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# Quantification of genetic variability of cotton genotypes as affected by different sowing dates under agro-climatic condition of north-west Pakistan

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For developing superior cultivars genotype (G), environment (E) interaction, is of major concern to plant breeders. G x 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 randomized complete block design (RCBD) having three replications. Analysis of variance presented highly significant differences for genotypes and sowing dates for almost all the agronomic traits except seed index, where the mean differences were non-significant for sowing dates. G x E interaction effects were highly significant ($P \leq 0.01$) for seeds locule$^{-1}$ while for rest of the traits the G × E interactions were non-significant. Significant G x E interaction effects for these traits could be due to different environments in which the genotypes were examined. Overall, in genotypes and G x 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 per boll (33.21), seeds per locule (7.54), boll weight (4.76 g) and seed cotton yield per plant (83.24g). The $F_5$ population CIM-554 × CIM-473 $S_2$ produced maximum seeds boll$^{-1}$(31.95), seeds locule$^{-1}$ (7.42) and lint % (35.85%). Parental cultivar CIM-496 showed maximum sympodia plant$^{-1}$ (16.10), bolls sympodia$^{-1}$ (1.17), bolls plant$^{-1}$ (18.89) and seed index (9.37 g). $F_5$ 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 and lint yields.

**Keywords: Cotton, sowing dates, genotypes, environment, lint %**

## INTRODUCTION

Cotton is very sensitive to environmental conditions and grown in a wide range of ecological zones and thus, a number of factors; cultivars, plant density, sowing time, nutrients and water management practices are involved in cotton yield Therefore, a better crop growth ensures with the appropriate coordination of different agronomic practices and judicious use of various inputs and among these, planting date is important to explore the potential of a cultivar in the region (Ali et al. 2009). The cultivar selection is also a key management component in any cropping system even more critical in plant spacing and sowing date for cotton production, although high yield potential is a predominant consideration however, maturity and plant size are also major factor to consider (Nichols et al. 2004).

Agronomists have also developed new cultivation practices adapted to late planting with the aiming of accelerating the crop cycle, while reducing the vegetative vigor, thus, agronomic management does not promote excessive crop growth that delay maturity. Therefore, optimum sowing date for a cultivar in a region is considered to be the most important manageable factor in cotton crop (Bozbek et al. 2006). Early sowing produced 10% more flowers, 23% more open bolls and 18% more seed cotton yield than late sowing (Arshad, et al. 2007). Similarly, Akhter et al. (2002) investigated the sowing dates from May 01 to June 16 with six cotton cultivars and reported that regardless of the cultivars, best results were obtained with the crop planted on May 16.

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 (Khan et al. 2012). During 2013-14, the cotton crop was cultivated on an area of 2.806 millions 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 (Kakar et al. 2007). 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 (Sharma et al. 1987).

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 (Gul, 2013). 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 (Gul et al. 2014). 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 (Romagosa et al. 1996).

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 (Iqbal et al. 2006). 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. 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 material and experimental design

Genotype × environment interaction 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. 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.

#### 1. Locules boll$^{-1}$

Five bolls from each plant were randomly selected and averaged over five to get the average number of locules per boll.

#### 2. Seeds locule$^{-1}$

The number of seeds in each locule, were counted from five selected bolls of each plant and their average were calculated to get the average number of seeds locule$^{-1}$.

#### 3. Seeds boll$^{-1}$

Similarly the number of seeds per boll were calculated, by counting the number of seeds in randomly selected five bolls of each plant and averaged over five to get the average number of seeds boll$^{-1}$.

#### 4. Lint % (Ginning outturn)

Dry and clean seed cotton picked and obtained from bolls was ginned with the help of 8-saw-gin. The obtained lint was weighed separately for each sample of seed cotton and percent lint was computed with the following formula:

$$Lint\ \%\ (G.O.T) = \frac{Weight\ of\ Lint\ in\ a\ Sample}{Weight\ of\ Seed\ Cotton\ Sample} \times 100$$

**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 $S_2$ |

### 5. Seed index (g)

Seed index was computed by weighing on electric balance 100 seeds fully free from lint, inert matter and biological matter like insects and pathogens.

### 6. Lint index (g)

Similarly the lint obtained from 100 seeds were weighed and expressed as lint index. The formula used for calculating the lint index is given below.

$$Lint\ Index = \frac{Seed\ Index \times Lint\%}{100 - Lint\%}$$

### Statistical Analysis

The data obtained were subjected to analysis of variance for genotype × environment interaction (Gomez and Gomez, 1984) by using following G × E interaction ANOVA (Table 2). After getting the significant variations among genotypes performance across environments for all the studied traits, the genotype means for each variable were further separated and compared by using the least significant difference (LSD) test at 5% probability level.

**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 except seed index, where non-significant (P>0.05) differences for sowing dates were recorded (Table 3). 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.

### Locules boll$^{-1}$

Genotypes mean values for locules boll$^{-1}$ ranged from 4.07 to 4.61, while the said range for genotype × environment interaction was 4.03 to 4.67 (Table 4 ). In view of the genotype means, genotype CIM-499 × CIM-554 $S_1$ (4.61) showed maximum number of locules boll$^{-1}$ and was found at par with genotype CIM-499 × CIM-554 $S_2$ (4.60). Genotype CIM-707 × CIM-499 $S_1$ (4.07) showed minimum number of locules boll$^{-1}$ and was found at par with genotype CIM-707 × SLH-284 $S_1$ (4.13).

Concerning sowing date means, the genotypes produced maximum locules boll$^{-1}$ (4.43) during normal sowing and minimum (4.33) during late sowing. In genotype × environment interaction, $F_5$ population CIM-499 × CIM-554 $S_1$ (4.67) showed maximum number of locules boll$^{-1}$ and was found at par with the genotype CIM-499 × CIM-554 $S_2$ (4.65) with normal sowing. Genotype CIM-707 × CIM-499 $S_1$ (4.03) showed minimum number of locules boll$^{-1}$ and was found at par with genotype CIM-707 × SLH-284 $S_1$ (4.08) during late sowing. Overall, in genotypes and G × E interaction means, $F_5$ populations CIM-499 × CIM-554 $S_1$ and CIM-499 × CIM-554 $S_2$ showed maximum number of locules boll$^{-1}$.

