Research Article

Genotype × environment interaction studies in F_5 populations of upland cotton under agro-climatic condition of Peshawar

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Abstract

Genotype (G) × Environment (E) interaction and correlation studies were carried out in F_5 populations along with parental genotypes at two different sowing dates i.e. normal (mid-May) and late (mid-June) in upland cotton during crop season 2013-14 at The University of Agriculture, Peshawar, Pakistan. The experimental material comprised 37 genotypes including 29 $F_{4:5}$ populations and eight parental genotypes. The experiment was conducted in a RCB Design having three replications. ANOVA presented highly significant differences for genotypes and sowing dates for almost all the traits except seed index, where the mean differences were non-significant for sowing dates. G × E interaction effects were highly significant for sympodia plant^{-1}, bolls sympodia^{-1}, bolls plant^{-1} and seeds locule^{-1}. Seed cotton yield plant^{-1} revealed significant positive association with most of the traits. Overall, in genotypes and G × E interactions, F_5 population CIM-506 × CIM-554 S_2 exhibited highest seed cotton yield plant^{-1}(85.05g), bolls sympodia^{-1} (2.27), bolls plant^{-1} (18.63) and seed index (9.53 g). The F_5 population CIM-554 × CIM-707 S_1 revealed maximum seeds boll^{-1} (33.21), seeds locule^{-1} (7.54), boll weight (4.76 g) and seed cotton yield plant^{-1} (83.24g). The F_5 population CIM-554 × CIM-473 S_2 produced maximum seeds boll^{-1}(31.95), seeds locule^{-1} (7.42). Parental cultivar CIM-496 showed maximum sympodia plant^{-1} (16.10), bolls sympodia^{-1} (1.17) and bolls plant^{-1} (18.89). F_5 population CIM-506 × CIM-554 S_2 was found more responsive to both environments followed by F_5 populations CIM-554 × CIM-707 S_1, CIM-554 × CIM-473 S_2 and parental genotype CIM-496 which could be used in future breeding programme for improvement in seed cotton.

Keywords: Cotton; Environment; Genotype; Seed-cotton

Introduction

Cotton belongs to genus *Gossypium*, family *Malvaceae* and tribe *Gossypieae*. *Gossypium* has about 50 species, out of which four species are cultivated and the remaining 46 species are distributed throughout the world in wild form. Upland cotton (*Gossypium hirsutum* L.) is a tetraploid specie which was first found at high lands of Georgia. Wild species of *Gossypium* are important sources of useful traits such as cytoplasmic male sterility and resistance to biotic and abiotic stresses. In four cultivated species, two are diploids i.e. *G. arboreum* L. and *G. herbaceum* L. and called as old world cotton, while two are tetraploids viz., *G. hirsutum* L. and *G. barbadense* L. are termed as new world cotton [1]

Upland cotton contributes approximately 90% of the total world fiber production. Pakistan is the fourth biggest cotton producer participating about 1.6% to GDP and 7.8% to Agriculture and earns 45-60% foreign exchange depending upon the production and utilization [1]. During 2013-14, the cotton crop was cultivated on an area of 2.806 million hectare and seed cotton production was 12.8 million bales having seed cotton yield of 773 kg ha^{-1}. Cottonseed oil was considered to be useful in a variety of food products and therefore cotton is regarded as second to soybean in edible oil production. Cottonseed has oil and protein contents with ratio of 21:23%, respectively. Cottonseed fatty acid profile includes about 55% polyunsaturated fatty acids, 18% monounsaturated fatty acids, and 27% saturated fatty acids. Cottonseed oil has good steadiness as cooking oil and can endure high temperatures without deterioration.

Genotype by environment interaction refers to the relative performance of a genotype across different environments. Genotype × environment interaction (GEI) is of major concern to plant breeders for developing superior cultivars. Growth and yield contributing variables and fiber quality traits are directly associated with environments encouraging for higher yield [2]. A cultivar, to be commercially successful, must perform better across the range of environments. Occurrence of GE interaction reduces the association between phenotype and genotype, and makes it very difficult to evaluate the genetic potential of a genotype [3].

Genotypes and some environmental factors (fertilizer, plant population, pest control, etc.) are controllable, however, other factors of natural environment such as day length and sunshine, rainfall, and some soil properties are generally fixed and difficult to alter for a given location and planting season [4]. Consequence of uncontrollable factors on crop performance is as important as that of controllable factors. However, the uncontrollable factors are likely to change with season and location, and the quantification of their effects on different variables of a crop is vital and measurable [5]. In crop research, most commonly used way to estimate the effects of uncontrollable environmental factors on crop response is to repeat the experiments at numerous sites or several crop seasons and or both.

Differential genotypic expression across environments, frequently referred to genotype × environment interaction, is one of the unifying challenges facing by plant breeders. Most of important traits are end-point measurements, reflecting the cumulative effects of large numbers of genes acting independently or in gene complexes. However, throughout the life cycle of an organism, the external factors at any time may change the development and function of an organism in ways that may not be expected. The extent to which G × E affects a trait is an important determinant of the degree of testing over years and locations that must be employed to adequately quantify the performance of a crop genotype. Because testing is a major factor in the instance and cost of developing new crop varieties, and G × E interactions and their consequences have received much concentration from crop scientists [6].

Sowing time is the main factor affecting yield, and considered as key element to explore the appropriate sowing time of crop cultivars under the particular agro-climatic conditions. Sowing time linearly affects the seed cotton yield, because early maturing cultivars start flowering and boll development well before as compared to late ones. Understanding of correlation in various traits influencing yield is a pre-requisite for designing a successful plant breeding programme. It helps in the recognition of the yield components, however they do not provide accurate information regarding the relative significance of direct and indirect influence of each componential trait [7]. If correlation among traits is very high, then selection for one trait will equally result in changes of other trait. This correlation may be either harmful or valuable, depending upon the direction of association and objectives of the plant breeder. The traits i.e. number of sympodia, boll weight and bolls plant^{-1} presented significant and positive association with seed cotton yield plant^{-1} in earlier studies [7]. Therefore, in light of above review, the current research was designed with the following objectives, to assess the performance of F$_5$ upland cotton populations for their adaptability and genetic potential over two sowing times.To study the correlation of component traits with seed cotton yield

Materials and methods
Plant materials and experimental design
Genotype × environment interaction and correlation studies of F$_5$ populations along with parental genotypes of upland cotton were carried out, at two different sowing dates i.e. normal (mid-May) and late (mid-June) during crop season 2013-14 at The University of Agriculture, Peshawar. Breeding material comprised 37 genotypes including 29 F$_{4:5}$ populations and eight parental genotypes (Table 1). The experiment was conducted in a randomized complete block (RCB) design with three replications, (combined over sowing dates) (Table 2). Each genotype was having two

rows of five meters length with 30 and 75 cm plant and row spacing, respectively. Cultural practices were carried out as per recommended package for cotton production. Recommended inputs including fertilizer and irrigation have been applied same to all the entries. Severe attack of sucking and chewing insect pests has been observed, and controlled with spraying of different insecticides. Picking was made during the month of November on single plant basis.

