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Full Length Article



Genotype by Environment and Biplot Analyses for Yield and Fiber Traits in Upland Cotton

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Abstract

Stability and desired response of genotypes across different environments is very important for plant breeders. Therefore, plant breeders always test their breeding material across diverse environments to assess consistency of superior genotypes for wider adaptation. Twenty-eight upland cotton genotypes (G) were studied across six environments (E) during two crop seasons (2012 and 2013) at three locations i.e., Peshawar, Dera Ismail Khan (D.I. Khan) and Faisalabad, Pakistan. Genotypes, genotype \times year, genotype \times location and genotype \times year \times location (G \times Y \times L) showed significant ($p \le 0.01$) differences for all the traits. On an average, genotypes produced significantly more bolls per plant and lint % during 2013 than 2012. By comparing the locations, overall the genotypes performed better for yield and lint traits at Peshawar. In $G \times Y \times L$ interactions, maximum bolls per plant produced by cultivar CIM-473 grown during 2013 at Peshawar. For lint %, genotypes CIM-506 and IR-NIBGE-3701-38 were leading, grown during 2012 and 2013 at D.I. Khan. According to genotype, genotype by environment (GGE) biplot analysis, the genotype CIM-473 was found as best cultivar during 2012 at D.I. Khan and Faisalabad as confirmed by genotype by environment interaction (GEI). During 2012 and 2013 at Peshawar and 2013 at D.I. Khan, the genotypes CIM-554 and IR-NIBGE-3701-38 were the vertex cultivars and more stable with high lint yield. Cultivars CIM-554 and CIM-506 were identified as best genotypes across all the environments for lint %. Genotypes CIM-554 and CIM-506 were relatively steady across environments thus, identified as ideal genotypes for lint %. However, majority of the cotton genotypes were inconsistent. Therefore, this study emphasizes that efforts should be made to synthesize the cotton cultivars for the specific environment rather than mere broad adaptation. © 2018 Friends Science Publishers

Keywords: Cultivars performance; Stability of cultivars; GGE-biplot analysis; Yield and lint traits; Gossypium hirsutum L.

Introduction

Cotton is the major fiber crop of the world used extensively in the textile industry and as oilseed crop for edible oil purpose. Cotton is one of the oldest cultivated crops of the world grown for fiber and feed (Iqbal *et al.*, 2017). Cotton being a major cash crop earns a lot of foreign exchange for Pakistan. Globally, Pakistan is the fourth largest producer of raw cotton and one of the biggest exporters of cotton yarn. This achievement was facilitated by the unceasing efforts of cotton breeders of the country. In 2016–17, cotton crop was grown on 2.489 million hectares and seed cotton production was 10.671 million bales with average seed cotton yield of 730 kg ha⁻¹ (PBS, 2017). However, in our country, the cotton production is low per unit area in contrast to other advanced cotton grown countries of the world. Seed cotton and lint yields being complex characters are managed by the

interaction between its attributes accompanied by varying environmental conditions (Ahmad *et al.*, 2008; Khan, 2013). Realizing the importance of this crop in economy, various efforts have been made in order to boost up its production around the country. Therefore, besides developing of high yielding cotton cultivars we also earnestly need to explore more potential areas to increase its productivity.

Desired response of genotypes across different environments is very crucial for plant breeders. Crop performance depends on genotype and the environment in which it is grown and genotype × environment (GE) interaction (Gomez and Gomez, 1984; Gul *et al.*, 2014). Some environmental factors can be controlled but some other factors of the environment are fixed and hard to change (Gul *et al.*, 2016). The uncontrollable factors are expected to change with location and crop season. Therefore, measuring the performance of a genotype,

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the effects of uncontrollable factors are as important as that of controllable factors and their evaluation is essential (Yang *et al.*, 2009). Such uncontrollable effects on genotypes are measurable in the form of variations. In crop research, the most commonly used way to evaluate the effects of uncontrollable environmental factors on crop response is to repeat the experiments at several sites and crop seasons or may be both.

Phenotypic performance of a genotype is determined by the interaction of said genotype with environment where it grown. Genotype expression over environments may arise when certain genotypes are grown in a diverse set of environments (Paterson et al., 2003). In the study of major crops grown in a wide range of environments, genotype by environment interaction is of great importance (Saranga et al., 2001; Ali et al., 2017). Genotype by environment interaction is a differential response of genotypes across environments and is important to breeders because the interaction components provide basic information concerning the adaptability of a given genotype. Interactions due to genotype by environment have assumed greater importance in plant breeding as they reduce the stability of genotype values under diverse environments (Romagosa and Fox, 1993). A significant GE interaction for quantitative traits can seriously limit the efforts on selecting superior genotypes for cultivar development (Kang and Gorman, 1989; Gul et al., 2016). However, G × E interactions become more important and challenging when the ranking of breeding lines change in different environments (Baker and Leon, 1988; Ali et al., 2017). The impact of environment on phenology and growth varies which depends on crop species, variety, and growth stages (Ali et al., 2005). Therefore, the extent of environmental effects on phenotypic performance of a genotype determines the importance of screening over locations and years.

Several studies has advocated the use of GGE biplot in multi-environment trials (METs). GGE biplot is believed to be very effective in explaining complex patterns of GE interaction and usually first choice of plant breeders to identify best performing genotypes for environments (Yan et al., 2007). The GGE biplot analysis is the graphical approach to assess genotypes main effects integrated with genotype by environment interactions (GEI) for evaluation of genotypes under diverse environments (Yan and Holland, 2010). The GGE biplot has very useful features such as visually assessing the discrimination ability of environments (ability to differentiate the genotypes); relationship among the genotypes and environments; ideal environment and genotype (Yan, 2001). Similarly, genotypes are ranked in ranking biplot to visually identify best and consistent performing genotypes. In the current study, cotton genotypes collected from reputable research institutes of Pakistan were used to; a) assess their relative performance of genotypes across diverse environments using GGE biplot analysis, and b) identify high yielding stable genotypes in terms of lint %. Majority of these genotypes were field-tested for the first time in Peshawar and D.I. Khan for their potential use in these localities.

Materials and Methods

Experimental Sites and Environmental Conditions

This two years study was conducted during 2012 and 2013 at three different locations i.e., a) University of Agriculture, Peshawar, b) Cotton Research Station, D.I. Khan, and c) National Institute for Biotechnology and Genetic Engineering (NIBGE), Faisalabad, Pakistan. Soil analysis of these locations revealed that soil was clay loam both at Faisalabad and D.I. Khan while silty clay loam at Peshawar (Table 1). Maximum and minimum temperatures and rainfall data of cotton crop seasons 2012 and 2013 at three locations are provided in Fig. 1 and 2.

Breeding Material and Procedure

Twenty-eight upland cotton genotypes were grown in the field for two years (2012 and 2013) at three locations of Pakistan (Table 2). Sowing was made during the 2nd week of May at all the locations during both years. All the experiments were laid out in a randomized complete block design (RCBD) with three replications. Each genotype was grown in four rows having five-meter length, with plants and rows spacing of 30 and 75 cm, respectively.