In upland cotton, highly significant genotypic differences were observed for parental genotypes and $F_1$ populations for locules boll$^{-1}$ and $F_1$ populations presented best performance for locules boll$^{-1}$ and seeds locule$^{-1}$ with positive association of seed cotton yield and locules boll$^{-1}$ (Bibi et al. 2011). Highly significant differences were reported among genotypes for all the traits except locules boll$^{-1}$, however, seed cotton yield presented nonsignificant negative correlation with locules boll$^{-1}$ (Khan et al. 2009b). Conflicting results may be due to varied genetic makeup of cotton populations used under different environmental conditions. Moreover, positive association of locules boll$^{-1}$ with seed cotton yield was mainly due to boll weight.

**Table 3: Mean squares of genotypes, sowing dates and G × E interaction for various traits in upland cotton**

| Variables | Mean squares | | | | |
|---|---|---|---|---|---|
| | Sowing dates | Genotypes | G × E Interaction | Error | CV % |
| Degree of freedom | 1 | 36 | 36 | 144 | - |
| Locules boll$^{-1}$ | 0.636** | 0.119** | 0.001$^{NS}$ | 0.042 | 4.67 |
| Seeds locule$^{-1}$ | 5.186** | 1.051** | 0.042** | 0.020 | 2.15 |
| Seeds boll$^{-1}$ | 316.878** | 25.198** | 0.668$^{NS}$ | 1.749 | 4.47 |
| Lint % | 261.474** | 20.136** | 1.137$^{NS}$ | 1.785 | 4.03 |
| Seed index | 0.171$^{NS}$ | 0.804** | 0.000$^{NS}$ | 0.185 | 4.92 |
| Lint index | 11.693** | 0.755** | 0.052$^{NS}$ | 0.115 | 7.82 |

**, * significant at P≤0.01 & P≤0.05, respectively, NS = Non-Significant

**Table 4: Mean performance of parental cultivars and their $F_5$ populations for locules boll$^{-1}$ in G × E interaction studies in upland cotton.**

| Parental genotypes | Normal Sowing | Late sowing | Means (#) |
|---|---|---|---|
| SLH-284 | 4.48 | 4.36 | 4.42 |
| CIM-446 | 4.51 | 4.34 | 4.42 |
| CIM-473 | 4.37 | 4.23 | 4.30 |
| CIM-496 | 4.43 | 4.31 | 4.37 |
| CIM-499 | 4.43 | 4.32 | 4.38 |
| CIM-506 | 4.42 | 4.29 | 4.36 |
| CIM-554 | 4.36 | 4.28 | 4.32 |
| CIM-707 | 4.20 | 4.12 | 4.16 |
| **$F_5$ populations** | | | |
| CIM-496 × CIM-446 $S_1$ | 4.33 | 4.22 | 4.28 |
| CIM-496 × CIM-473 $S_1$ | 4.62 | 4.52 | 4.57 |
| CIM-496 × CIM-554 $S_1$ | 4.46 | 4.35 | 4.41 |
| CIM-499 × CIM-446 $S_1$ | 4.54 | 4.44 | 4.49 |
| CIM-499 × CIM-496 $S_1$ | 4.61 | 4.49 | 4.55 |
| CIM-499 × CIM-496 $S_2$ | 4.58 | 4.46 | 4.52 |
| CIM-499 × CIM-554 $S_1$ | 4.67 | 4.55 | 4.61 |
| CIM-499 × CIM-554 $S_2$ | 4.65 | 4.56 | 4.60 |
| CIM-499 × CIM-707 $S_1$ | 4.60 | 4.44 | 4.52 |
| CIM-506 × CIM-446 $S_1$ | 4.46 | 4.35 | 4.41 |
| CIM-506 × CIM-446 $S_2$ | 4.51 | 4.42 | 4.47 |
| CIM-506 × CIM-499 $S_1$ | 4.59 | 4.45 | 4.52 |
| CIM-506 × CIM-499 $S_2$ | 4.51 | 4.40 | 4.45 |
| CIM-506 × CIM-554 $S_1$ | 4.59 | 4.51 | 4.55 |
| CIM-506 × CIM-554 $S_2$ | 4.39 | 4.26 | 4.33 |
| CIM-554 × SLH-284 $S_1$ | 4.50 | 4.39 | 4.45 |
| CIM-554 × CIM-473 $S_1$ | 4.25 | 4.15 | 4.20 |
| CIM-554 × CIM-473 $S_2$ | 4.53 | 4.43 | 4.48 |
| CIM-554 × CIM-496 $S_1$ | 4.30 | 4.20 | 4.25 |
| CIM-554 × CIM-506 $S_1$ | 4.44 | 4.30 | 4.37 |
| CIM-554 × CIM-506 $S_2$ | 4.30 | 4.18 | 4.24 |
| CIM-554 × CIM-506 $S_3$ | 4.30 | 4.19 | 4.25 |
| CIM-554 × CIM-707 $S_1$ | 4.41 | 4.33 | 4.37 |
| CIM-707 × SLH-284 $S_1$ | 4.17 | 4.08 | 4.13 |
| CIM-707 × SLH-284 $S_2$ | 4.33 | 4.24 | 4.28 |
| CIM-707 × CIM-499 $S_1$ | 4.11 | 4.03 | 4.07 |
| CIM-707 × CIM-499 $S_2$ | 4.56 | 4.48 | 4.52 |
| CIM-707 × CIM-506 $S_1$ | 4.17 | 4.11 | 4.14 |
| CIM-707 × CIM-506 $S_2$ | 4.35 | 4.27 | 4.31 |
| **Means (#)** | 4.43 | 4.33 | - |

**Seeds locule$^{-1}$**

For seeds locule$^{-1}$, genotypes mean values varied from 6.11 to 7.54, while the mean values for genotype × environment interaction ranged from 5.89 to 7.69 (Table 5). Considering genotype means, three $F_5$ populations i.e. CIM-554 × CIM-707 $S_1$ (7.54), CIM-506 × CIM-446 $S_1$ (7.46) and CIM-554 × CIM-473 $S_2$ (7.42) showed maximum and similar seeds locule$^{-1}$.