Traits measurement
Data was recorded on randomly selected ten plants for the variables listed below.
Plant height (cm)
The height of individual plants was measured at physiological maturity from ground level to the tip of the plant by using a meter rod.
Monopodia plant^{-1}
Vegetative branches arising at the base of the main stem during early stage are known as monopodial branches. These monopodial branches were counted for randomly selected individual plants and recorded as monopodia plant^{-1}.
Sympodia plant^{-1}
These branches arise from main stem as well as from vegetative branches. They are flowering branches. These branches were counted and expressed as sympodia plant^{-1}.
Bolls sympodia^{-1}
Bolls on each sympodia were counted and treated as bolls sympodia^{-1} in each respective plant.
Bolls plant^{-1}
Fully open and mature bolls from all the picks for each selected plant were counted and recorded as bolls plant^{-1}.
Boll weight (g)
Ten bolls were randomly selected, and after weighing with electric balance and dividing with sample size, the average boll weight was computed in grams.
Seed cotton yield plant^{-1} (g)
A total of two picks at regular interval were taken from each selected plant and weighed on electric balance in grams as seed cotton yield plant^{-1} on individual plant

basis.
Correlation
Correlation between seed cotton yield with

morphological and yield related traits was worked out through MSTATC programme.

Table 1. List of genotypes used in the G × E interaction studies

S. No.	Genotypes	S. No.	Genotypes
Parental cultivars		**F$_5$ populations**	
T1	SLH-284	T19	CIM-506 × CIM-446 S$_2$
T2	CIM-446	T20	CIM-506 × CIM-499 S$_1$
T3	CIM-473	T21	CIM-506 × CIM-499 S$_2$
T4	CIM-496	T22	CIM-506 × CIM-554 S$_1$
T5	CIM-499	T23	CIM-506 × CIM-554 S$_2$
T6	CIM-506	T24	CIM-554 × SLH-284 S$_1$
T7	CIM-554	T25	CIM-554 × CIM-473 S$_1$
T8	CIM-707	T26	CIM-554 × CIM-473 S$_2$
F$_5$ populations		T27	CIM-554 × CIM-496 S$_1$
T9	CIM-496 × CIM-446 S$_1$	T28	CIM-554 × CIM-506 S$_1$
T10	CIM-496 × CIM-473 S$_1$	T29	CIM-554 × CIM-506 S$_2$
T11	CIM-496 × CIM-554 S$_1$	T30	CIM-554 × CIM-506 S$_3$
T12	CIM-499 × CIM-446 S$_1$	T31	CIM-554 × CIM-707 S$_1$
T13	CIM-499 × CIM-496 S$_1$	T32	CIM-707 × SLH-284 S$_1$
T14	CIM-499 × CIM-496 S$_2$	T33	CIM-707 × SLH-284 S$_2$
T15	CIM-499 × CIM-554 S$_1$	T34	CIM-707 × CIM-499 S$_1$
T16	CIM-499 × CIM-554 S$_2$	T35	CIM-707 × CIM-499 S$_2$
T17	CIM-499 × CIM-707 S$_1$	T36	CIM-707 × CIM-506 S$_1$
T18	CIM-506 × CIM-446 S$_1$	T37	CIM-707 × CIM-506 S$_2$

Table 2. ANOVA Table for G × E interaction studies

Source of Variation	D.F	Mean Square	Computed F-Value
Sowing dates (S)	S-1	S MS	S MS / RMS
Reps within sowing dates (R)	S (R-1)	R MS	-
Genotypes (G)	G-1	G MS	G MS / E MS
S x G	(S-1) (G-1)	S x G MS	S x G MS / E MS
Pooled Error	S (R-1) (G-1)	E MS	-
Total	SRG-1	-	-

Results and discussion
Analysis of variance exhibited highly significant (P≤0.01) differences for genotypes and sowing dates for almost all the studied traits. Genotype × environment interaction effects were highly significant (P≤0.01) for sympodia plant[-1], bolls sympodia[-1], bolls plant[-1] and seeds locule[-1], while non-significant (P>0.05) for rest of the traits. Significant genotype × environment interaction effect might be due to diverse genetic makeup and the

environmental conditions in which the genotypes were examined.

Plant height (cm)

Genotypes mean values for plant height ranged from 76.59 to 153.45 cm, while for genotype × environment interaction the mean values varied from 69.58 to 157.53 cm (Table 3). For genotype means, cultivar SLH-284 (76.59 cm) exhibited minimum plant height. The F_5 population CIM-499 × CIM-707 S_1 revealed maximum plant height of 153.45 cm. For sowing dates, on average, the genotypes produced minimum plant height (113.59 cm) during late sowing (mid-June) and maximum (122.24 cm) during normal sowing (mid-May). In

genotype × environment interactions, minimum plant height was observed in cultivar SLH-284 (69.58 cm) during late sowing. Maximum plant height was observed for F_5 population CIM-499 × CIM-707S_1 (157.53 cm) and it was found at par with F_5 population CIM-554 × CIM-506 S_1 (152.94 cm) during normal sowing. Overall, the cultivar SLH-284 revealed minimum plant height in genotype means and G × E interactions. Plant height showed highly significant (P≤0.01) positive correlation (r = 0.334) with seed cotton yield (Table 4).

Table 3. Mean performance of parental cultivars and their F_5 populations for plant height in GEI studies in upland cotton.

Parental genotypes	Normal Sowing	Late Sowing	Means (cm)
SLH-284	83.60	69.58	76.59
CIM-446	111.51	99.49	105.50
CIM-473	103.48	93.95	98.71
CIM-496	116.93	105.42	111.18
CIM-499	87.97	79.62	83.80
CIM-506	98.53	88.51	93.52
CIM-554	112.31	103.56	107.93
CIM-707	127.65	115.16	121.40
F_5 populations			
CIM-496 × CIM-446 S_1	117.76	111.12	114.44
CIM-496 × CIM-473 S_1	107.07	99.95	103.51
CIM-496 × CIM-554 S_1	109.82	101.63	105.72
CIM-499 × CIM-446 S_1	118.61	104.14	111.38
CIM-499 × CIM-496 S_1	126.67	115.06	120.87
CIM-499 × CIM-496 S_2	111.47	100.79	106.13
CIM-499 × CIM-554 S_1	121.33	114.38	117.86
CIM-499 × CIM-554 S_2	124.22	117.02	120.62
CIM-499 × CIM-707 S_1	157.53	149.38	153.46
CIM-506 × CIM-446 S_1	119.40	114.84	117.12
CIM-506 × CIM-446 S_2	120.47	112.11	116.29
CIM-506 × CIM-499 S_1	116.48	109.55	113.02
CIM-506 × CIM-499 S_2	117.28	111.44	114.36
CIM-506 × CIM-554 S_1	127.26	120.41	123.84
CIM-506 × CIM-554 S_2	108.82	99.94	104.38
CIM-554 × SLH-284 S_1	134.02	119.97	126.99
CIM-554 × CIM-473 S_1	144.55	133.43	138.99
CIM-554 × CIM-473 S_2	124.55	120.60	122.58
CIM-554 × CIM-496 S_1	147.67	141.33	144.50