Crop Husbandry

Cotton is a deep-rooted crop which needs fine good tilth and well prepared soil for successful germination and growth of crop. To get this, field was ploughed with deep plough then harrowed with planking each time to make the soil loose, fine, leveled and pulverized. The stubbles of the previous crop left in the field were also removed. The fertilizer was applied at the rate of 100:60:60 kg ha⁻¹ of NPK, respectively. All P₂O₅, K₂O and 1/3 of the N were applied at sowing time and the remaining N was applied in two split doses i.e., with first irrigation and at the pre-flowering stage. However, the doses of N and P were increased or decreased keeping in view the fertility of soil at different locations. Overall, 5–6 irrigations (from June to September) have been given to the crops at all the locations. The weeds at all the locations were removed and controlled manually. For the control of sucking pests i.e., Whitefly (Bemisia tabaci), Jassids (Amrasca biguttula devastans) and Thrips (Thrips tabaci), the insecticides viz., Confidor 200 SL (625 mL ha⁻¹) and Baythroid TM 525 EC (1250 mL ha⁻¹) were used in the experiments at all the locations during both years. In chewing insects, the American Bollworm (Helicoverpa armigera) was more prominent at all the locations and which was controlled by the insecticides i.e., larvin 80 DF (1125 g ha⁻¹) and deltaphos 36 EC (1500 mL ha⁻¹). Picking was done during the month of November on the single plant basis.

Table 1: Soil analysis of the three locations used in the studies

Locations	Soil texture	pН	Organic matter (%)	N (%)	P ₂ O ₅ (ppm)	K ₂ O (ppm)
The Univ. Agri. Peshawar	Silty Clay Loam	8.2	0.81	0.063	7.18	112
ARI, D.I. Khan	Clay Loam	7.9	0.87	0.047	7.8	147
NIBGE, Faisalabad	Clay Loam	7.4	0.93	0.038	9.05	179

Table 2: Pedigree of 28 upland cotton genotypes used in the studies

Genotypes	Parentage	Breeding center	Released / under approval
IR-NIBGE-901	PGMB-33/FH-90	NIBGE, Faisalabad, Pakistan	2011
IR-NIBGE-1524-4	PGMB-33/NIBGE-2	-do-	2010
IR-NIBGE-3	PGMB-33/FH-100	-do-	2012
IR-NIBGE-4	PGMB-33/CIM-448	-do-	2011
IR-NIBGE-5	PGMB-33/CIM496	-do-	Under approval
IR 3300-24	PGMB-33/BH-160	-do-	Under approval
IR 3300-13	PGMB-33/BH-160	-do-	Under approval
NIBGE-115	S-12/LRA-5166	-do-	2012
NN-3	S-12/LRA-5166	-do-	Under approval
NIBGE-2472	S-12/LRA-5166	-do-	Germplasm
NIBGE-2	LRA/S-12	-do-	2006
IR-2379	PGMB-33/FH-100	-do-	Germplasm
IR-NIBGE-3701-38	PGMB-33/CIM-448	-do-	2010
IR 1526	PGMB-33/NIBGE-2	-do-	Germplasm
NIBGE-314	S-12/LRA	-do-	Under approval
NIBGE-5	S-12/LRA	-do-	Germplasm
NIBGE-4	S-12/ CIM-448	-do-	Germplasm
IR NIBGE-2620	IR-901/Rajhans	-do-	Germplasm
NIBGE 758-8	S-12/ CIM-448	-do-	Germplasm
IR NIBGE-3701-33-6	PGMB-33/CIM-448	-do-	2010
SLH-284	-	CRS, Sahiwal, Pakistan	Under approval
CIM-446	$CP 15/2 \times S 12$	CCRI, Multan, Pakistan	1998
CIM-473	CIM-402 × LRA 5166	-do-	2002
CIM-496	$CIM-425 \times 755-6/93$	-do-	2005
CIM-499	CIM-433 \times 755-6/93	-do-	2003
CIM-506	CIM-360 \times CP 15/2	-do-	2004
CIM-554	2579-04/97 × W-1103	-do-	2009
CIM-707	CIM-243 × 738-6/93	-do-	2004

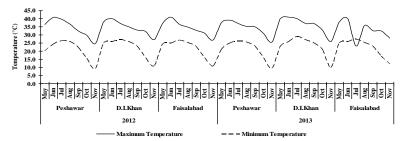


Fig. 1: Maximum and minimum temperatures during the cotton crop seasons at three locations

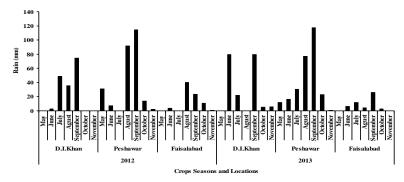


Fig. 2: Rainfall data during the cotton crop seasons at three locations

Data Collection

Ten plants were randomly selected from central two rows in each genotype/replication to record the data during both years at all locations. Data were recorded on plant height with the help of meter rod by measuring from ground level to the tip of the plant, bolls per plant recorded through counting the total number of mature and open bolls per plant, seeds per boll determined by taking average of total seeds in ten bolls (Shah *et al.*, 2016). For lint (%), in each plant, the dry and clean seed cotton was picked and weighed. The ginning was made separately with 8-saw gin machine. The lint obtained from each plant was weighed and lint (%) was calculated by the following formula:

$$Lint \% (G.O.T) = \frac{Weight of \ lint in \ a \ sample}{Weight of \ seed \ cotton \ sample} \times 100$$

Statistical Analyses

All the data were subjected to analysis of variance to test the null hypothesis of no differences among various genotypes, years, locations and their interactions ($G \times Y \times L$) (Hicks, 1982; Gomez and Gomez, 1984). The genotypes, years, locations and their interaction mean squares for each trait were further separated and compared by using the least significant difference (LSD) test at 5% level of probability. Significant $G \times L \times Y$ justified further analysis. Locations within each year were considered as six separate environments namely Peshawar 2012 (E-1), D.I. Khan 2012 (E-2), Faisalabad 2012 (E-3), Peshawar 2013 (E-4), D.I. Khan 2013 (E-5) and Faisalabad 2013 (E-6). GGE biplot analysis (Yan, 2001) was used to interpret the genotype by environment interaction using Gen-Stat V.12 computer software (Gen-Stat, 2009). Correlation of lint % with plant height, bolls per plant and seeds per boll was worked out through computer software Statistix version 8.1.

Results

Genotype by Environment Interaction (GEI) Study

Genotype by environment interaction study was carried out for 28 upland cotton genotypes across two years and three locations. Combined analysis of variance revealed that years and locations showed significant (p \leq 0.01) differences for all the traits (Table 3). The year × location interactions were significant (\leq 0.01) for seeds per boll and lint % while nonsignificant for plant height and bolls per plant. Genotypes, genotype by year, genotypes by location and genotype × year × location interactions were significant ($p \leq$ 0.01) for all the traits (Fig. 1 and 2).

Overall, the genotypes mean across years and locations for plant height ranged from 125.29 to 148.08 cm (Table 4). Minimum plant height was observed for genotype

IR-NIBGE-2620 (125.29 cm) and it was found same with nine other genotypes ranging from 125.51 to 133.86 cm (Table 4). Maximum plant height was observed in genotype IR-NIBGE-3701-33-6 (148.08 cm); however, it was found similar in stature with four other genotypes. For year means, on average the genotypes revealed minimum plant height during 2012 (131.52 cm) and more during 2013 (139.86 cm). For location means, on average the genotypes revealed minimum plant height at Faisalabad (129.09 cm) and D.I. Khan (136.43 cm). However, at Peshawar, the genotypes showed maximum plant height (141.55 cm). In genotype × year × location interactions, the mean values for plant height ranged from 100.87 to 161.67 cm. Minimum plant height was observed for genotype NIBGE-4 (100.87 cm) planted during 2012 at Faisalabad. However, maximum plant height was noted for genotype IR-NIBGE-3 (161.67 cm) grown at Peshawar during 2013. Highly significant positive correlation ($r = 0.05^{**}$) was observed between plant height and lint % (Table 8).