**Table 5: Mean performance of parental cultivars and their $F_5$ populations for seeds locule$^{-1}$ in GEI studies in upland cotton.**

| Parental genotypes | Normal Sowing | Late Sowing | Means (#) Means (#) |
|---|---|---|---|
| SLH-284 | 6.39 | 5.91 | 6.15 |
| CIM-446 | 6.36 | 5.89 | 6.12 |
| CIM-473 | 6.68 | 5.96 | 6.32 |
| CIM-496 | 6.48 | 5.96 | 6.22 |
| CIM-499 | 6.43 | 6.06 | 6.24 |
| CIM-506 | 7.18 | 6.93 | 7.06 |
| CIM-554 | 6.57 | 5.90 | 6.23 |
| CIM-707 | 6.55 | 5.91 | 6.23 |
| **$F_5$ populations** | | | |
| CIM-496 × CIM-446 $S_1$ $S_1$ | 6.82 | 6.32 | 6.57 |
| CIM-496 × CIM-473 $S_1$ | 6.48 | 5.89 | 6.19 |
| CIM-496 × CIM-554 $S_1$ | 6.42 | 6.19 | 6.30 |
| CIM-499 × CIM-446 $S_1$ | 7.32 | 7.03 | 7.18 |
| CIM-499 × CIM-496 $S_1$ | 7.13 | 6.94 | 7.04 |
| CIM-499 × CIM-496 $S_2$ | 6.20 | 6.01 | 6.11 |
| CIM-499 × CIM-554 $S_1$ | 6.61 | 6.34 | 6.48 |
| CIM-499 × CIM-554 $S_2$ | 6.81 | 6.54 | 6.67 |
| CIM-499 × CIM-707 $S_1$ | 6.80 | 6.51 | 6.66 |
| CIM-506 × CIM-446 $S_1$ | 7.58 | 7.33 | 7.46 |
| CIM-506 × CIM-446 $S_2$ | 6.94 | 6.50 | 6.72 |
| CIM-506 × CIM-499 $S_1$ | 6.81 | 6.37 | 6.59 |
| CIM-506 × CIM-499 $S_2$ | 6.77 | 6.57 | 6.67 |
| CIM-506 × CIM-554 $S_1$ | 6.81 | 6.64 | 6.73 |
| CIM-506 × CIM-554 $S_2$ | 7.15 | 7.00 | 7.08 |
| CIM-554 × SLH-284 $S_1$ | 6.68 | 6.59 | 6.64 |
| CIM-554 × CIM-473 $S_1$ | 6.58 | 6.43 | 6.51 |
| CIM-554 × CIM-473 $S_2$ | 7.52 | 7.31 | 7.42 |
| CIM-554 × CIM-496 $S_1$ | 7.23 | 7.15 | 7.19 |
| CIM-554 × CIM-506 $S_1$ | 6.86 | 6.65 | 6.75 |
| CIM-554 × CIM-506 $S_2$ | 6.76 | 6.61 | 6.69 |
| CIM-554 × CIM-506 $S_3$ | 6.39 | 6.22 | 6.30 |
| CIM-554 × CIM-707 $S_1$ | 7.69 | 7.38 | 7.54 |
| CIM-707 × SLH-284 $S_1$ | 6.32 | 6.07 | 6.20 |
| CIM-707 × SLH-284 $S_2$ | 6.48 | 6.18 | 6.33 |
| CIM-707 × CIM-499 $S_1$ | 7.25 | 7.05 | 7.15 |
| CIM-707 × CIM-499 $S_2$ | 7.18 | 7.01 | 7.10 |
| CIM-707 × CIM-506 $S_1$ | 6.59 | 6.36 | 6.47 |
| CIM-707 × CIM-506 $S_2$ | 6.22 | 6.03 | 6.13 |
| **Means (#)** | 6.78 | 6.48 | - |

Genotypes $LSD_{0.05}$ = 0.16, Environments $LSD_{0.05}$ = 0.04, GEI $LSD_{0.05}$ = 0.23

However, $F_5$ populations viz., CIM-499 × CIM-496 $S_2$ (6.11), CIM-446 (6.12) and CIM-707 × CIM-506 $S_2$ (6.13) exhibited minimum and same number of seeds locule$^{-1}$. However, the above three genotypes were found at par with genotype SLH-284 (6.15) for minimum number of seeds locule$^{-1}$. For sowing dates, on average, during normal sowing the genotypes produced maximum seeds locule$^{-1}$ (6.78) and minimum (6.48) during late sowing.

In genotype × environment interaction, genotype CIM-554 × CIM-707 $S_1$ (7.69) showed maximum number of seeds locule$^{-1}$ during normal sowing. The above genotype was found at par with two other $F_5$ populations i.e. CIM-506 × CIM-446 $S_1$ (7.58) and CIM-554 × CIM-473 $S_2$ (7.52) for maximum number of seeds locule$^{-1}$ during normal sowing. Five genotypes i.e. CIM-446 (5.89), CIM-496 × CIM-473 $S_1$ (5.89), CIM-554 (5.90), CIM-707 (5.91) and SLH-284 (5.91) exhibited minimum and similar seeds locule$^{-1}$ during late sowing. However, these genotypes were found at par with alike values of two other parental cultivars i.e. CIM-496 (5.96) and CIM-473 (5.96) for minimum seeds locule$^{-1}$ during late sowing. Overall, the $F_5$ populations CIM-554 × CIM-707 $S_1$, CIM-506 × CIM-446 $S_1$ and CIM-554 × CIM-473 $S_2$ showed maximum number of seeds locule$^{-1}$ in genotypes and G × E interaction means.