CIM-554 × CIM-506 S_1	152.94	146.03	149.48
CIM-554 × CIM-506 S_2	141.64	133.45	137.55
CIM-554 × CIM-506 S_3	134.14	128.65	131.39
CIM-554 × CIM-707 S_1	151.49	145.25	148.37
CIM-707 × SLH-284 S_1	131.35	121.15	126.25
CIM-707 × SLH-284 S_2	136.17	129.11	132.64
CIM-707 × CIM-499 S_1	99.00	93.72	96.36
CIM-707 × CIM-499 S_2	125.38	114.25	119.82
CIM-707 × CIM-506 S_1	144.97	137.90	141.44
CIM-707 × CIM-506 S_2	108.82	100.78	104.80
Means (cm)	122.24	113.59	-

Genotypes $LSD_{0.05} = 3.94$, Environments $LSD_{0.05} = 0.92$, GEI $LSD_{0.05} = 5.57$

Table 4. Correlation of seed cotton yield per plant with various traits in G × E interactions of upland cotton

Parameters	Correlation of seed cotton yield with other traits	Probability
Plant height	0.334**	<0.001
Monopodia plant^{-1}	0.140*	0.038
Sympodia plant^{-1}	0.146*	0.029
Bolls sympodia^{-1}	0.435**	<0.001
Bolls plant^{-1}	0.662**	<0.001
Boll weight	0.545**	<0.001

**, * significant at P≤0.01 & P≤0.05, respectively.

Kakar *et al.* [2] observed significant effect of genotypes and sowing dates, while non-significant genotype × environment interaction effect for plant height in upland cotton. They observed that normal sowing results in maximum plant height, while late sowing adversely affected plant height, seed cotton yield and other characters. Our results were also in close resemblance with the earlier findings of Awan *et al.* [8] who noticed that different sowing dates and plant spacing significantly affected the plant height, while their interaction effect was non-significant. They also concluded that seed cotton yield and other characters showed maximum effect during normal sowing as compared to late sowing. Significant mean squares for genotypes and genotype × environment interactions for plant height in upland cotton were recorded. These results are in line with Gul *et al.* [5]. However, non-significant positive association of plant height and seed cotton yield was also noticed which might be due

to no lodging of cotton plants. Cotton breeders are mostly interested in minimum plant height due to lodging and picking problems. Though, plant height can play constructive role in bolls setting and seed cotton yield if lodging did not happen.

Positive correlation was observed between seed cotton yield and plant height in upland cotton. These results are in line with Ahmad *et al.* [9], which exhibited that selection for plant height could be effective in breeding for seed cotton yield when it is paired with sympodia plant^{-1}. Plant height is an important trait and has close relationship with bolls plant^{-1}, so has ultimate positive effect on seed cotton yield plant^{-1}. Significant positive association of plant height with seed cotton yield was also observed in past studies of upland cotton. These results are supported by Naveed *et al.* [10], Salahuddin *et al.* [11]. However, in present studies highly significant positive correlation of plant height with seed cotton yield might be due to no lodging.

Monopodia plant^{-1}

Genotypes mean values for monopodia plant^{-1} ranged from 1.15 to 2.62, while mean values for genotype $\times$ environment interaction ranged from 1.11 to 2.65 (Table 5). In case of genotype means, F_5 population CIM-506 $\times$ CIM-499 S_2 (1.15) showed minimum monopodia plant^{-1} and was found at par with F_5 population CIM-707 $\times$ SLH-284 S_2 (1.17). Genotype CIM-554 $\times$ CIM-506 S_3 (2.62) showed maximum monopodia plant^{-1} followed by at par values of the F_5 populations CIM-707 $\times$ CIM-506 S_2 (2.31), CIM-707 $\times$ SLH-284S_1 (2.27) and CIM-506 $\times$ CIM-446 S_2 (2.26). Considering sowing dates, on average, genotypes produced minimum (1.75) monopodia plant^{-1} during late sowing (mid-June) and maximum (1.81) during normal sowing (mid-May). In genotype $\times$ environment interaction, minimum monopodia plant^{-1} (1.11) were observed for genotype CIM-506 $\times$ CIM-499 S_2 during late sowing. Four other genotypes were also at par with above F_5 population for minimum monopodia plant^{-1} i.e. CIM-707 $\times$ SLH-284 S_2 (1.14) and CIM-499 $\times$ CIM-446 S_1 (1.23) with late sowing, and CIM-506 $\times$ CIM-499 S_2 (1.19) and CIM-707 $\times$ SLH-284 S_2 (1.21) with normal sowing. However, genotype CIM-554 $\times$ CIM-506 S_3 exhibited maximum and minimum monopodia plant^{-1} (2.65, 2.60) during normal and late sowing, respectively. All other interactions for monopodia plant^{-1} showed medium values. Overall, F_5 populations CIM-506 $\times$ CIM-499 S_2 and CIM-707 $\times$ SLH-284 S_2 revealed minimum monopodia plant^{-1} in genotypes and G $\times$ E interaction means. Monopodia plant^{-1} showed significant positive correlation (r = 0.14) with seed cotton yield (Table 4).

Table 5. Mean performance of parental cultivars and their F_5 populations for monopodia plant^{-1} in GEI studies in upland cotton

Parental genotypes	Normal Sowing	Late Sowing	Means (#)
SLH-284	1.51	1.43	1.47
CIM-446	1.47	1.41	1.44
CIM-473	1.33	1.27	1.30
CIM-496	1.49	1.45	1.47
CIM-499	1.93	1.89	1.91
CIM-506	2.04	1.98	2.01
CIM-554	1.45	1.40	1.43
CIM-707	2.14	2.08	2.11
F_5 populations			
CIM-496 $\times$ CIM-446 S_1	1.79	1.73	1.76
CIM-496 $\times$ CIM-473 S_1	1.50	1.43	1.46
CIM-496 $\times$ CIM-554 S_1	1.45	1.41	1.43
CIM-499 $\times$ CIM-446 S_1	1.27	1.23	1.25
CIM-499 $\times$ CIM-496 S_1	1.28	1.24	1.26
CIM-499 $\times$ CIM-496 S_2	1.78	1.74	1.76
CIM-499 $\times$ CIM-554 S_1	1.51	1.47	1.49
CIM-499 $\times$ CIM-554 S_2	2.28	2.22	2.25
CIM-499 $\times$ CIM-707 S_1	1.69	1.63	1.66
CIM-506 $\times$ CIM-446 S_1	1.85	1.81	1.83
CIM-506 $\times$ CIM-446 S_2	2.28	2.23	2.26
CIM-506 $\times$ CIM-499 S_1	1.64	1.60	1.62
CIM-506 $\times$ CIM-499 S_2	1.19	1.11	1.15