For bolls per plant across years and locations, overall mean values of the genotypes ranged from 35.84 to 54.46 (Table 5). Maximum bolls per plant were observed in cultivar NIBGE-4 (54.46) and it was found same in performance with genotype IR-NIBGE-2620 (53.17). However, minimum bolls per plant were produced by genotype IR-3300-13 (35.84) and it was found same in performance with six other genotypes ranging from 37.37 to 39.51. For year means, overall the genotypes produced maximum bolls per plant grew during 2013 (52.92) and minimum during 2012 (33.62). For locations, on average the genotypes produced maximum bolls per plant grown at Peshawar (47.95) followed by D.I. Khan (42.44) and minimum at Faisalabad (39.44). For genotype × year × location interactions, bolls per plant ranged from 12.67 to 71.13. Maximum bolls per plant were exhibited by cultivar CIM-473 (71.13) grown during 2013 at Peshawar and it was found same in performance with some other genotypes grown during 2012 and 2013 at three locations ranging from 62.33 to 69.67. However, least bolls per plant were observed in cultivar CIM-446 (12.67) during 2012 at Faisalabad. Significant ($p \le 0.01$) association (r = 0.177) of bolls per plant was observed with lint % (Table 8).

For seeds per boll, averaged over years and locations, all the genotypes ranged from 24.00 to 28.52 (Table 6). Maximum and similar seeds per boll were observed in cultivars IR-2379 (28.52) and IR-3300-13 (28.46), and these two genotypes were found same in performance with six other cultivars ranging from 27.49 to 28.29. However, minimum seeds per boll were observed in cultivar NIBGE-314 (24.00) and it was found at par with three other genotypes i.e., IR-NIBGE-2620 (24.03), NIBGE-758-8 (24.12) and IR-1526 (24.48). For year means, overall the genotypes produced maximum seeds per boll grown during 2013 (27.57) and minimum in 2012 (25.74). For locations, on average the genotypes produced maximum seeds per boll grown at Peshawar (27.80) followed by

Table 3: Mean squares for various traits in upland cotton genotypes evaluated for two years at three locations

Sources of variations	df	Plant height (cm)	Bolls / plant	Seeds / boll	Lint (%)
Years	1	8763.338 [*]	46947.251**	422.401**	16.194**
Locations	2	6594.437 [*]	3128.141*	666.905**	137.257**
Years × Locations	2	107.976	208.032	208.092**	82.773**
Years \times Loc. \times Reps	12	1037.034	591.286	27.72	1.64
Genotypes	27	582.269**	377.588***	29.717**	53.707**
Genotypes × Years	27	206.155	145.415**	6.698^{**}	20.578**
Genotypes × Locations	54	666.162**	177.059**	25.603**	8.499**
Genotypes \times Years \times Loc.	54	218.324	296.818**	8.942**	11.337**
Error $(Y \times L \times R \times G)$	324	181.512	34.854	3.105	1.942
CV (%)		9.93	13.64	6.61	3.87
df = degree of freedom					

Table 4: Mean performance of upland cotton genotypes for plant height (cm) across $G \times Y \times L$ interactions

Genotypes		2012			2013		Means (cm)
• •	Peshawar	D.I. Khan	Faisalabad	Peshawar	D.I. Khan	Faisalabad	
IR-NIBGE-901	144.00	122.07	134.33	136.13	141.73	131.20	134.91 d-g
IR-NIBGE-1524-4	134.40	122.67	131.20	156.80	142.67	120.67	134.73 d-g
IR-NIBGE-3	133.00	121.47	117.80	161.67	131.47	124.00	131.57 e-h
IR-NIBGE-4	142.20	130.33	132.33	149.87	140.33	133.47	138.09 c-f
IR-NIBGE-5	129.87	107.67	118.33	145.33	130.67	153.00	130.81 e-h
IR-3300-24	131.00	122.60	111.00	145.33	132.60	153.33	132.64 e-h
IR-3300-13	133.13	131.93	139.87	136.13	141.93	135.87	136.48 c-f
NIBGE-115	153.80	149.87	120.33	156.80	159.87	142.67	147.22 ab
NN-3	158.67	143.27	115.73	161.67	153.27	133.67	144.38 a-c
NIBGE-2472	150.87	135.87	120.00	153.87	145.87	128.13	139.10 b-e
NIBGE-2	146.53	131.13	127.13	149.53	141.13	127.00	137.08 c-f
IR-2379	143.00	116.40	129.60	146.00	126.40	147.53	134.82 d-g
IR-NIBGE-3701-38	142.33	118.33	145.53	145.33	128.33	137.33	136.20 c-f
IR-1526	142.33	125.80	147.00	145.33	135.80	141.53	139.63 a-e
NIBGE-314	139.13	122.80	122.27	142.13	145.20	143.00	135.76 c-g
NIBGE-5	135.80	136.67	109.87	138.80	132.87	123.27	129.54 f-h
NIBGE-4	153.20	139.00	100.87	156.20	139.80	103.20	132.04 e-h
IR-NIBGE-2620	133.80	107.80	120.60	136.80	136.13	116.60	125.29 h
NIBGE-758-8	152.53	157.33	110.20	155.53	156.80	129.00	143.57 a-d
IR-NIBGE-3701-33-6	154.00	154.67	129.93	157.00	161.67	131.20	148.08 a
SLH-284	129.27	147.67	126.27	132.27	153.27	120.67	134.90 d-g
CIM-446	116.87	154.20	147.33	119.87	145.87	130.80	135.82 c-g
CIM-473	107.87	132.80	145.93	141.93	141.13	133.47	133.86 e-h
CIM-496	127.60	138.33	139.87	159.87	126.40	142.80	139.14 b-e
CIM-499	118.80	132.47	120.33	153.27	128.33	147.67	133.48 e-h
CIM-506	129.40	123.93	115.73	145.87	135.80	111.73	127.08 gh
CIM-554	132.87	141.67	122.67	141.13	151.67	135.33	137.56 c-f
CIM-707	118.53	120.53	121.47	121.53	143.87	127.13	125.51 h
Year means (cm)	2012 = 131.5	52 b		2013 = 139.8	86 a		
Location means (cm)	Peshawar = 1	141.55 a	D.I. Khan = 13	36.43 ab	Faisalabad =	129.09 b	

Faisalabad (26.29) and minimum at D.I. Khan (24.87). For genotype \times year \times location interactions, the mean values of all the genotypes ranged from 19.71 to 32.32. Maximum and same seeds per boll (32.32) were exhibited by cultivars IR-3300-13 and CIM-499 grown during 2013 at D.I. Khan and IR-2379 (32.32) grown at Peshawar during the same cropping season. Least seeds per boll were observed in genotype NIBGE-2472 (19.71) grown during 2012 at D.I. Khan. The association between seeds per boll and lint % was significantly ($p \le 0.01$) negative (Table 8).