Significant variations among genotypes, environments and genotypes × environments interaction effects for morpho-yield traits suggested that genotypes showed differential responses over diverse environmental conditions (Elsiddig et al. 2004). Bibi et al. (2011) determined genetic differences, yield potential and correlation of seed cotton yield with different morpho-yield traits in $F_1$ diallel populations and observed highly significant genotypic differences for seeds locule$^{-1}$, and significant positive association of yield with seeds locule$^{-1}$. Khan et al. (2010) observed nonsignificant differences between the genotypes for seeds per locule. On the other hand, seed cotton yield presented nonsignificant negative correlation with seeds per locule. Conflicting findings may be due to varied genetic makeup of the cotton populations used under different environments.

### Seeds boll$^{-1}$

Genotypes mean values for seeds boll$^{-1}$ ranged from 24.04 to 33.22, while genotype × environment interaction mean values varied from 22.26 to 34.78 (Table 6). Considering genotype means, $F_5$ population CIM-554 × CIM-707 $S_1$ (33.22) showed maximum seeds boll$^{-1}$, however, it was found at par with three other $F_5$ populations viz., CIM-554 × CIM-473 $S_1$ (32.80), CIM-707 × CIM-499 $S_2$ (32.64) and CIM-554 × CIM-473 $S_2$ (31.95) for maximum seeds boll$^{-1}$. Genotype CIM-473 exhibited minimum seeds boll$^{-1}$ (24.04) and was found at par with two other genotypes i.e. CIM-707 × CIM-499 $S_1$ (25.49) and CIM-707 (25.52). Regarding sowing time means, on average the genotypes produced maximum seeds boll$^{-1}$ (30.79) during normal sowing and minimum (28.40) during late sowing.

In genotype × environment interaction, $F_5$ population CIM-554 × CIM-707 $S_1$ (34.78) showed maximum seeds boll$^{-1}$ during normal sowing. The above genotype was found at par with two other $F_5$ populations i.e. CIM-554 × CIM-473 $S_1$ (34.54) and CIM-707 × CIM-499 $S_2$ (33.65) sown at normal time. However, these genotypes were found at par with the similar values of two other genotypes i.e. CIM-554 × CIM-473 $S_2$ (32.88) and CIM-554 × CIM-496 $S_1$ (32.87) for maximum number of seeds boll$^{-1}$ during normal sowing. Genotype CIM-473 (22.26) exhibited minimum seeds boll$^{-1}$ and was found at par with the genotype CIM-554 × CIM-506 $S_2$ (24.36) during late sowing. Overall, in genotypes and G × E interaction means, $F_5$ populations CIM-554 × CIM-707 $S_1$, CIM-554 × CIM-473 $S_1$, CIM-707 × CIM-499 $S_2$ and CIM-554 × CIM-473 $S_2$ showed maximum number of seeds boll$^{-1}$. Dewdar et al. (2013) also reported significant difference among cotton genotypes. He noticed significant differences between cotton genotypes for lint %, lint index, boll weight, number of open bolls and lint yield per plant. Through combine analysis of variance, he observed highly significant differences among the genotypes, environments and for gene-environment interaction for all the studied traits.

Present results were in close resemblance with earlier findings Awan et al. (2011) who noticed that different sowing dates and plant spacing and their interaction significantly affected seed cotton yield in upland cotton. Elsiddig et al. (2004) 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 (Gul et al. 2014;

Dewdar et al. (2013)). In view of above, positive correlation of seed cotton yield with majority of traits was also encouraging for improvement in yield.

**Table 6: Mean performance of parental cultivars and their $F_5$ populations for seeds $boll^{-1}$ in G × E interaction studies in upland cotton.**

| Parental genotypes | Normal Sowing | Late Sowing | Means (#) |
|---|---|---|---|
| SLH-284 | 32.53 | 29.31 | 30.92 |
| CIM-446 | 31.37 | 29.65 | 30.51 |
| CIM-473 | 25.82 | 22.26 | 24.04 |
| CIM-496 | 32.11 | 29.11 | 30.61 |
| CIM-499 | 31.44 | 28.91 | 30.17 |
| CIM-506 | 30.87 | 28.15 | 29.51 |
| CIM-554 | 31.39 | 28.81 | 30.10 |
| CIM-707 | 26.55 | 24.49 | 25.52 |
| **$F_5$ populations** | | | |
| CIM-496 × CIM-446 $S_1$ | 29.64 | 27.36 | 28.50 |
| CIM-496 × CIM-473 $S_1$ | 30.37 | 28.50 | 29.44 |
| CIM-496 × CIM-554 $S_1$ | 29.54 | 27.86 | 28.70 |
| CIM-499 × CIM-446 $S_1$ | 31.68 | 30.17 | 30.93 |
| CIM-499 × CIM-496 $S_1$ | 31.70 | 29.55 | 30.63 |
| CIM-499 × CIM-496 $S_2$ | 31.43 | 29.69 | 30.56 |
| CIM-499 × CIM-554 $S_1$ | 30.45 | 28.46 | 29.45 |
| CIM-499 × CIM-554 $S_2$ | 31.39 | 28.14 | 29.77 |
| CIM-499 × CIM-707 $S_1$ | 30.42 | 28.14 | 29.28 |
| CIM-506 × CIM-446 $S_1$ | 31.57 | 28.34 | 29.96 |
| CIM-506 × CIM-446 $S_2$ | 31.67 | 28.22 | 29.94 |
| CIM-506 × CIM-499 $S_1$ | 29.86 | 27.94 | 28.90 |
| CIM-506 × CIM-499 $S_2$ | 30.24 | 28.32 | 29.28 |
| CIM-506 × CIM-554 $S_1$ | 31.12 | 28.30 | 29.71 |
| CIM-506 × CIM-554 $S_2$ | 31.36 | 29.10 | 30.23 |
| CIM-554 × SLH-284 $S_1$ | 31.53 | 29.75 | 30.64 |
| CIM-554 × CIM-473 $S_1$ | 34.54 | 31.05 | 32.80 |
| CIM-554 × CIM-473 $S_2$ | 32.88 | 31.01 | 31.95 |
| CIM-554 × CIM-496 $S_1$ | 32.87 | 30.56 | 31.71 |
| CIM-554 × CIM-506 $S_1$ | 30.59 | 28.03 | 29.31 |
| CIM-554 × CIM-506 $S_2$ | 27.91 | 24.36 | 26.14 |
| CIM-554 × CIM-506 $S_3$ | 27.80 | 26.53 | 27.17 |
| CIM-554 × CIM-707 $S_1$ | 34.78 | 31.65 | 33.21 |
| CIM-707 × SLH-284 $S_1$ | 30.91 | 28.74 | 29.83 |
| CIM-707 × SLH-284 $S_2$ | 32.63 | 29.69 | 31.16 |
| CIM-707 × CIM-499 $S_1$ | 26.30 | 24.68 | 25.49 |
| CIM-707 × CIM-499 $S_2$ | 33.65 | 31.62 | 32.64 |
| CIM-707 × CIM-506 $S_1$ | 26.88 | 25.61 | 26.24 |
| CIM-707 × CIM-506 $S_2$ | 31.26 | 28.57 | 29.92 |
| **Means (#)** | 30.79 | 28.40 | |