CIM-506 × CIM-554 S_1	2.20	2.11	2.16
CIM-506 × CIM-554 S_2	1.81	1.76	1.79
CIM-554 × SLH-284 S_1	2.27	2.23	2.25
CIM-554 × CIM-473 S_1	1.36	1.29	1.33
CIM-554 × CIM-473 S_2	2.30	2.13	2.22
CIM-554 × CIM-496 S_1	2.17	2.13	2.15
CIM-554 × CIM-506 S_1	2.27	2.14	2.21
CIM-554 × CIM-506 S_2	2.20	2.13	2.17
CIM-554 × CIM-506 S_3	2.65	2.60	2.62
CIM-554 × CIM-707 S_1	1.93	1.86	1.89
CIM-707 × SLH-284 S_1	2.30	2.24	2.27
CIM-707 × SLH-284 S_2	1.21	1.14	1.17
CIM-707 × CIM-499 S_1	1.69	1.63	1.66
CIM-707 × CIM-499 S_2	1.33	1.29	1.31
CIM-707 × CIM-506 S_1	2.15	2.10	2.12
CIM-707 × CIM-506 S_2	2.33	2.28	2.31
Means (#)	1.81	1.75	-

Genotypes $LSD_{0.05}$ = 0.02, Environments $LSD_{0.05}$ = 0.09, GEI $LSD_{0.05}$ = 0.12

Significant variances due to G, E and GEI were observed for most of the traits including monopodial branches in upland cotton. These results are in line with Satish *et al*. [12], Gul, [4]. Abbas *et al*. [13] recorded significant positive correlation of monopodia plant[-1] with yield contributing traits, while studying upland cotton genotypes for genetic variability, heritability, genetic advance and correlation. Plant height, monopodia plant[-1] and bolls plant[-1] manifested significant correlation with seed cotton yield. These results are in line with Hussain *et al*. [14]. Greater genetic variability was reported among cotton genotypes for monopodia plant[-1] however, its association was negative with seed cotton yield. These results are supported by Iqbal *et al*. [7], Batool *et al*. [15]. Contradictory findings might be due to different genetic makeup of the cotton populations used under varied environmental conditions. However, positive association of monopodia plant[-1] with seed cotton yield might be due to some indirect effect of vegetative branches.

Sympodia plant[-1]

For sympodia plant[-1], genotypes mean values were ranging from 7.75 to 16.10, while genotype × environment interaction means varied from 7.40 to 17.46 (Table 6).

For genotype means, the parental cultivar CIM-496 (16.10) exhibited maximum number of sympodia plant[-1] followed by parental cultivars CIM-707 (14.15), CIM-473 (12.73) and F_5 population CIM-506 × CIM-446 S_1 (13.03). F_5 populations CIM-707 × SLH-284 S_1 (10.68) and CIM-499 × CIM-496 S_1 (10.52) showed medium and at par number of sympodia plant[-1]. Genotype CIM-506 × CIM-499 S_2 (7.75) showed minimum number of sympodia plant[-1] and was analogous with genotypes CIM-499 (7.77), CIM-707 × CIM-499 S_1 (7.97) and CIM-554 × CIM-473 S_2 (8.01). In case of sowing dates, on average, the genotypes produced maximum (11.32) sympodia plant[-1] during normal sowing and minimum (9.96) during late sowing.

In view of genotype × sowing time interaction, cultivar CIM-496 (17.47) showed maximum number of sympodia plant[-1] during normal sowing, followed by at par values of parental cultivars CIM-707 (15.23) with normal sowing and CIM-496 (14.73) under late sowing. The F_5 population CIM-554 × CIM-707 S_1 (7.40) revealed minimum number of sympodia plant[-1] during late sowing. However, genotypes CIM-506 × CIM-499 S_2 (7.53) and CIM-499 (7.60) were found at par with above genotype and exhibited minimum

number of sympodia plant[-1] during late sowing. Overall, in genotypes and G × E interaction means, genotypes CIM-496 and CIM-707 exhibited maximum number of sympodia plant[-1]. Sympodia plant[-1] revealed positive significant correlation (r = 0.146) with seed cotton yield (Table 4). Significant differences were observed among cotton genotypes for sympodia plant[-1], which might be due to varied nature of cotton genotypes and environmental conditions. These results are in line with Ehsan *et al.* [16]. Variances due to genotype × environment interaction were significant for sympodia plant[-1] and yield related traits in upland cotton genotypes. These results are supported by Kalli *et al.* and Killi &

Harem [17, 18]. Memon *et al.* [19] observed highly significant positive correlation between sympodial branches and seed cotton yield of upland cotton cultivars. Genetic variability and significant positive correlation of sympodial branches with seed cotton yield were observed Arshad *et al.* [20], Djaboutou *et al.* [21]. Genotype by environment interaction was significant for sympodia plant[-1] and that might be due to genetic base and environmental conditions in which the genotypes were grown. Significant positive correlation of sympodia plant[-1] with seed cotton yield was due to boll number.

Table 6. Mean performance of parental cultivars and their F₅ populations for sympodia plant[-1] in G × E interaction studies in upland cotton

Parental genotypes	Normal Sowing	Late Sowing	Means (#)
SLH-284	11.93	10.33	11.13
CIM-446	12.13	10.80	11.47
CIM-473	13.27	12.20	12.73
CIM-496	17.47	14.73	16.10
CIM-499	7.95	7.60	7.77
CIM-506	12.07	10.60	11.33
CIM-554	11.07	9.87	10.47
CIM-707	15.23	13.07	14.15
F₅ populations			
CIM-496 × CIM-446 S₁	12.63	12.00	12.32
CIM-496 × CIM-473 S₁	10.23	8.31	9.27
CIM-496 × CIM-554 S₁	10.90	8.67	9.78
CIM-499 × CIM-446 S₁	11.43	9.27	10.35
CIM-499 × CIM-496 S₁	11.11	9.93	10.52
CIM-499 × CIM-496 S₂	11.85	11.07	11.46
CIM-499 × CIM-554 S₁	12.80	11.00	11.90
CIM-499 × CIM-554 S₂	10.80	9.60	10.20
CIM-499 × CIM-707 S₁	12.18	10.33	11.26
CIM-506 × CIM-446 S₁	14.07	12.00	13.03
CIM-506 × CIM-446 S₂	11.98	10.60	11.29
CIM-506 × CIM-499 S₁	8.71	8.00	8.35
CIM-506 × CIM-499 S₂	7.97	7.53	7.75
CIM-506 × CIM-554 S₁	12.98	10.53	11.76
CIM-506 × CIM-554 S₂	8.55	7.87	8.21
CIM-554 × SLH-284 S₁	11.37	10.33	10.85
CIM-554 × CIM-473 S₁	12.01	10.40	11.20