For lint %, overall the genotype means across years and locations, ranged from 32.52 to 38.72 % (Table 7). Maximum lint % was observed in cultivar CIM-554

(32.52%) while minimum in NIBGE-2472 (32.52%). For year means, on average the genotypes produced maximum lint % grown during 2013 (36.21%) and minimum in 2012 (35.85%). For locations, overall the genotypes produced maximum lint % grown at D.I. Khan (36.80%) followed by Peshawar (36.26%) while minimum at Faisalabad (35.04%). For genotype × year × location interaction, the lint % ranged from 28.60 to 42.77%. Maximum lint % was exhibited by cultivar CIM-506 (42.77%) grown during 2012 at D.I. Khan and it was found same in performance with eight other genotypes ranging from 40.83 to 42.68%. However, minimum lint % was observed in genotype IR-NIBGE-12 (28.60%) grown during 2012 at Peshawar.

Table 5: Mean performance of upland cotton genotypes for bolls per plant across $G \times Y \times L$ interactions

Genotypes		2012	2		2013		
	Peshawar	D.I. Khan	Faisalabad	Peshawar	D.I. Khan	Faisalabad	_
IR-NIBGE-901	39.27	33.80	21.93	59.00	55.33	46.67	42.67 f-j
IR-NIBGE-1524-4	30.60	30.33	25.80	64.67	65.13	42.60	43.19 e-j
IR-NIBGE-3	36.20	32.27	20.87	54.33	57.33	47.33	41.39 g-k
IR-NIBGE-4	42.47	34.13	18.73	48.93	56.33	57.13	42.96 e-j
IR-NIBGE-5	33.93	19.67	21.93	47.87	64.33	49.33	39.51 j-m
IR-3300-24	33.67	26.87	21.13	38.33	55.87	48.33	37.37 lm
IR-3300-13	34.07	30.13	23.27	43.80	61.53	22.27	35.84 m
NIBGE-115	32.60	25.73	40.73	54.67	68.87	39.73	43.72 d-i
NN-3	37.53	28.20	35.67	50.60	68.33	47.33	44.61 c-h
NIBGE-2472	39.33	29.33	38.07	55.33	57.80	48.20	44.68 c-h
NIBGE-2	41.60	27.40	29.87	65.13	62.33	49.93	46.04 b-f
IR-2379	40.67	38.40	36.40	57.33	38.33	48.87	43.33 e-j
IR-NIBGE-3701-38	40.60	26.40	41.47	56.33	58.00	53.87	46.11 b-f
IR-1526	42.33	32.53	35.47	64.33	54.67	56.33	47.61 bc
NIBGE-314	48.73	36.93	43.73	55.87	50.60	47.87	47.29 b-d
NIBGE-5	43.67	39.27	39.93	61.53	55.33	53.53	48.88 b
NIBGE-4	41.47	50.27	40.13	68.87	65.13	60.87	54.46 a
IR-NIBGE-2620	46.27	40.33	46.40	68.33	57.33	60.33	53.17 a
NIBGE-758-8	44.20	31.60	20.00	57.80	56.33	49.80	43.29 e-j
IR-NIBGE-3701-33-6	41.13	43.27	15.33	62.33	64.33	54.33	46.79 b-e
SLH-284	45.07	39.93	18.87	52.70	55.87	57.13	44.93 c-g
CIM-446	30.00	35.60	12.67	69.67	30.20	49.33	37.91 k-m
CIM-473	31.07	35.40	16.27	71.13	28.80	48.33	38.50 k-m
CIM-496	35.40	33.40	27.93	62.73	28.20	56.33	40.67 i-l
CIM-499	34.07	42.53	17.60	53.00	31.47	47.87	37.76 k-m
CIM-506	40.33	32.93	20.00	54.00	25.07	53.53	37.64 k-m
CIM-554	41.27	30.87	36.13	45.47	28.00	60.87	40.43 i-l
CIM-707	37.40	33.20	32.27	56.00	34.67	52.00	40.92 h-1
Year means	2012 = 33.62	2 b		2013 = 52.93	a		
Location means	Peshav	var = 47.95 a	D.I. Khan:	= 42.44 ab	Faisalabad	= 35.99 b	

Table 6: Mean performance of upland cotton genotypes for seeds per boll across $G \times Y \times L$ interactions

Genotypes		2012		2013			Means
	Peshawar	D.I. Khan	Faisalabad	Peshawar	D.I. Khan	Faisalabad	
IR-NIBGE-901	24.56	22.36	28.23	26.56	28.73	28.61	26.51 c-f
IR-NIBGE-1524-4	26.45	21.88	28.33	28.45	29.28	28.53	27.16 a-d
IR-NIBGE-3	26.85	20.39	26.27	28.85	29.23	27.05	26.44 c-f
IR-NIBGE-4	28.01	23.40	27.77	30.01	27.63	30.89	27.95 ab
IR-NIBGE-5	29.56	22.69	26.16	31.56	27.09	30.49	27.93 ab
IR-3300-24	26.73	25.21	24.93	28.73	27.93	30.99	27.42 a-c
IR-3300-13	27.28	24.49	26.61	29.28	32.32	28.80	28.13 a
NIBGE-115	27.23	22.88	26.08	29.23	29.32	30.08	27.47 a-c
NN-3	25.63	22.67	28.35	27.63	26.08	29.97	26.72 с-е
NIBGE-2472	25.09	19.71	28.84	27.09	28.35	28.19	26.21 d-g
NIBGE-2	25.93	22.61	28.61	27.93	22.61	32.00	26.62 c-f
IR-2379	30.32	24.28	28.53	32.32	24.28	29.32	28.18 a
IR-NIBGE-3701-38	27.32	24.49	27.05	29.32	24.43	26.08	26.45 c-f
IR-1526	24.08	23.01	20.43	26.08	23.01	28.35	24.16 hi
NIBGE-314	26.35	22.93	20.75	28.35	22.93	20.75	23.68 i
NIBGE-5	26.84	22.17	27.08	28.84	22.17	27.08	25.70 e-g
NIBGE-4	26.61	24.72	25.04	28.61	24.72	25.04	25.79 e-g
IR-NIBGE-2620	26.53	20.43	23.13	28.53	20.43	23.13	23.70 i
NIBGE-758-8	25.05	20.75	20.57	27.05	28.73	20.57	23.79 i
IR-NIBGE-3701-33-6	28.89	27.08	23.47	30.89	29.28	23.47	27.18 a-d
SLH-284	28.49	25.04	22.61	30.49	29.23	22.61	26.41 c-f
CIM-446	28.99	23.13	24.93	30.99	27.63	24.93	26.77 с-е
CIM-473	26.80	20.57	26.61	28.80	27.09	26.61	26.08 d-g
CIM-496	28.08	23.47	21.60	30.08	27.93	21.60	25.46 fg
CIM-499	27.97	22.61	23.99	29.97	32.32	23.99	26.81 b-e
CIM-506	26.19	19.92	27.88	28.19	29.32	27.88	26.56 c-f
CIM-554	25.51	22.76	28.48	27.51	26.08	28.48	26.47 c-f
CIM-707	23.01	20.20	27.16	25.01	28.35	27.16	25.15 gh
Year means	2012 = 25.07 b)		2013 = 27.57	7 a		-
Location means	Peshawar	= 27.80 a	D.I. Khan =	24.87 c	Faisala	bad = 26.29 b	