Genotypes $LSD_{0.05}$ = 1.50, Environments $LSD_{0.05}$ = 0.35, GEI $LSD_{0.05}$ = 2.12

**Lint %**

For lint %, genotypes mean values ranged from 29.54 to 36.19%, while mean values for genotype × environment interaction varied from 28.86 to 37.56% (Table 7).

**Table 7: Mean performance of parental cultivars and their $F_5$ populations for lint% in G × E interaction studies in upland cotton.**

| Parental genotypes Genotypes | Normal Sowing | Late Sowing | Means (%) |
|---|---|---|---|
| SLH-284 | 35.38 | 32.56 | 33.97 |
| CIM-446 | 35.56 | 32.95 | 34.26 |
| CIM-473 | 30.69 | 29.12 | 29.91 |
| CIM-496 | 32.76 | 30.16 | 31.46 |
| CIM-499 | 32.64 | 31.16 | 31.90 |
| CIM-506 | 30.29 | 29.39 | 29.84 |
| CIM-554 | 32.82 | 31.69 | 32.26 |
| CIM-707 | 31.20 | 29.91 | 30.56 |
| **$F_5$ populations** | | | |
| CIM-496 × CIM-446 $S_1$ | 34.27 | 32.94 | 33.61 |
| CIM-496 × CIM-473 $S_1$ | 37.11 | 34.14 | 35.63 |
| CIM-496 × CIM-554 $S_1$ | 35.89 | 33.21 | 34.55 |
| CIM-499 × CIM-446 $S_1$ | 31.40 | 30.10 | 30.75 |
| CIM-499 × CIM-496 $S_1$ | 37.24 | 33.86 | 35.55 |
| CIM-499 × CIM-496 $S_2$ | 33.02 | 31.23 | 32.13 |
| CIM-499 × CIM-554 $S_1$ | 34.63 | 32.28 | 33.46 |
| CIM-499 × CIM-554 $S_2$ | 32.95 | 30.82 | 31.88 |
| CIM-499 × CIM-707 $S_1$ | 37.50 | 34.87 | 36.19 |
| CIM-506 × CIM-446 $S_1$ | 32.10 | 30.94 | 31.52 |
| CIM-506 × CIM-446 $S_2$ | 34.20 | 31.84 | 33.02 |
| CIM-506 × CIM-499 $S_1$ | 32.60 | 31.44 | 32.02 |
| CIM-506 × CIM-499 $S_2$ | 33.68 | 32.42 | 33.05 |
| CIM-506 × CIM-554 $S_1$ | 37.56 | 34.14 | 35.85 |
| CIM-506 × CIM-554 $S_2$ | 33.40 | 31.50 | 32.45 |
| CIM-554 × SLH-284 $S_1$ | 33.31 | 31.12 | 32.22 |
| CIM-554 × CIM-473 $S_1$ | 37.04 | 32.37 | 34.71 |
| CIM-554 × CIM-473 $S_2$ | 37.13 | 34.57 | 35.85 |
| CIM-554 × CIM-496 $S_1$ | 35.62 | 33.09 | 34.35 |
| CIM-554 × CIM-506 $S_1$ | 33.30 | 31.80 | 32.55 |
| CIM-554 × CIM-506 $S_2$ | 30.21 | 28.86 | 29.54 |
| CIM-554 × CIM-506 $S_3$ | 33.31 | 29.52 | 31.42 |
| CIM-554 × CIM-707 $S_1$ | 34.20 | 32.25 | 33.22 |
| CIM-707 × SLH-284 $S_1$ | 35.28 | 33.31 | 34.30 |
| CIM-707 × SLH-284 $S_2$ | 35.45 | 32.81 | 34.13 |
| CIM-707 × CIM-499 $S_1$ | 36.79 | 34.87 | 35.83 |
| CIM-707 × CIM-499 $S_2$ | 33.85 | 31.12 | 32.48 |
| CIM-707 × CIM-506 $S_1$ | 35.99 | 32.75 | 34.37 |
| CIM-707 × CIM-506 $S_2$ | 35.12 | 34.09 | 34.61 |
| **Means (%)** | 34.20 | 32.03 | - |