CIM-554 × CIM-473 S$_2$	8.23	7.80	8.01
CIM-554 × CIM-496 S$_1$	11.77	10.67	11.22
CIM-554 × CIM-506 S$_1$	13.14	11.20	12.17
CIM-554 × CIM-506 S$_2$	10.81	9.89	10.35
CIM-554 × CIM-506 S$_3$	11.00	9.13	10.07
CIM-554 × CIM-707 S$_1$	8.88	7.40	8.14
CIM-707 × SLH-284 S$_1$	10.97	10.40	10.68
CIM-707 × SLH-284 S$_2$	12.35	10.40	11.37
CIM-707 × CIM-499 S$_1$	8.14	7.80	7.97
CIM-707 × CIM-499 S$_2$	10.73	9.40	10.07
CIM-707 × CIM-506 S$_1$	9.23	8.27	8.75
CIM-707 × CIM-506 S$_2$	11.03	9.47	10.25
Means (#)	11.32	9.96	-

Genotypes LSD$_{0.05}$ = 0.63, Environments LSD$_{0.05}$ = 0.15, GEI LSD$_{0.05}$ = 0.88

Bolls sympodia^{-1}

Genotypes mean values for bolls sympodia^{-1} ranged from 1.03 to 2.35, while for genotype × environment interaction the said range was 1.03 to 2.48 (Table 7). In case of genotype means, the cultivar CIM-499 (2.35) and F$_5$ population CIM-506 × CIM-554 S$_2$ (2.26) showed maximum and same number of bolls sympodia^{-1}. The F$_5$ population CIM-506 × CIM-499 S$_2$ (2.12) also followed the above two genotypes in maximum number of bolls sympodia^{-1}. Genotypes CIM-707 (1.03) and CIM-554 (1.03) revealed minimum and same number of bolls sympodia^{-1}. However, the above two genotypes were found at par with alike values of three other genotypes i.e. CIM-499 × CIM-446 S$_1$ (1.05), CIM-554 × CIM-506 S$_2$ (1.05) and CIM-496 × CIM-554 S$_1$ (1.05) for minimum number of bolls sympodia^{-1}. Regarding sowing dates, overall, during normal sowing the genotypes produced maximum (1.44) number of bolls sympodia^{-1} and minimum (1.35) during late sowing.

Table 7. Mean performance of parental cultivars and their F$_5$ populations for bolls sympodia^{-1} in GEI studies in upland cotton

Parental genotypes	Normal Sowing	Late Sowing	Means (#)
SLH-284	1.47	1.43	1.45
CIM-446	1.15	1.06	1.10
CIM-473	1.44	1.42	1.43
CIM-496	1.18	1.17	1.17
CIM-499	2.47	2.22	2.35
CIM-506	1.22	1.11	1.17
CIM-554	1.04	1.03	1.04
CIM-707	1.03	1.03	1.03
F$_5$ populations			
CIM-496 × CIM-446 S$_1$	1.14	1.10	1.12
CIM-496 × CIM-473 S$_1$	1.15	1.14	1.14
CIM-496 × CIM-554 S$_1$	1.05	1.05	1.05
CIM-499 × CIM-446 S$_1$	1.05	1.05	1.05
CIM-499 × CIM-496 S$_1$	1.16	1.10	1.13
CIM-499 × CIM-496 S$_2$	1.38	1.23	1.31
CIM-499 × CIM-554 S$_1$	1.31	1.30	1.31

CIM-499 × CIM-554 S_2	1.36	1.33	1.34
CIM-499 × CIM-707 S_1	1.32	1.27	1.29
CIM-506 × CIM-446 S_1	1.35	1.34	1.35
CIM-506 × CIM-446 S_2	1.26	1.24	1.25
CIM-506 × CIM-499 S_1	1.75	1.41	1.58
CIM-506 × CIM-499 S_2	2.29	1.95	2.12
CIM-506 × CIM-554 S_1	1.23	1.21	1.22
CIM-506 × CIM-554 S_2	2.37	2.17	2.27
CIM-554 × SLH-284 S_1	1.36	1.24	1.30
CIM-554 × CIM-473 S_1	1.07	1.07	1.07
CIM-554 × CIM-473 S_2	2.14	1.81	1.98
CIM-554 × CIM-496 S_1	1.25	1.18	1.22
CIM-554 × CIM-506 S_1	1.50	1.43	1.46
CIM-554 × CIM-506 S_2	1.05	1.05	1.05
CIM-554 × CIM-506 S_3	1.57	1.56	1.57
CIM-554 × CIM-707 S_1	2.06	1.92	1.99
CIM-707 × SLH-284 S_1	1.26	1.26	1.26
CIM-707 × SLH-284 S_2	1.28	1.24	1.26
CIM-707 × CIM-499 S_1	1.55	1.53	1.54
CIM-707 × CIM-499 S_2	1.87	1.69	1.78
CIM-707 × CIM-506 S_1	1.73	1.57	1.65
CIM-707 × CIM-506 S_2	1.28	1.19	1.24
Means (#)	1.44	1.35	-

Genotypes LSD$_{0.05}$ = 0.02, Environments LSD$_{0.05}$ = 0.10, GEI LSD$_{0.05}$ = 0.14

For genotype × environment interaction, genotype CIM-499 (2.48) exhibited maximum number of bolls sympodia^{-1} and was found at par with F$_5$ population CIM-506 × CIM-554 S_2 (2.36) during normal sowing. However, the above genotypes were followed by at par values of two other genotypes i.e. CIM-506 × CIM-499 S_2 (2.29) with normal sowing and CIM-499 (2.22) during late sowing. Genotype CIM-707 (1.03) during late sowing revealed minimum number of bolls sympodia^{-1}. Three other genotypes having same values i.e. CIM-554 (1.03) and with normal sowing and CIM-554 (1.03) during late sowing were found at par with the above genotype for minimum number of bolls sympodia^{-1}. Overall, in genotypes and G × E interaction means, the genotypes CIM-499, CIM-506 × CIM-554 S_2 and CIM-506 × CIM-499 S_2 showed maximum number of bolls sympodia^{-1}. Bolls sympodia^{-1} showed highly significant positive correlation (r = 0.435) with seed cotton yield (Table 4).