Table 7: Mean performance of upland cotton genotypes for lint (%) across $G \times Y \times L$ interactions

Genotypes		2012				2013		
	Peshawar	D.I. Khan	Faisalabad	Peshawar	D.I. Khan	Faisalabad		
IR-NIBGE-901	37.35	35.62	32.97	33.87	36.56	35.27	35.27 hi	
IR-NIBGE-1524-4	36.12	34.45	31.27	33.99	37.69	36.56	35.01 hi	
IR-NIBGE-3	35.53	34.66	32.03	37.12	34.68	37.69	35.29 hi	
IR-NIBGE-4	34.23	39.63	35.27	42.12	36.33	32.62	36.70 f	
IR-NIBGE-5	28.60	32.12	29.70	37.32	36.87	32.63	32.87k	
IR-3300-24	32.62	34.11	31.47	34.81	37.14	37.38	34.59 ij	
IR-3300-13	32.63	32.92	30.67	36.71	36.79	34.83	34.09 j	
NIBGE-115	37.38	32.88	31.27	37.56	38.86	31.43	34.90 h-j	
NN-3	34.83	36.01	33.20	34.83	36.01	33.20	34.68 h-j	
NIBGE-2472	31.43	33.87	32.27	31.43	33.87	32.27	32.52 k	
NIBGE-2	34.23	33.99	30.63	34.23	33.99	30.63	32.95 k	
IR-2379	35.27	37.12	33.00	35.27	37.12	35.53	35.55 gh	
IR-NIBGE-3701-38	36.56	42.12	37.33	36.56	42.12	36.56	38.55 ab	
IR-1526	37.69	37.32	34.67	37.69	37.32	37.69	37.06 d-f	
NIBGE-314	34.68	34.81	33.20	34.68	34.81	34.68	34.48 ij	
NIBGE-5	36.33	36.71	35.13	36.33	36.71	36.33	36.26 fg	
NIBGE-4	36.87	37.56	33.53	36.87	37.56	36.33	36.46 fg	
IR-NIBGE-2620	37.14	36.30	34.77	37.14	36.30	36.87	36.42 fg	
NIBGE-758-8	36.79	36.46	33.87	36.79	36.46	37.14	36.25 fg	
IR-NIBGE-3701-33-6	38.86	38.56	35.00	38.86	38.56	36.79	37.77 b-e	
SLH-284	39.50	38.43	36.00	39.50	35.53	38.86	37.97 a-c	
CIM-446	37.69	40.83	38.40	37.69	34.23	38.40	37.87 a-d	
CIM-473	37.25	42.68	38.43	37.25	28.60	38.43	37.11 c-f	
CIM-496	37.38	42.12	36.40	37.38	32.62	36.40	37.05 d-f	
CIM-499	35.35	41.36	36.47	35.35	36.33	36.47	36.89 ef	
CIM-506	37.02	42.77	37.00	37.02	36.87	37.00	37.95 a-d	
CIM-554	38.47	41.11	38.57	38.47	37.14	38.57	38.72 a	
CIM-707	38.04	40.33	36.47	38.04	36.79	36.47	37.69 b-e	
Year means (%)	2012 = 35.85	бЪ		2013 = 36.21	l a			
Location means (%)	Peshav	var = 36.26 b	D.I. Kh	an = 36.80 a	Faisala	abad = 35.04 c		

Table 8: Correlation of lint percent with yield traits

Parameters	Correlation coefficients	$P \le 0.05$
Plant height	0.054	0.000
Bolls per plant	0.177	0.000
Seeds per boll	-0.121	0.000

GGE-Biplot Analysis

Polygon view of biplot analysis: Which-won-where pattern of biplot is visualized in Fig. 3. Twenty-eight genotypes were distributed in six sectors. Sectors of genotypes where environments were included indicated specific interaction of genotypes with those environments. Genotypes CIM-473, CIM-554, IR-NIBGE-3701-38, NIBGE-115, IR-NIBGE-5 and NIBGE-2472 were on the vertices of polygon suggesting their specific adaptability. Environment E-2 (2012, D.I. Khan) and E-3 (2012, NIBGE) fell into the sector in which genotype CIM-473 was the vertex cultivar. This means that genotype CIM-473 was the best cultivar in environment E-3 and E-2. Other three environments viz., E-1 (2012, Peshawar), E-4 (2013, Peshawar) and E-5 (2013, D.I. Khan) fell into the sector in which genotypes CIM-554 and IR-NIBGE-3701-38 were the vertex cultivars, means that these genotypes had significant interaction with these three environments. Environment E-6 (2013, NIBGE) fell into the sector in which none of the genotypes was the vertex cultivar which means that said environment was not the best for any cultivar. No environment fell into sectors

with genotypes NIBGE-2472, IR-NIBGE-5 and NIBGE-115 which mean that these three cultivars were not the good performers in any of the environment and might be poor performers in some/all of the environments. Genotypes which were located near the origin were also found as less responsive to the environments than the corner (vertex) genotypes such as NIBGE-5 and IR-NIBGE-4.

Average Lint (%) and Stability of the Cultivars

An average tester coordinate (ATC) based on the average environment is shown in Fig. 4. The ATC X-Axis passes through the biplot origin and the marker of the average environment which is defined by the PC1 and PC2 scores overall environments. The ATC Y-Axis passes the plot origin and is perpendicular to the ATC X-Axis. The average lint % of the cultivar is approximated by the projections of their markers to the ATC X-Axis. Thus, the genotype CIM-554 had the highest average lint % followed by genotype SLH-284. However, genotype NIBGE-2472 had the lowest lint % followed by IR-NIBGE-5. The stability of the cultivar is measured by their projection to the ATC Y-Axis.

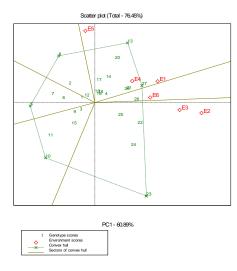


Fig. 3: "Which-won-where" pattern of GGE biplot for 28 upland cotton genotypes evaluated across multiple environments. Genotypes at the vertices of the polygon are responsive to particular environments. Key: Genotypes with Sr. No. 1-28 (Table 2), Environments: E1 (Peshawar 2012), E2 (D.I. Khan 2012), E3 (Faisalabad 2012), E4 (Peshawar 2013), E5 (D.I. Khan 2013), E6 (Faisalabad 2013)

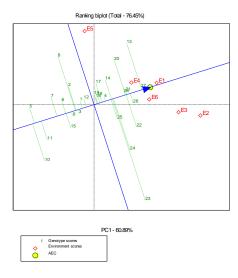


Fig. 4: Ranking biplot of GGE biplot based on genotype focused scaling for 28 upland cotton genotypes. Genotypes on the extreme right are highest yielding; those having smaller projection on the ordinate are relatively stable. Key: Genotypes with Sr. No. 1-28 (Table 2), Environments: E1 (Peshawar 2012), E2 (D.I. Khan 2012), E3 (Faisalabad 2012), E4 (Peshawar 2013), E5 (D.I. Khan 2013), E6 (Faisalabad 2013)

The greater the absolute length of the projection of a cultivar, less stable it is. Therefore, NIBGE-2472 was found as the least stable cultivar while CIM-554 was identified as the most stable genotype followed by SLH-284.