Genotypes $LSD_{0.05}$ = 1.52, Environments $LSD_{0.05}$ = 0.35, GEI $LSD_{0.05}$ = 2.15

The $F_5$ populations CIM-499 × CIM-707 $S_1$ (36.19) showed maximum lint %. The above genotype was found at par with three other $F_5$ populations i.e. CIM-554 × CIM-473 $S_2$ (35.85%), CIM-506 × CIM-554 $S_1$ (35.85%) and CIM-707 × CIM-499 $S_1$ (35.83%) for maximum lint %. Genotypes CIM-554 × CIM-506 $S_2$ (29.54%) and CIM-506 (29.84%) exhibited minimum and similar lint %. The above genotypes were found at par with three other genotypes i.e. CIM-473 (29.91%), CIM-707 (30.56%) and CIM-499 × CIM-446 $S_1$ (30.75%) for minimum lint %. Regarding sowing times, genotypes produced maximum (34.20%) lint % during normal sowing and minimum (32.03%) during late sowing.

In genotype × environment interaction, $F_5$ population CIM-506 × CIM-554 $S_1$ (37.56%) showed maximum lint % with normal sowing and was found at par with genotype CIM-499 × CIM-707 $S_1$ (37.50%) at same sowing. However, these genotypes were found at par with four other $F_5$ populations i.e. CIM-499 × CIM-496 $S_1$ (37.24%), CIM-554 × CIM-473 $S_2$ (37.13%), CIM-496 × CIM-473 $S_1$ (37.12%) and CIM-554 × CIM-473 $S_1$ (37.04%) for maximum lint % during normal sowing. Genotype CIM-554 × CIM-506 $S_2$ (28.86%) exhibited minimum lint % and was found at par with the genotype CIM-473 (29.12%) during late sowing. Overall, in genotypes and G × E interaction means, $F_5$ populations CIM-506 × CIM-554 $S_1$, CIM-499 × CIM-707 $S_1$, CIM-499 × CIM-496 $S_1$, CIM-554 × CIM-473 $S_2$, CIM-496 × CIM-473 $S_1$ and CIM-554 × CIM-473 $S_1$ showed maximum lint %. Lint % showed non-significant negative correlation (r = -0.095) with seed cotton yield (Table 17). Analysis of variance across the environments exhibited significant variations among genotypes, environments and genotype by environment interaction for lint % (Awan et al. 2011; Campbell and Jones, 2005) findings revealed that sowing time and plant spacing significantly affected lint %, while their interaction effects were nonsignificant. Present results were also supported by findings of Naveed et al. (2004) who observed nonsignificant negative association of lint % with seed cotton yield. Correlation of yield and fiber quality traits in upland cotton genotypes was determined and lint % showed significant positive association with seed cotton yield (Hussain et al. 2010). Contradiction in between present and past findings might be due to genotype by environment interaction and diverse environmental conditions.

**Seed index**

Genotypes mean values for seed index varied from 7.98 to 9.53 g, while mean values for genotype × environment interaction varied from 7.96 to 9.56 g (Table 8). In case of genotype means, $F_5$ population CIM-506 × CIM-554 $S_2$ (9.53 g) showed maximum seed index and it was found at par with two other genotypes i.e. CIM-496 (9.37 g) and CIM-499 × CIM-496 $S_1$ (9.33 g) for maximum seed index. Genotype SLH-284 (7.98 g) exhibited minimum seed index, and was found similar in performance with two other genotypes i.e. CIM-496 × CIM-554 $S_1$ (8.12 g) and CIM-499 × CIM-554 $S_2$ (8.30 g) for minimum seed index. Concerning sowing dates, on average, during normal sowing the genotypes produced maximum seed index (8.77 g) and minimum (8.71 g) during late sowing.

In genotype × environment interaction, $F_5$ population CIM-506 × CIM-554 $S_2$ (9.56 g) showed maximum seed index during normal sowing. The above genotype was found at par with two other genotypes i.e. CIM-506 × CIM-554 $S_2$ (9.49 g) with late sowing and CIM-496 (9.40 g) during normal sowing for maximum seed index. However, these genotypes were found parallel with two other genotypes i.e. CIM-499 × CIM-496 $S_1$ (9.36 g) in normal sowing and CIM-496 (9.33 g) during late sowing. Genotypes SLH-284 (7.96 g) with late sowing and SLH-284(8.00 g) during normal sowing exhibited minimum and same values for seed index. Theses genotypes were found at par with two other genotypes i.e. CIM-496 × CIM-554 $S_1$ (8.09 g) under late sowing and CIM-496 × CIM-554 $S_1$ (8.14 g) during normal sowing for minimum seed index. Overall, in genotypes and G × E interaction means, two $F_5$ populations CIM-506 × CIM-554 $S_2$, CIM-499 × CIM-496 $S_1$ and parental cultivar CIM-496 showed maximum seed index. Seed index showed non-significant positive correlation (r = 0.058) with seed cotton yield (Table 17). Earlier studies showed that during the last 50 years, the variances due to G, E and GEI have been altered little in upland cotton (Meredith et al. 2012). Components of variations i.e. G, E and G × E interactions equally influenced yield, however, fiber quality traits and yield components (seed weight, boll weight, lint yield) were not as much influenced by environments and G × E interactions. Our results were also in corroboration with previous findings of Kakar et al. (2012), who noticed significant differences for genotypes, sowing dates and nonsignificant genotypes × sowing dates effects for seed index.