Ali *et al*. [22] observed highly significant mean squares for genotypes, environments and genotype × environment interactions in upland cotton. However, these significant differences in cotton genotypes might be due to their different genetic background. Positive correlation of bolls sympodia^{-1} with seed cotton yield in upland cotton genotypes was also observed during earlier studies of Khan *et al*. [1], Tariq *et al*. [23], Dewdar *et al*. [24]. Conflicting findings might be due to different genetic makeup of cotton populations and environmental conditions. Highly significant positive correlation of bolls sympodia^{-1} with seed cotton yield was mainly due to direct effect of bolls sympodia^{-1} on seed cotton yield.

Bolls plant^{-1}

Parental cultivars and F$_5$ populations mean values for bolls plant^{-1} varied from 10.27 to 18.89, while the mean values for genotype

$\times$ environment interaction ranged from 9.07 to 20.58 (Table 8). Genotype CIM-496 (18.89) showed maximum number of bolls plant^{-1} and was found at par with two F$_5$ populations viz., CIM-506 $\times$ CIM-554 S$_2$ (18.63), CIM-499 (18.24) and one parental cultivar CIM-473 (18.22). Four F$_5$ populations CIM-496 $\times$ CIM-554 S$_1$ (10.27), CIM-496 $\times$ CIM-473 S$_1$ (10.60),

CIM-554 $\times$ CIM-506 S$_2$ (10.87), CIM-499 $\times$ CIM-446 S$_1$ (10.87) and one cultivar CIM-554 (10.86) exhibited minimum and same number of bolls plant^{-1}. For sowing dates, on average, the genotypes produced maximum (15.76) bolls plant^{-1} during normal sowing and minimum (13.17) during late sowing.

Table 8. Mean performance of parental cultivars and their F$_5$ populations for bolls plant^{-1} in GEI studies in upland cotton

Parental genotypes	Normal Sowing	Late Sowing	Means (#)
SLH-284	17.51	14.73	16.12
CIM-446	13.98	11.40	12.69
CIM-473	19.16	17.27	18.22
CIM-496	20.58	17.20	18.89
CIM-499	19.67	16.80	18.24
CIM-506	14.74	11.80	13.27
CIM-554	11.52	10.20	10.86
CIM-707	15.76	13.67	14.71
F$_5$ populations			
CIM-496 $\times$ CIM-446 S$_1$	14.42	13.20	13.81
CIM-496 $\times$ CIM-473 S$_1$	11.73	9.47	10.60
CIM-496 $\times$ CIM-554 S$_1$	11.47	9.07	10.27
CIM-499 $\times$ CIM-446 S$_1$	12.00	9.73	10.87
CIM-499 $\times$ CIM-496 S$_1$	12.90	10.93	11.92
CIM-499 $\times$ CIM-496 S$_2$	16.47	13.60	15.03
CIM-499 $\times$ CIM-554 S$_1$	16.77	14.33	15.55
CIM-499 $\times$ CIM-554 S$_2$	14.67	12.73	13.70
CIM-499 $\times$ CIM-707 S$_1$	16.02	13.13	14.58
CIM-506 $\times$ CIM-446 S$_1$	18.87	16.13	17.50
CIM-506 $\times$ CIM-446 S$_2$	15.06	13.13	14.10
CIM-506 $\times$ CIM-499 S$_1$	15.25	11.27	13.26
CIM-506 $\times$ CIM-499 S$_2$	18.37	14.67	16.52
CIM-506 $\times$ CIM-554 S$_1$	15.94	12.73	14.34
CIM-506 $\times$ CIM-554 S$_2$	20.26	17.00	18.63
CIM-554 $\times$ SLH-284 S$_1$	15.47	12.80	14.13
CIM-554 $\times$ CIM-473 S$_1$	12.87	11.13	12.00
CIM-554 $\times$ CIM-473 S$_2$	17.67	14.13	15.90
CIM-554 $\times$ CIM-496 S$_1$	14.76	12.53	13.65
CIM-554 $\times$ CIM-506 S$_1$	19.67	15.93	17.80
CIM-554 $\times$ CIM-506 S$_2$	11.40	10.33	10.87
CIM-554 $\times$ CIM-506 S$_3$	17.31	14.20	15.76
CIM-554 $\times$ CIM-707 S$_1$	18.24	14.20	16.22
CIM-707 $\times$ SLH-284 S$_1$	13.85	13.07	13.46

CIM-707 × SLH-284 S_2	15.78	12.87	14.33
CIM-707 × CIM-499 S_1	12.71	11.93	12.32
CIM-707 × CIM-499 S_2	20.15	15.87	18.01
CIM-707 × CIM-506 S_1	15.96	12.93	14.45
CIM-707 × CIM-506 S_2	14.11	11.27	12.69
Means (#)	15.76	13.17	-

Genotypes $LSD_{0.05}$ = 0.76, Environments $LSD_{0.05}$ = 0.18, GEI $LSD_{0.05}$ = 1.08

In genotype × environment interaction, genotypes CIM-496 (20.58) and CIM-506 × CIM-554 S_2 (20.26) produced maximum and similar number of bolls plant^{-1} during normal sowing. However, these genotypes were found similar in performance with three other genotypes i.e. CIM-707 × CIM-499 S_2 (20.15), CIM-499 (19.67) and CIM-554 × CIM-506 S_1 (19.67) for maximum number of bolls plant^{-1} during normal sowing. Genotype CIM-496 × CIM-554 S_1 (9.07) produced minimum number of bolls plant^{-1} during late sowing and was found at par with two other F_5 populations i.e. CIM-496 × CIM-473 S_1 (9.47) and CIM-499 × CIM-446 S_1 (9.73) during late sowing. Overall, in genotypes and G × E interaction means, the F_5 population CIM-506 × CIM-554 S_2 and cultivars CIM-496 and CIM-499 produced maximum number of bolls plant^{-1}. Bolls plant^{-1} showed positive significant (P≤0.01) correlation (r = 0.662) with seed cotton yield (Table 4).

Highly significant genotypes, environments and genotypes × environments interaction effects for bolls plant^{-1} among cotton genotypes were also recorded Dewdar *et al.* [24]. Furthermore, the bolls plant^{-1} has important role in cotton yield and thus, selection should be made for larger number of bolls plant^{-1}. However, positive highly significant association of bolls plant^{-1} with seed cotton yield was also recorded. In view of the fact that genotype by environment interaction was significant for bolls plant^{-1}, so it might be due to genetic makeup and the environmental conditions in which the genotypes were studied.

Mushtaq *et al.* [25] observed highly significant positive association of number of bolls plant^{-1} and seed cotton yield. However, correlation of yield and fiber quality traits in upland cotton genotypes was determined during studies Hussain *et al.* [14]. In their studies, bolls plant^{-1} showed positive significant association with seed cotton yield. Highly significant positive correlation of bolls plant^{-1} with seed cotton yield was mainly due to direct effect of bolls plant^{-1} on seed cotton yield.