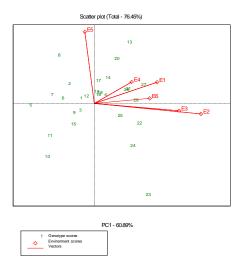


Fig. 5: GGE biplot for the evaluation of the relationships among the six environments. Environmental vectors having smaller angles are closely related. Environments having longer vectors are discriminating. Key: Genotypes with Sr. No. 1-28 (Table 2). Environments: E1 (Peshawar 2012), E2 (D.I. Khan 2012), E3 (Faisalabad 2012), E4 (Peshawar 2013), E5 (D.I. Khan 2013), E6 (Faisalabad 2013)

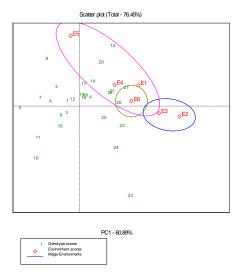


Fig. 6: Visualization of mega-environment using GGE biplot for 28 upland cotton genotypes evaluated across multiple environments. Key: Genotypes with Sr. No. 1-28 (Table 2). Environments: E1 (Peshawar 2012), E2 (D.I. Khan 2012), E3 (Faisalabad 2012), E4 (Peshawar 2013), E5 (D.I. Khan 2013), E6 (Faisalabad 2013)

The Representative and Discriminating Ability of the Environments

The vector length i.e., absolute distance between the markers of an environment and the plot origin is the

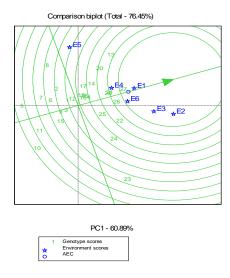


Fig. 7: Visulization of 'ideal genotype' using GGE biplot with scaling focussed on genotypes. Concentric circles showing the location of ideal genotype. Genotypes closer to the ideal spot are ideal genotypes. Key: Genotypes with S. No. 1-28 (Table 2). Environments: E1 (Peshawar 2012), E2 (D.I. Khan 2012), E3 (Faisalabad 2012), E4 (Peshawar 2013), E5 (D.I. Khan 2013), E6 (Faisalabad 2013)

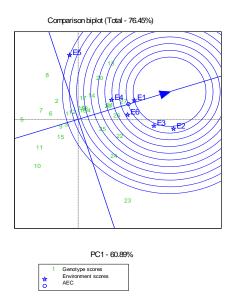


Fig. 8: Visulization of 'ideal environment' using GGE biplot. Concentric circles showing the position of ideal environment. Environments closer to the ideal spot are ideal environments. Key: Genotypes with Sr. No. 1-28 (Table 2). Environments: E1 (Peshawar 2012), E2 (D.I. Khan 2012), E3 (Faisalabad 2012), E4 (Peshawar 2013), E5 (D.I. Khan 2013), E6 (Faisalabad 2013)

measure of its discriminating ability, longer the vector higher the discriminating power of that environment (Fig. 5). In environment E-2 (2012, D.I. Khan), the

vector was long which means that the variation among the genotypes was high in this environment and the angle with other four environments was less which revealed the high relationship between E-2 (2012, D.I. Khan) and four other environments. In the remaining environment E-5 (2013, D.I. Khan), the angle was high and having less relationship with all other environments. For said observations, all the six environments divided into two mega-environments, and the larger environment containing four environments viz., E-1 (2012, Peshawar), E-4 (2013, Peshawar), E-5 (2013, D.I. Khan) and E-6 (2013, NIBGE) while the smaller one having two environments i.e., E-2 (2012, D.I. Khan) and E-3 (2012, NIBGE) (Fig. 6).

Evaluation of Ideal Genotypes and Ideal Environments

In the GGE-biplot analysis, the genotypes found in the first concentric circle are considered as ideal genotypes. Desirable genotypes are ones lying closer to the ideal genotype. In the present study, genotype CIM-554 was close to the ideal genotype and located on the first concentric circle followed by CIM-506 located in the second circle. Genotypes IR-NIBGE-5 and NIBGE-2472 were undesirable genotypes and were found distant from the first concentric circle (Fig. 7). Similar to the ideal genotype, the ideal environment is located on the first concentric circle in the environment focused biplot and the desirable environment is always close to the ideal environment. In the present study, E-1 (2012, Peshawar) was located on the first concentric circle followed by E-2 (2012, D.I. Khan) and E-3 (2012, NIBGE) which were identified as desirable environments and found close to the ideal environment (Fig. 8).

Discussion

Significant mean squares due to genotypes, environments and G × E interaction for various traits revealed greater genetic variability among the cotton genotypes due to their diverse genetic background, as well as environments under which the genotypes were grown. In previous studies, genotype x year and genotype × year × location interaction means were observed significant for various morphological and yield traits in four groups of cotton genotypes (Machado et al., 2002; Ali et al., 2017). In various environments, the genotypes performed differently and significant G × E interactions in upland cotton (Satish et al., 2009). Mean squares due to genotypes, environments and G × E interactions were reported to be significant for various agronomic traits in G. hirsutum L (Gul et al., 2014, 2016).

Plant height is an important trait and has a close relationship with bolls per plant, as has an ultimately

positive effect on lint %. In present studies, for plant height, the genotypes, years, locations, and genotypes × locations revealed significant $(p \le 0.01)$ differences while other components of variance were nonsignificant. It revealed that genotypes have the significant role in the said studies at different locations. A significant effect of genotypes and nonsignificant variances due to G × E interactions were observed for plant height in upland cotton (Kakar et al., 2012). However, some studies revealed that environmental factors had a significant influence on plant height in upland cotton (Singh and Gill, 1982). Some of the previous studies manifested nonsignificant mean squares for genotypes and genotype × environment interactions for plant height in upland cotton (Unay et al., 2004; Shah et al., 2005; Gul et al., 2014). Plant height can be used as selection criteria because of its positive association with seed cotton yield and lint % which might be due to no lodging of cotton plants (Khan et al., 2005; Ali et al., 2017). Cotton breeders are mostly interested in minimum plant height due to lodging threat and picking problems. However, plant height can play a constructive role in boll setting and lint yield if lodging did not occur.

Bolls per plant have an important role in managing lint yields and thus, selection should be made for larger number bolls per plant because of its significant positive association with lint yields. In present studies, genotypes, years, locations and interactions (genotypes \times years, genotypes \times locations and genotypes \times years \times locations) were found significant ($p \le 0.01$) for bolls per plant which might be due to the broad genetic base of the genotypes and the environments in which these genotypes were grown. Present findings also revealed that promising genotypes might be area specific and bolls per plant were significantly positive associated with lint %. Significant differences were observed among genotypes, environments, and genotype × environment interactions for bolls per plant in upland cotton genotypes (Dewdar, 2013; Gul et al., 2016). Past studies revealed the significant positive association of bolls per plant with lint yields in upland cotton (Khan et al., 2005; Ahmad et al., 2011).