**Table 8: Mean performance of parental cultivars and their $F_5$ populations for seed index in G × E interaction studies in upland cotton.**

| Parental Genotypes | Normal Sowing | Late Sowing | Means (g) |
|---|---|---|---|
| SLH-284 | 8.00 | 7.96 | 7.98 |
| CIM-446 | 8.49 | 8.44 | 8.47 |
| CIM-473 | 9.13 | 9.07 | 9.10 |
| CIM-496 | 9.40 | 9.33 | 9.37 |
| CIM-499 | 8.87 | 8.79 | 8.83 |
| CIM-506 | 9.27 | 9.22 | 9.25 |
| CIM-554 | 9.28 | 9.21 | 9.24 |
| CIM-707 | 9.04 | 9.00 | 9.02 |
| **$F_5$ populations** | | | |
| CIM-496 × CIM-446 $S_1$ | 8.79 | 8.74 | 8.76 |
| CIM-496 × CIM-473 $S_1$ | 8.95 | 8.88 | 8.91 |
| CIM-496 × CIM-554 $S_1$ | 8.14 | 8.09 | 8.12 |
| CIM-499 × CIM-446 $S_1$ | 8.85 | 8.79 | 8.82 |
| CIM-499 × CIM-496 $S_1$ | 9.36 | 9.31 | 9.33 |
| CIM-499 × CIM-496 $S_2$ | 8.79 | 8.73 | 8.76 |
| CIM-499 × CIM-554 $S_1$ | 8.91 | 8.86 | 8.88 |
| CIM-499 × CIM-554 $S_2$ | 8.32 | 8.27 | 8.30 |
| CIM-499 × CIM-707 $S_1$ | 8.48 | 8.42 | 8.45 |
| CIM-506 × CIM-446 $S_1$ | 8.83 | 8.77 | 8.80 |
| CIM-506 × CIM-446 $S_2$ | 8.48 | 8.42 | 8.45 |
| CIM-506 × CIM-499 $S_1$ | 8.69 | 8.63 | 8.66 |
| CIM-506 × CIM-499 $S_2$ | 8.52 | 8.47 | 8.50 |
| CIM-506 × CIM-554 $S_1$ | 8.85 | 8.80 | 8.83 |
| CIM-506 × CIM-554 $S_2$ | 9.56 | 9.49 | 9.53 |
| CIM-554 × SLH-284 $S_1$ | 8.38 | 8.31 | 8.35 |
| CIM-554 × CIM-473 $S_1$ | 8.45 | 8.41 | 8.43 |
| CIM-554 × CIM-473 $S_2$ | 8.47 | 8.39 | 8.43 |
| CIM-554 × CIM-496 $S_1$ | 8.84 | 8.80 | 8.82 |
| CIM-554 × CIM-506 $S_1$ | 8.85 | 8.80 | 8.83 |
| CIM-554 × CIM-506 $S_2$ | 8.99 | 8.95 | 8.97 |
| CIM-554 × CIM-506 $S_3$ | 9.12 | 9.06 | 9.09 |
| CIM-554 × CIM-707 $S_1$ | 8.43 | 8.38 | 8.40 |
| CIM-707 × SLH-284 $S_1$ | 8.35 | 8.29 | 8.32 |
| CIM-707 × SLH-284 $S_2$ | 8.64 | 8.60 | 8.62 |
| CIM-707 × CIM-499 $S_1$ | 9.21 | 9.16 | 9.19 |
| CIM-707 × CIM-499 $S_2$ | 8.44 | 8.38 | 8.41 |
| CIM-707 × CIM-506 $S_1$ | 8.64 | 8.59 | 8.61 |
| CIM-707 × CIM-506 $S_2$ | 8.61 | 8.56 | 8.59 |
| **Means (g)** | 8.77 | 8.71 | - |

Genotypes $LSD_{0.05}$ = 0.49, Environments $LSD_{0.05}$ = 0.11, GEI $LSD_{0.05}$ = 0.69

Hassan et al. (2005) found that seed index was significantly positively correlated with seed cotton yield, while studying the performance of Egyptian cotton genotypes. However, positive correlation of seed index with seed cotton yield was also observed (Khan et al. 2010). Contradiction in findings might be due to different genetic makeup of cotton populations used under different environmental conditions.

### Lint index

For lint index, the genotypes mean values ranged from 3.76 to 5.17 g, while the said range for genotype × environment interaction was 3.63 to 5.57 g (Table 9). The $F_5$ populations CIM-499 × CIM-496 $S_1$ (5.17 g) and CIM-707 × CIM-499 $S_1$ (5.14 g) showed maximum and similar lint index.

**Table 9: Mean performance of parental cultivars and their $F_5$ populations for lint index in G × E interaction studies in upland cotton.**

| Parental genotypes Genotypes | Normal Sowing | Late Sowing | Means (g) |
|---|---|---|---|
| SLH-284 | 4.38 | 3.84 | 4.11 |
| CIM-446 | 4.69 | 4.15 | 4.42 |
| CIM-473 | 4.03 | 3.73 | 3.88 |
| CIM-496 | 4.59 | 4.04 | 4.32 |
| CIM-499 | 4.30 | 3.98 | 4.14 |
| CIM-506 | 4.03 | 3.85 | 3.94 |
| CIM-554 | 4.53 | 4.27 | 4.40 |
| CIM-707 | 4.12 | 3.85 | 3.98 |
| **$F_5$ populations** | | | |
| CIM-496 × CIM-446 $S_1$ | 4.58 | 4.29 | 4.44 |
| CIM-496 × CIM-473 $S_1$ | 5.29 | 4.61 | 4.95 |
| CIM-496 × CIM-554 $S_1$ | 4.57 | 4.02 | 4.30 |
| CIM-499 × CIM-446 $S_1$ | 4.05 | 3.79 | 3.92 |
| CIM-499 × CIM-496 $S_1$ | 5.57 | 4.77 | 5.17 |
| CIM-499 × CIM-496 $S_2$ | 4.35 | 3.97 | 4.16 |
| CIM-499 × CIM-554 $S_1$ | 4.71 | 4.23 | 4.47 |
| CIM-499 × CIM-554 $S_2$ | 4.10 | 3.69 | 3.89 |
| CIM-499 × CIM-707 $S_1$ | 5.08 | 4.50 | 4.79 |
| CIM-506 × CIM-446 $S_1$ | 4.17 | 3.93 | 4.05 |
| CIM-506 × CIM-446 $S_2$ | 4.41 | 3.93 | 4.17 |
| CIM-506 × CIM-499 $S_1$ | 4.21 | 3.96 | 4.09 |
| CIM-506 × CIM-499 $S_2$ | 4.32 | 4.07 | 4.19 |
| CIM-506 × CIM-554 $S_1$ | 5.33 | 4.56 | 4.95 |
| CIM-506 × CIM-554 $S_2$ | 4.81 | 4.37 | 4.59 |
| CIM-554 × SLH-284 $S_1$ | 4.20 | 3.75 | 3.98 |
| CIM-554 × CIM-473 $S_1$ | 4.98 | 4.03 | 4.51 |
| CIM-554 × CIM-473 $S_2$ | 5.00 | 4.43 | 4.72 |
| CIM-554 × CIM-496 $S_1$ | 4.90 | 4.36 | 4.63 |
| CIM-554 × CIM-506 $S_1$ | 4.41 | 4.10 | 4.26 |
| CIM-554 × CIM-506 $S_2$ | 3.89 | 3.63 | 3.76 |
| CIM-554 × CIM-506 $S_3$ | 4.56 | 3.79 | 4.17 |
| CIM-554 × CIM-707 $S_1$ | 4.40 | 3.99 | 4.19 |