Boll weight (g)

For boll weight, genotypes were having range of 2.76 to 4.76 g, while the mean values for genotype × environment interaction varied from 2.74 to 4.79 g (Table 9). Genotypes CIM-554 × CIM-707 S_1 (4.76 g) and CIM-506 × CIM-446 S_1 (4.72 g) showed maximum and alike boll weight. The above two genotypes were found at par with same values of three other genotypes viz., CIM-496 × CIM-446 S_1 (4.69 g), CIM-554 × CIM-506 S_3 (4.66 g) and CIM-496 × CIM-473 S_1 (4.64 g) for maximum boll weight. Genotypes SLH-284 (2.76 g), CIM-499 (2.82 g) and CIM-554 × CIM-473 S_2 (2.91 g) exhibited minimum and same boll weight. However, these genotypes were followed by same values of two other genotypes i.e. CIM-506 × CIM-554 S_1 (3.16 g) and CIM-554 × CIM-496 S_1 (3.17 g) for minimum boll weight. Regarding sowing date means, genotypes produced maximum boll weight (3.88 g) during normal sowing and minimum (3.83 g) during late sowing.

Table 9. Mean performance of parental cultivars and their F$_5$ populations for boll weight in G × E interaction studies in upland cotton

Parental genotypes	Normal Sowing	Late Sowing	Means (g)
SLH-284	2.79	2.74	2.76
CIM-446	3.85	3.80	3.83
CIM-473	3.64	3.60	3.62
CIM-496	3.27	3.21	3.24
CIM-499	2.84	2.80	2.82
CIM-506	3.53	3.49	3.51
CIM-554	3.74	3.65	3.70
CIM-707	3.67	3.64	3.66
F$_5$ populations			
CIM-496 × CIM-446 S$_1$	4.71	4.68	4.69
CIM-496 × CIM-473 S$_1$	4.65	4.62	4.64
CIM-496 × CIM-554 S$_1$	4.29	4.26	4.27
CIM-499 × CIM-446 S$_1$	4.20	4.16	4.18
CIM-499 × CIM-496 S$_1$	4.15	4.09	4.12
CIM-499 × CIM-496 S$_2$	3.45	3.39	3.42
CIM-499 × CIM-554 S$_1$	3.43	3.37	3.40
CIM-499 × CIM-554 S$_2$	4.58	4.50	4.54
CIM-499 × CIM-707 S$_1$	3.67	3.58	3.62
CIM-506 × CIM-446 S$_1$	4.74	4.69	4.72
CIM-506 × CIM-446 S$_2$	4.15	4.09	4.12
CIM-506 × CIM-499 S$_1$	4.53	4.46	4.49
CIM-506 × CIM-499 S$_2$	3.38	3.33	3.35
CIM-506 × CIM-554 S$_1$	3.18	3.13	3.16
CIM-506 × CIM-554 S$_2$	4.42	4.38	4.40
CIM-554 × SLH-284 S$_1$	4.38	4.34	4.36
CIM-554 × CIM-473 S$_1$	4.37	4.32	4.35
CIM-554 × CIM-473 S$_2$	2.92	2.89	2.91
CIM-554 × CIM-496 S$_1$	3.19	3.15	3.17
CIM-554 × CIM-506 S$_1$	3.69	3.62	3.65
CIM-554 × CIM-506 S$_2$	4.07	4.03	4.05
CIM-554 × CIM-506 S$_3$	4.70	4.63	4.66
CIM-554 × CIM-707 S$_1$	4.79	4.72	4.76
CIM-707 × SLH-284 S$_1$	3.65	3.59	3.62
CIM-707 × SLH-284 S$_2$	4.21	4.18	4.20
CIM-707 × CIM-499 S$_1$	3.22	3.18	3.20
CIM-707 × CIM-499 S$_2$	3.34	3.28	3.31
CIM-707 × CIM-506 S$_1$	4.35	4.29	4.32
CIM-707 × CIM-506 S$_2$	3.71	3.67	3.69
Means (g)	3.88	3.83	-

Genotypes LSD$_{0.05}$ = 0.22, Environments LSD$_{0.05}$ = 0.05, GEI LSD$_{0.05}$ = 0.31

Genotype × environment interaction revealed that genotype CIM-554 × CIM-707 S$_1$(4.79 g) showed maximum boll weight and was found at par with genotype

CIM-506 × CIM-446 S_1(4.74 g) during normal sowing. However, these genotypes were found at par with similar values of four other genotypes i.e. CIM-554 × CIM-707 S_1 (4.72 g) and CIM-506 × CIM-446 S_1 (4.69 g) during late sowing, CIM-496 × CIM-446 S_1(4.71 g) and CIM-554 × CIM-506 S_3(4.70 g) under normal sowing. The three genotypes i.e. SLH-284(2.74 g) during late sowing, SLH-284(2.79 g) under normal sowing and CIM-499(2.80 g) during late sowing, exhibited minimum and similar boll weight. The above genotypes were found at par with three other genotypes viz., CIM-499 (2.84 g) and CIM-554 × CIM-473 S_2 (2.92 g) with normal sowing, and CIM-554 × CIM-473 S_2 (2.89 g) during late sowing. All other interactions exhibited medium values for boll weight. Overall, in genotypes and G × E interaction means, genotypes CIM-554 × CIM-707 S_1, CIM-506 × CIM-446 S_1, CIM-496 × CIM-446 S_1 and CIM-554 × CIM-506 S_3 showed maximum boll weight. Boll weight indicated significant positive correlation (r = 0.545) with yield (Table 4).

Deshmukh *et al.* [26] recorded significant differences for environments and genotype by environment interactions, which revealed differential response of genotypes in diverse environmental conditions. Genetic variability among cotton genotypes for boll weight was recorded in previous finding of Taohua *et al.* [27], Meena *et al.* [28]. Batool *et al.* [15] noticed highly

significant differences for boll weight among upland cotton genotypes. Rao and Mary [29] also recorded significant differences for boll weight and its positive correlation with seed cotton yield. Bibi *et al.* [30] found highly significant positive correlation of boll weight with seed cotton yield in upland cotton. Highly significant positive correlation of boll weight with seed cotton yield was mainly due to direct effect of boll weight on seed cotton yield. Boll weight is an important yield contributing trait like bolls plant[-1]. Therefore, attention should be paid to boll weight during selection of genotypes for higher seed cotton yield.