Seeds per boll and lint yield are important yield contributing traits and have a direct contribution to boll weight. Present studies revealed that genotypes, years, locations and their interactions were significant ($p \le 0.01$) for seeds per boll and lint %, which manifesting greater genetic variability in the genotypes and the diverse environments where these genotypes were studied. Lint % is one of the important yield components and high lint yield is always the primary goal in cotton. Significant differences were observed among the genotypes for seeds per boll and lint %, and significant positive association of seeds per boll with lint yield (Ahmad et al., 2008). Correlation analysis describes the strength of association between different traits. Significant differences were observed among genotypes for seeds per boll and lint yield, with a significant positive association of lint yield with seeds per boll in upland cotton (Meredith *et al.*, 2012; Vinodhana *et al.*, 2013; Ul-Allah *et al.*, 2017). Furthermore, significant positive associations of seeds per boll with lint yield mainly due to boll weight. However, some past studies revealed significant differences among the genotypes for seeds per boll and lint %, while seeds per boll showed the negative association with lint % in upland cotton genotypes (Hussain *et al.*, 2010). The polygenic architecture of the lint % makes it extremely difficult to manipulate and improve (Gapare *et al.*, 2018). The cotton crop is mainly grown for fiber and major output after ginning of seed cotton is lint %, however, edible oil is also extracted as a byproduct from cottonseed. Therefore, cottonseed has the major share in the edible oil industry of cotton growing countries.

Contradictory findings might be due to different cotton genotypes and the diverse environmental conditions. Previous studies revealed that selection of superior and promising genotypes for lint yield in cotton performance trials is impacted by $G \times E$ interaction (Geng et al., 1987; Mustafa et al., 2007; Ehsan et al., 2008). To widen the genetic base upon which selection is practiced, large and diverse germplasm needs to be screened. Both qualitative and quantitative types of interaction were observed in this study. In quantitative interaction, the promising genotypes performs best even if there may be a universal change in the mean performance of all of the genotypes tested across different environments, which do not affect the genotype to be selected. Qualitative (crossover) interaction, however, also a type of interaction that makes multiple environments testing (MET) data interpretation and makes selection complex (Yan et al., 2007). The vector length and direction represent the extension of the genotypes response to the tested environments (Farias et al., 2016; Ali et al., 2017).

Test environments can be divided into a group of locations (mega-environments) that share the same best genotype and whenever there is a consistent differential ranking of genotypes (Yan et al., 2007). Previous studies revealed that mega-environment split up the crop growing area into different targeted regions (Gauch and Zobel, 1997). In present studies, Peshawar (2012) was identified as representative site and hence, was found more effective for evaluation and identifying superior cotton varieties. The location of Peshawar favored as new crop area (by having less pressure of insect pests), and due to silty clay loam soil, more nitrogen and rain, and ultimately low temperature which are necessary for boll retention. Past studies revealed that line passing through the biplot origin is called average environment coordinate (AEC), which is defined by the average PC1 and PC2 scores, for all the environments (Yan and Kang, 2003). environments having long vectors and large angles with AEC abscissa are good in culling unstable genotypes. However, sites with long vector and smaller angles with average environment axis are suitable for selecting superior genotypes (Yan et al., 2007).

An environment that has the representative

identification of all other environments for widely adapted variety and discriminating ability among genotypes is an ideal test environment (Yan, 2001). Based on the present findings, the E-1 (2012, Peshawar) was a near ideal site having high discriminating power and very low angle from the average environment axis, which might be due to distinct environmental condition i.e., silty clay loam soil, more nitrogen and rain, and ultimately low temperature. Overall desirability of a genotype is a combination of high yield and stability in performance (Yan and Kang, 2003). An ideal genotype is one that has the highest yield and an absolute stability. In GGE-biplot methodology, the estimation of yield and stability of genotypes can be worked out through AEC methods (Yan et al., 2007). Closer to the ideal genotype, are the most desirable genotypes (Yan et al., 2007). Based on this criterion, genotypes CIM-554 and CIM-707 were the only genotypes under the category of the desirable genotypes for wider adaptation. For MET data, the GGE biplot analysis was found to be a handy tool (Kaya et al., 2006; Yan and Tinker, 2006)

Based on the present study, genotype CIM-707 was the most stable and widely adapted genotype in terms of yield and lint traits for regional release. Trials across several years and locations will enable to firmly conclude the presence of the mega-environments. The criterion for an ideal genotype is high yield and high stability across environments (Farshadfar et al., 2012; Ali et al., 2017). The ideal genotype is located on the first concentric circle in biplot. Some of the past studies revealed that starting from the middle concentric circle pointed with arrow concentric circles were drawn to help in visualizing the distance between the genotypes and ideal genotype (Yan and Kang, 2003). Some previous studies revealed that ideal environment is the representative and has the highest discriminating power (Yan and Tinker, 2006). For selection, the ideal genotype can be used as a benchmark. The genotypes which are close to the ideal genotype can be used and studied further in the future breeding program, while those which are far away from the ideal genotype can be rejected in early breeding cycles (Yan and Kang, 2003).

Conclusion

Based on genotype × environment interaction and GGE-biplot analysis, the cultivars CIM-473, CIM-506, and CIM-554 were declared as best performers and ideal genotypes. Similarly, Peshawar-2012 was identified as an ideal environment, while crop season 2013 was found more prolific in terms of lint %. Moreover, significant correlation of lint % was observed with plant height and bolls per plant. This study further explored Peshawar as one of the potential areas for cotton cultivation. This could bring significant and positive change in cropping pattern of Peshawar in specific and Khyber Pakhtunkhwa in general.

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References

- Ahmad, M., N.U. Khan, F. Mohammad, S.A. Khan, I. Munir, Z. Bibi and S. Shaheen, 2011. Genetic potential and heritability studies for some polygenic traits in cotton (G. hirsutum L.). Pak. J. Bot., 43: 1713–1718
- Ahmad, W., N.U. Khan, M.R. Khalil, A. Parveen, U. Aiman, M. Saeed, S. Ullah and S.A. Shah, 2008. Genetic variability and correlation analysis in upland cotton. Sarhad J. Agric., 24: 573–580
- Ali, I., N.U. Khan, F. Mohammad, M.A. Iqbal, A. Abbas, Farhatullah, Z. Bibi, S. Ali, I.A. Khalil, S. Ahmad and M. ur Rahman, 2017. Genotype by environment and GGE-biplot analysis for seed cotton yield in upland cotton. *Pak. J. Bot.*, 49: 2273–2283
- Ali, Y., Z. Aslam and F. Hussain, 2005. Genotype and environment interaction effect on yield of cotton under naturally salt stress condition. Int. J. Environ. Sci. Technol., 2: 169–173
- Baker, H.C. and J. Leon, 1988. Stability analysis in plant breeding. *Plant Breed.*, 101: 11–23
- Dewdar, M.D.H., 2013. Stability analysis and genotype x environment interactions of some Egyptian cotton cultivars. *Afr. J. Agric. Res.*, 8: 5156–5160
- Ehsan, F., A. Ali, M.A. Nadeem, M. Tahir and A. Majeed, 2008. Comparative yield performance of new cultivars of cotton (G. hirsutum L.). Pak. J. Life Soc. Sci., 6: 1–3
- Farias, F.J.C., L.P. Carvalho, J.L.S. Filho and P.E. Teodoro, 2016. Biplot analysis of phenotypic stability in upland cotton genotypes in Mato Grosso. *Genet. Mol. Res.*, 15: gmr.15028009
- Farshadfar, E., R. Mohammadi, M. Aghaee and Z. Vaisi, 2012. GGE biplot analysis of genotype x environment interaction in wheat-barley disomic addition lines. *Aust. J. Crop Sci.*, 6: 1074–1079
- Gapare, W., S. Liu, W. Conaty, Q.H. Zhu, V. Gillespi, D. Llewellyn, W. Stiller and I. Wilson, 2018. Historical datasets support genomic selection models for the prediction of cotton fiber quality phenotypes across multiple environments. G3: Genes Genom. Genet., doi:10.1534/g3. 118.200140
- Gauch, J.H.G. and R.W. Zobel, 1997. Identifying mega-environments and targeting genotypes. Crop Sci., 37: 311–326
- Geng, S., Q.F. Zhang and D.M. Basset, 1987. Stability in yield and fiber quality of California cotton. Crop Sci., 27: 1004–1010
- Gen-Stat, 2009. Gen-Stat for Windows Introduction, 12th edition. VSN International, Hemel Hempstead
- Gomez, K.A. and A.A. Gomez, 1984. Statistical Procedures for Agricultural Research, 2nd edition. John Wiley & Sons Inc. New York. USA
- Gul, S., N.U. Khan, R. Gul, M. Baloch, A. Latif and I.A. Khan, 2016. Genotype by environment and phenotypic adaptability studies for yield and fiber variables in upland cotton. J. Anim. Plant Sci., 26: 776–786
- Gul, S., N.U. Khan, S. Batool, M.J. Baloch, S.H. Ghaloo, M. Munir, Z.A. Soomro, A.A. Khakwani, M. Sajid and S.F. Kazmi, 2014. Genotype by environment interaction and association of morpho-yield variables in upland cotton. J. Anim. Plant Sci., 24: 262–271
- Hicks, C.R., 1982. Fundamental Concepts in the Design of Experiments. CBS College Publication, New York, USA