| | | | |
|---|---|---|---|
| CIM-707 × SLH-284 $S_1$ | 4.55 | 4.14 | 4.34 |
| CIM-707 × SLH-284 $S_2$ | 4.75 | 4.20 | 4.47 |
| CIM-707 × CIM-499 $S_1$ | 5.37 | 4.91 | 5.14 |
| CIM-707 × CIM-499 $S_2$ | 4.33 | 3.79 | 4.06 |
| CIM-707 × CIM-506 $S_1$ | 4.87 | 4.19 | 4.53 |
| CIM-707 × CIM-506 $S_2$ | 4.65 | 4.42 | 4.54 |
| **Means (g)** | 4.57 | 4.11 | - |

Genotypes $LSD_{0.05}$ = 0.39, Environnements $LSD_{0.05}$ = 0.09, GEI $LSD_{0.05}$ = 0.54

The above genotypes were also found at par with two other genotypes i.e. CIM-496 × CIM-473 $S_1$ (4.95 g) and CIM-506 × CIM-554 $S_1$ (4.95 g) for maximum lint index. Genotype CIM-554 × CIM-506 $S_2$ (3.76 g) exhibited minimum lint index and was found at par with two other genotypes i.e. CIM-473 (3.88 g) and CIM-499 × CIM-554 $S_2$ (3.89 g) for minimum lint index. Regarding sowing dates, genotypes produced maximum (4.57 g) lint index during normal sowing and minimum (4.11 g) during late sowing.

In genotype × environment interactions, $F_5$ population CIM-499 × CIM-496 $S_1$ (5.57 g) showed maximum lint index during normal sowing. The above genotype was found at par with four other $F_5$ populations viz., CIM-707 × CIM-499 $S_1$ (5.37 g), CIM-506 × CIM-554 $S_1$ (5.33 g), CIM-496 × CIM-473 $S_1$ (5.29 g) and CIM-499 × CIM-707 $S_1$ (5.08 g) for maximum lint index during normal sowing. The genotype CIM-554 × CIM-506 $S_2$ (3.63 g) exhibited minimum lint index during late sowing. The above genotype was found at par with three other genotypes i.e. CIM-499 × CIM-554 $S_2$ (3.69 g), CIM-473(3.73 g) and CIM-554 × SLH-284 $S_1$ (3.76 g) for minimum lint index during late sowing. Overall, $F_5$ populations CIM-499 × CIM-496 $S_1$, CIM-707 × CIM-499 $S_1$, CIM-506 × CIM-554 $S_1$, CIM-496 × CIM-473 $S_1$ and CIM-499 × CIM-707 $S_1$ showed maximum lint index. Lint index showed non-significant negative correlation (r = -0.065) with seed cotton yield (Nadeem et al. 2018)**.**

Significant mean squares were observed due to genotypes, environments and genotype by environment interactions for seed cotton yield and its components in upland cotton (Satish et al. 2009). However, the major share of genotype by environment interactions was noticed for majority of the traits apart from lint index, sympodia $plant^{-1}$ and bolls $plant^{-1}$. Elsiddig et al. (2006) observed significant variances due to genotype × environment interactions for lint index and lint % in upland cotton genotypes. Lint index was found significantly positively correlated with seed cotton yield (Khan et al. 2009). Lint index is an important trait due to its contribution in the lint % and seed cotton yield. Conflicting views could be due to different genetic makeup of the cotton populations used under different environmental conditions.

## CONCLUSION

Overall, in genotypes and G x 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 per boll (33.21), seeds per locule (7.54), boll weight (4.76 g) and seed cotton yield per plant (83.24g). The $F_5$ population CIM-554 × CIM-473 $S_2$ produced maximum seeds $boll^{-1}$(31.95), seeds $locule^{-1}$ (7.42) and lint % (35.85%). Parental cultivar CIM-496 showed maximum sympodia $plant^{-1}$ (16.10), bolls $sympodia^{-1}$ (1.17), bolls $plant^{-1}$ (18.89) and seed index (9.37 g). $F_5$ 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 and lint yields.

## CONFLICT OF INTEREST

The authors declared that present study was performed in absence of any conflict of interest.

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## AUTHOR CONTRIBUTIONS

Conceived and designed the experiments: Naqib Ullah Khan. Performed the experiments: FN,NUK, SK. Analyzed the data: Imranuddin, NK, HB, Shabirullah,NK, Contributed, reagents/ materials/ analysis tools: Mifta-hu-din, Shabirullah, NK Wrote the paper: SN, SK



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