Seed cotton yield plant[-1]

For seed cotton yield plant[-1], genotypes mean values varied from 35.22 to 85.06 g, while the said range for genotype × environment interaction was 27.45 to 89.66 g (Table 10). Considering genotype means, three F_5 populations i.e. CIM-506 × CIM-554 S_2 (85.06 g), CIM-554 × CIM-707 S_1 (83.24 g) and CIM-506 × CIM-446 S_1 (83.00 g) showed maximum and similar seed cotton yield plant[-1]. Genotypes CIM-554 (35.22 g) and CIM-707 × CIM-499 S_1 (36.19 g) exhibited minimum and same seed cotton yield plant[-1]. Concerning sowing times, on average, the genotypes produced maximum (60.69 g) seed cotton yield plant[-1] during normal sowing and minimum (50.69 g) during late sowing.

Table 10. Mean performance of parental cultivars and their F_5 populations for seed cotton yield plant[-1] in GEI studies in upland cotton

Parental genotypes	Normal Sowing	Late Sowing	Means (g)
SLH-284	48.69	38.25	43.47
CIM-446	53.88	42.41	48.15
CIM-473	69.75	60.77	65.26
CIM-496	67.30	56.53	61.92
CIM-499	55.91	46.42	51.16
CIM-506	51.95	41.80	46.88
CIM-554	42.99	27.45	35.22
CIM-707	57.84	45.85	51.84
F_5 populations			
CIM-496 × CIM-446 S_1	67.90	59.01	63.46

CIM-496 × CIM-473 S_1	54.63	45.88	50.25
CIM-496 × CIM-554 S_1	49.29	40.52	44.90
CIM-499 × CIM-446 S_1	50.35	42.08	46.22
CIM-499 × CIM-496 S_1	53.54	44.98	49.26
CIM-499 × CIM-496 S_2	56.97	45.22	51.10
	57.53	46.15	51.84
CIM-499 × CIM-554 S_2	67.35	55.92	61.63
CIM-499 × CIM-707 S_1	58.76	51.59	55.17
CIM-506 × CIM-446 S_1	89.52	76.47	83.00
CIM-506 × CIM-446 S_2	62.46	51.87	57.17
CIM-506 × CIM-499 S_1	69.16	60.37	64.77
CIM-506 × CIM-499 S_2	62.06	50.06	56.06
CIM-506 × CIM-554 S_1	50.61	41.52	46.07
CIM-506 × CIM-554 S_2	89.66	80.45	85.05
CIM-554 × SLH-284 S_1	67.68	56.66	62.17
CIM-554 × CIM-473 S_1	56.26	45.31	50.78
CIM-554 × CIM-473 S_2	51.65	42.16	46.91
CIM-554 × CIM-496 S_1	47.16	36.86	42.01
CIM-554 × CIM-506 S_1	72.38	64.15	68.27
CIM-554 × CIM-506 S_2	46.38	38.04	42.21
CIM-554 × CIM-506 S_3	81.29	72.24	76.77
CIM-554 × CIM-707 S_1	87.55	78.93	83.24
CIM-707 × SLH-284 S_1	50.61	41.04	45.82
CIM-707 × SLH-284 S_2	66.55	58.49	62.52
CIM-707 × CIM-499 S_1	40.81	31.57	36.19
CIM-707 × CIM-499 S_2	67.23	56.63	61.93
CIM-707 × CIM-506 S_1	69.48	59.07	64.28
CIM-707 × CIM-506 S_2	52.26	42.80	47.53
Means (g)	60.69	50.69	-

Genotypes LSD$_{0.05}$ = 4.89, Environments LSD$_{0.05}$ = 1.14, GEI LSD$_{0.05}$ = 6.92

In genotype × environment interactions, two F$_5$ populations CIM-506 × CIM-554 S$_2$ (89.66 g) and CIM-506 × CIM-446 S$_1$ (89.52 g) showed maximum and alike seed cotton yield plant^{-1} during normal sowing. However, these genotypes were found at par with genotype CIM-554 × CIM-707 S$_1$ (87.55 g) for maximum seed cotton yield plant^{-1} during normal sowing. Genotype CIM-554 (27.45 g) exhibited minimum seed cotton yield plant^{-1} and was found at par with F$_5$ population CIM-707 × CIM-499 S$_1$ (31.57 g) during late sowing. Overall, in genotypes and G × E interaction means, F$_5$ populations CIM-506 × CIM-554 S$_2$, CIM-554 × CIM-707 S$_1$ and CIM-506 ×

CIM-446 S$_1$ showed maximum seed cotton yield plant^{-1}. Seed cotton yield plant^{-1} exhibited significant positive correlation with most of the traits except lint % and lint index where the correlation was negative (Table 4).

Present results were in close resemblance with earlier findings of Awan *et al*. [8] who noticed that different sowing dates and plant spacing and their interaction significantly affected seed cotton yield in upland cotton. Elsiddig *et al*. [31] studied genotype × environment interactions and observed that all the components of variation (G, E, G × E) exhibited highly significant differences among cotton

genotypes for seed cotton yield in upland cotton. Highly significant differences were recorded among genotypes, environments and genotypes × environments interaction and their effect on seed cotton yield in upland cotton. These results are in line with Dewdar *et al.* [24]. In view of above, positive correlation of seed cotton yield with majority of traits was also encouraging for improvement in yield.

Afiah and Ghoneim [32], Badr [33] and Soomro *et al*. [34] recorded highly significant positive correlation of yield with sympodia plant^{-1}, bolls plant^{-1} and boll weight. Seed cotton yield presented significant positive correlation with seed traits. These results are in line with Khan *et al.* [35]. Conflicting views may be due to different genetic makeup of the cotton populations used under different environmental conditions. In present studies, significant and positive correlation of seed cotton yield plant^{-1} with most of the traits might be due to direct/indirect effect of these traits on seed cotton yield.

Conclusion

Overall, in genotypes and genotype × environment interaction, F_5 population CIM-506 × CIM-554 S_2 exhibited maximum bolls sympodia^{-1} and bolls plant^{-1}. The F_5 population CIM-554 × CIM-707 S_1 revealed maximum seeds boll^{-1} and boll weight. Genotype CIM-554 × CIM-473 S_2 produced maximum seeds boll^{-1}. Parental genotype CIM-496 showed maximum sympodia plant^{-1}, bolls sympodia^{-1} and bolls plant^{-1}. The F_5 population CIM-506 × CIM-554 S_2 was found more responsive to both environments followed by genotypes CIM-554 × CIM-707 S_1, CIM-496 and CIM-554 × CIM-473 S_2 that could be used in future breeding programme for improvement of cotton.

Authors' contributions

Conceived and designed the experiments: F Nadeem & NU Khan, Performed the experiments: F Nadeem & NU Khan, Analyzed the data: Imranuddin, S Khalid & B Saeed. Contributed reagents/ materials/ analysis tools: Sikander, Imaranuddin, B Saeed, T Jan, K Khan & MR Khan, Wrote the paper: F Nadeem & S Khalid.

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