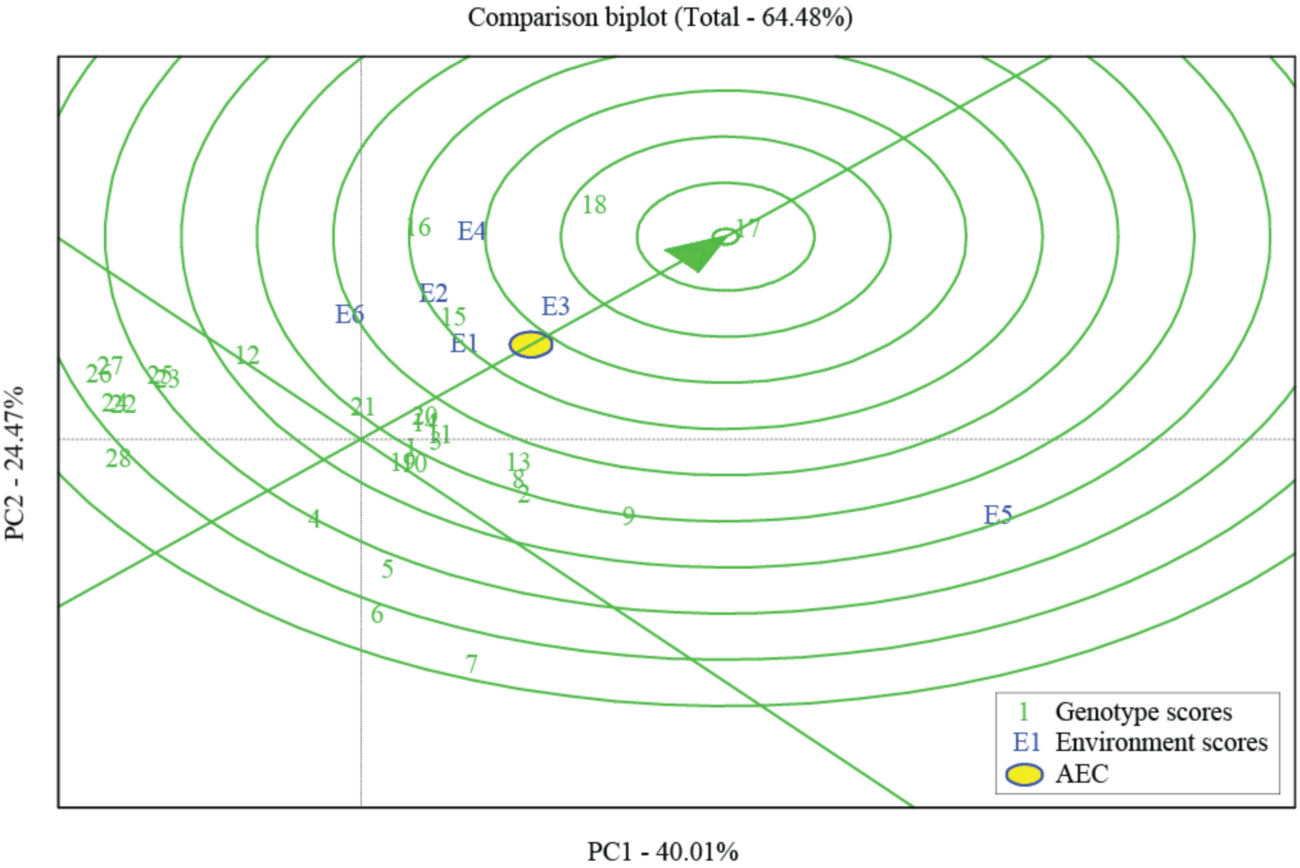

Fig. 6. GGE biplot with scaling focussed on genotypes.