- Hussain, K., I.A. Khan, H.A. Sadaqat and M. Amjad, 2010. Genotypic and phenotypic correlation analysis of yield, oil and protein contents in the seed of some Egyptian cotton cultivars grown at different locations. *Egypt. J. Agric. Res.*, 83: 735–750
- Iqbal, M., S. Ul-Allah, M. Naeem, M. Ijaz, A. Sattar and A. Sher, 2017. Response of cotton genotypes to water and heat stress from field to genes. *Euphytica*, 213: 131
- Kakar, N.U., F.C. Oad, S. Tunio, Q.U. Chachar and M.M. Kandhro, 2012. Response of sowing time to various cotton genotypes. Sarhad J. Agric., 28: 379–385
- Kang, M.S. and D.P. Gorman, 1989. Genotype × environment interaction in maize. Agron. J., 81: 662–664
- Kaya, Y., M. Akcura and S. Taner, 2006. GGE-biplot analysis of multienvironment yield trials in bread wheat. *Turk. J. Agric. For.*, 30: 325–337
- Khan, N.U., 2013. Diallel analysis of cotton leaf curl virus (CLCuV) disease, earliness, yield and fiber traits under CLCuV infestation in upland cotton. Aust. J. Crop Sci., 7: 1955–1966
- Khan, S.A., N.U. Khan, R. Gul, Z. Bibi, I.U. Khan, S. Gul, S. Ali and M. Baloch, 2005. Combining ability studies for yield and fiber traits in upland cotton. J. Anim. Plant Sci., 25: 698–707
- Machado, R.D.A., J.C.V. Penna, J. Fallieri, P.G. Santos and M.A. Lanza, 2002. Stability and adaptability of seed cotton yields of upland cotton genotypes in the state of Minas Gerais, Brazil. Crop Breed. Appl. Biotechnol., 2: 401–410
- Meredith, W.R.J., D.L. Boykin, F.M. Bourland, W.D. Caldwell, B.T. Campbell, J.R. Gannaway, K. Glass, L.M. May, A. Phillips, C.W. Smith and J. Zhang, 2012. Genotype by environment interactions over seven years for yield, yield components, fiber quality and gossypol traits in the regional high quality tests. *J. Cotton Sci.*, 16: 160–169
- Mustafa, A., Y.M.A. Elsheikh and E.A. Babiker, 2007. Genetic variability and character association and selection criteria in cotton (G. hirsutum L.). Sudan J. Agric. Res., 8: 43–50
- Paterson, A.H., Y. Saranga, M. Menz, C.X. Jiang and R.J. Wright, 2003. QTL analysis of genotype × environment interactions affecting cotton fiber quality. *Theor. Appl. Genet.*, 106: 384–396
- PBS, 2016–17. Year Book. Pakistan Bureau of Statistics (PBS), pp: 21–22. Ministry of Economic Affairs, Govt. of Pakistan, Islamabad, Pakistan
- Romagosa, I. and P. Fox, 1993. Genotype × environment interaction, and adaptation. *In: Plant Breeding Principles and Prospects*, pp: 373–390. Hayward, M.D., N.O. Bosemark and I. Romagosa (eds.). Chapman and Hall, London

- Saranga, Y., M. Menz, C.X. Jiang, R.J. Wright, D. Yakir and A.H. Paterson, 2001. Genomic dissection of genotype × environment interactions conferring adaptation of cotton to arid conditions. *Genom. Res.*, 11: 1988–1995
- Satish, Y., P.P. Jain and B.S. Chhabra, 2009. Stability analysis for yield and its component traits in American cotton (*G. hirsutum L.*). *J. Cott. Res. Dev.*, 23: 175–182
- Shah, M.A., M. Farooq and M. Hussain, 2016. Productivity and profitability of wheat-cotton system as influenced by relay intercropping of insect resistant transgenic cotton in bed planted wheat. Eur. J. Agron., 75: 33–41
- Shah, M.K.N., S.A. Malik and M. Saleem, 2005. Stability of cotton cultivars for early crop maturity across variable plant spacing and sowing times. *Pak. J. Bot.*, 37: 345–353
- Singh, T.H. and S.S. Gill, 1982. Genotype x environment interaction in upland cotton. *Crop Improv.*, 13: 213–215
- Ul-Allah, S., M. Iqbal, M. Naeem and W. Zahid, 2017. Genetic dissection of association among within-boll yield components and their relationship with seed cotton yield in F₃ populations of *Gossypium hirsutum L. Plant Genet. Resour.*, 15: 157–164
- Unay, A., H. Basal, A. Erkul and Z. Yuksekkaya, 2004. Stability analysis of upland cotton genotypes to the Aegean region in Turkey. Asian J. Plant Sci., 3: 36–38
- Vinodhana, N.K., M. Gunasekaran and P. Vindhiyavarman, 2013. Genetic studies of variability, correlation and path coefficient analysis in cotton genotypes. *Int. J. Pure Appl. Biol. Sci.*, 1: 6–10
- Yan, W., 2001. GGE biplot a windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agron. J.*, 93: 1111–1118
- Yan, W. and J.B. Holland, 2010, A heritability-adjusted GGE biplot for test environment evaluation. *Euphytica*, 171: 355–369
- Yan, W. and N. Tinker, 2006. Biplot analysis of multi-environment trial data: Principles and applications. *Can. J. Plant Sci.*, 86: 623–645
- Yan, W. and M.S. Kang, 2003. GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists. CRC Press LLC, Boca Raton, Florida, USA
- Yan, W., M.S. Kang, B. Ma, S. Woods and P.L. Cornelius, 2007. GGE biplot vs AMMI analysis of genotype-by-environment data. Crop Sci., 47: 643–655
- Yang, R.C., J. Crossa, P.L. Cornelius and J. Burgueño, 2009. Biplot analysis of genotype × environment interaction: proceed with caution. *Crop Sci.*, 49: 1564–1576

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