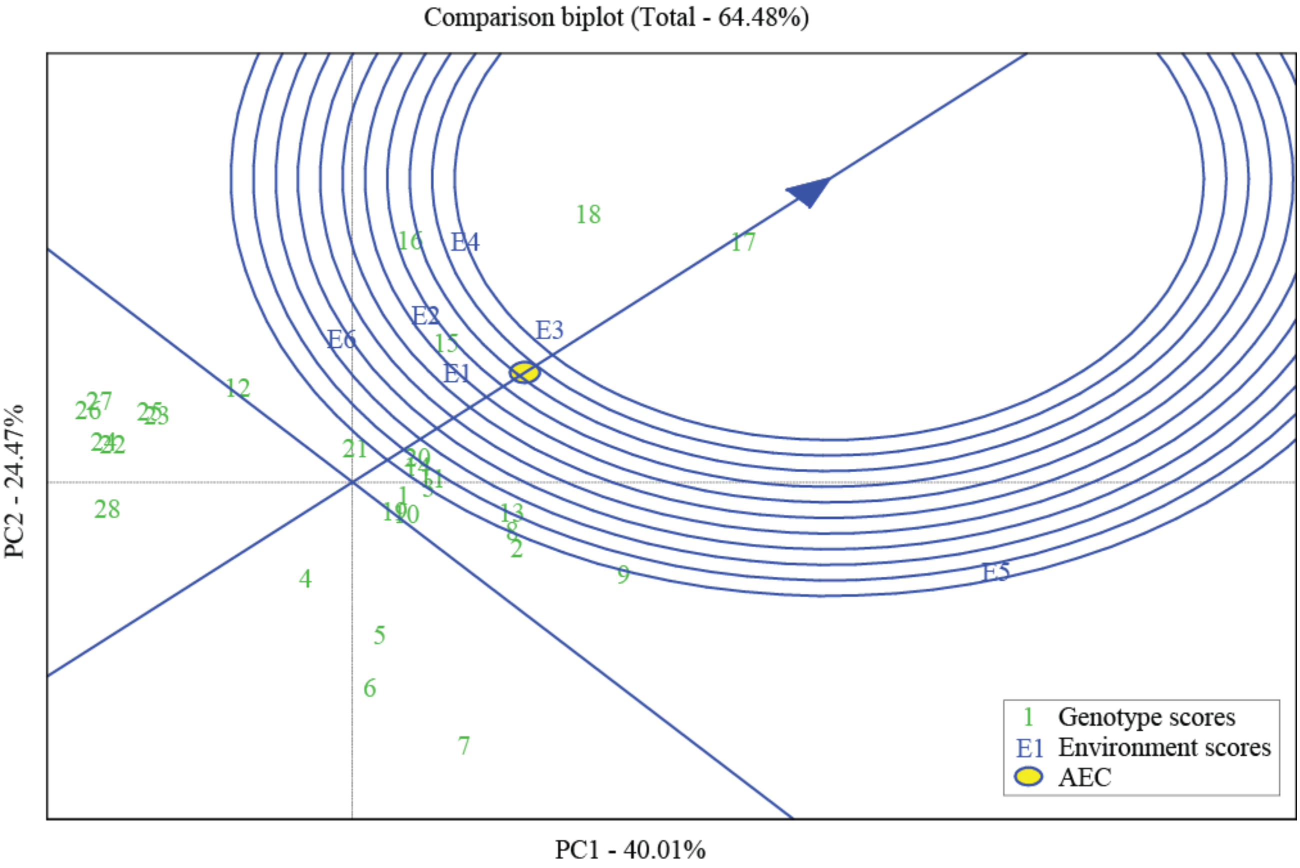

Fig. 7. GGE biplot with scaling focused on environments.

The G × E interaction measures the response of cultivars across different environments (Kerby *et al*., 2000; Blanche *et al*., 2006). In the present studies, overall, the variation was mainly governed by environmental - years followed by G × Y × L and genotypes. In the previous studies, the contribution towards sum of squares for environments was in the range of 11 to 92%, while for genotypes and G × E, it was 5 to 55% and 5 to 34%, respectively (Blanche *et al*., 2006). In another study, high positive effects of environment on various traits of upland cotton genotypes including boll number, seed cotton yield, and fruiting branches were reported (Gul *et al*., 2014).

Environments (year/location) impact on the performance of cotton genotypes—may fluctuate with the unpredictable environmental conditions i.e., cropping season, soil/location, rain, temperature, inputs and cultural practices etc. Significance of G × E interaction makes ineffective the correlation between the genotype and phenotype—a major handicap in bifurcating the genetic capability of cotton genotypes (Khan *et al*., 2007b; Gul *et al*., 2016). For example, significant G × Y and G × Y × L interactions were observed in the study of four different groups of genotypes in different environments for various morphological and yield traits (Maleia *et al*., 2010). Genotypes, years, locations and year × location interactions were significant for seed cotton yield in upland cotton (Killi & Harem, 2006).

Seed cotton yield of cotton genotypes is mostly affected by location and season and highly significant differences in yield and its components might be due to varieties and environmental components. Therefore, the environments alone and their interactions with the genotypes revealed significant differences which could help cotton breeders for selecting the best genotype for a particular environment. The differences among the upland cotton genotypes, environments (years/locations) and G × Y × L interactions were highly significant for yield traits (Unay *et al*., 2004). The G × E interaction showed different patterns of response among the genotypes across different environments (Blanche *et al*., 2006). However, Gul *et al*. (2016) observed that different climatic factors such as soil fertility, day length and temperature, moisture and sowing time of different seasons and locations affect the performance of cotton genotypes. In another investigation, the G × E interactions for seed cotton yield was found significant (Campbell *et al*., 2012).

In the present study, significant positive association of seed cotton yield with majority of the yield related traits might be due to direct and indirect effects of these independent components on seed cotton yield. Positive correlation was also reported in past studies between seed cotton yield and yield contributing traits (Khan *et al*., 2009d; 2010b). However, the fiber quality traits were found negatively correlated with seed cotton yield. Highly significant positive association of seed cotton yield was recorded with sympodia per plant, bolls per plant and boll weight in upland cotton genotypes (Afiah & Ghoneim, 2000; Soomro *et al*., 2008; Ullah *et al*., 2008; Khan *et al*., 2009a). In previous studies, seed cotton yield exhibited negative association with fiber quality traits in upland cotton (Khan *et al*., 2009b; 2009e).

Genotype × environment interaction over the phenotypic variation further make difficult the genetic improvement, and the phenotype will be no longer a good forecaster of genotype (Yan & Kang, 2003). To widen the genetic base of populations upon which selection is made, large and diverse germplasm should be screened in different crop seasons and locations. In this study, both type of interactions were observed i.e., qualitative and quantitative. In case of quantitative interaction, genotypes might show the varied performance across different environments, however, the best performing genotypes sustains their performance. Yan *et al*. (2007) findings revealed that qualitative (crossover) interaction was an interaction that compose multiple environments testing (MET) and selection become complex for high yielding genotype in all environments. Genotypes G-17 (NIBGE-4) and G-18 (IR-NIBGE-2620) were the best at E1 (Peshawar 2012), E2 (D.I.Khan 2012), E3 (NIBGE 2012) and E4 (Peshawar 2013) because these were the vertex genotypes in these environments (Fig. 1).

Genotype located at corner (vertex) was more responsive than those located near the origin. Yan & Tinker (2006) observed that vertex genotypes were the most responsive genotypes. In reliable differential ranking of genotypes, the test environments may be divided into location groups that share the same best genotype namely mega environments (Yan *et al*., 2007; Yan & Kang, 2003). Among the tested environments, E1 (Peshawar 2012), E2 (D.I.Khan 2012), E3 (NIBGE 2012), E4 (Peshawar 2013), E5 (D.I.Khan, 2013) and E6 (NIBGE 2013) were having a good discriminating power. The E3 (NIBGE 2012) was discriminating and representative site which was found useful to produce superior genotypes (Fig. 2). However, environments with long vectors and small angles, and with average environment axis are suitable for selecting best performing genotypes, while sites with long vector and large angles with the AEC abscissa are good in culling unstable genotypes (Yan *et al*., 2007).

In an ideal test environment, both discriminating abilities among genotypes and representative of all other environments are available for improvement of generally adapted variety (Yan, 2001; Yan *et al*., 2007). Present findings revealed that E3 (NIBGE 2012) was near to ideal site having low angle from the average environment axis and high discriminating power (Fig. 2). Overall, the desirability of a genotype is a combination of stability in performance and high yield (Yan & Kang, 2003). Yan *et al*. (2007) observed that in GGE biplot methodology, the estimation of yield and stability of genotypes was undertaken by using the average environment coordinate (AEC) methods. The line passing through the biplot origin is called AEC, which is defined by the average PC1 and PC2 scores, for all the environments (Yan & Kang, 2003). Past findings also revealed that genotypes found near to the ideal genotype were the most desirable genotypes for yield (Yan *et al*., 2007; Yan & Kang, 2003). Based on this criterion, genotypes G17 (NIBGE-4) and G15 (NIBGE-314) were found as desirable genotypes for wider adaptation. GGE biplot analysis was also reported to be more appropriate tool for MET data (Kaya *et al*., 2006; Yan & Tinker, 2006).

In the present study, genotype G17 (NIBGE-4) was found to be the most stable and widely adapted genotype for regional release to increase the seed cotton yield. Experiments across several years/locations will enable to identify the effect of the mega environments. Similar findings pertaining to harvesting maximum yields and stable response across different environments were reported (Farshadfar *et al*., 2012). The genotype falling in the first concentric circle of biplot is called as ideal genotype. Yan and Kang (2003) observed that starting from the middle concentric circle pointed with arrow concentric circles was drawn to help visualize the distance between genotypes and the ideal genotype. The ideal genotype could be used as a benchmark for selection. Yan & King (2003) observed that those genotypes which are close to the ideal genotype could be considered for further testing. It was also reported that an ideal environment has the highest ability to discriminate the genotypes (Yan & Tinker, 2006).

Conclusion

Genotype NIBGE-4 (G-17) showed best performance during both cotton growing seasons across all the locations. Comparing responses of genotypes through two years and three locations, all the genotypes performed well and produced more seed cotton yield during 2013 at Peshawar, Pakistan. Seed cotton yield showed highly significant positive correlation with the earliness, morphological and yield traits, while this association was negative with majority of the fiber quality traits. The G × E and GG-biplot analyses revealed that NIBGE-4 (G-17) followed by IR-NIBGE-2620 (G-18) were found as the ideal genotypes with respect to stability and producing maximum seed cotton yield in all environments.

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