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GENETIC ATTRIBUTES OF F_3 POPULATIONS AND THEIR PARENTAL LINES IN UPLAND COTTON

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ABSTRACT

The genetic potential, inbreeding depression, heritability, selection response and correlation were studied during 2011-12 in parental cultivars and their F_3 populations of upland cotton at the University of Agriculture, Peshawar, Pakistan. Eight upland cotton genotypes i.e., SLH-284, CIM-446, CIM-473, CIM-496, CIM-499, CIM-506, CIM-554 and CIM-707 and their 56 F_3 populations were sown in a randomized complete block design with three replications. Mean squares revealed significant differences among the parental lines and F_3 populations for all the characters. On average, the F_3 populations showed best performance than parental cultivars for yield contributing traits and eventually increased seed cotton yield. Majority of the F_3 populations revealed inbreeding depression for various traits. However, some of the F_3 populations revealed negative values for inbreeding depression by transgressing their F_2 populations in performance. The PCV and GCV values were comparable for almost all the traits which revealed that genotypes played greater role rather than environment and indicating less influence of environment on majority of the traits. Heritabilities (broad sense) were low to high with desirable selection response for all the traits. Seed cotton yield had significant positive correlation with all the traits, except days to first flowering where the association was non-significant. Parental cultivars viz., CIM-496, SLH-284, CIM-554 and CIM-707 and their F_3 populations i.e. CIM-506 × SLH-284, CIM-707 × CIM-554, CIM-473 × CIM-496, SLH-284 × CIM-707, SLH-284 × CIM-473 and CIM-473 × CIM-707 revealed maximum values for seed cotton yield and major yield contributing traits. The promising F_3 populations authenticated stability even after segregation which can be further studied for enhancement in seed cotton and lint yields.

Key words: Genetic variability; inbreeding depression; heritability; correlation; earliness and yield related traits; F_3 populations; upland cotton

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is one of the most important cash crops in Pakistan and is being grown in warmer regions of the country (Riaz *et al.*, 2013). Cotton has greater impact on foreign exchange earnings, textile industry development and employment generation (Khan, 2011). In Pakistan, during 2015-16 the cotton crop has failed and output is likely to be down by over 18% which was a major setback for the GDP growth rate (PBS, 2015-16). Cotton alone reduced the GDP growth rate by one percent which authenticated its role in the national economy. Upland cotton accounts for 90% of fiber production in the world and 2nd largest source of vegetable oil (Alishah *et al.*, 2008; Preetha and Raveendren, 2007). In Pakistan, beside its textiles use, it also provides edible oil and contributes about 60-70% to the local edible oil industry. Realizing the importance of this crop in economy, various efforts have been made in order to boost up its production around the country (Farooq *et al.,* 2013). Development of cultivars possessing tolerance to cotton leaf curl virus (CLCuV) along with earliness and yield potential are the prime objectives of the cotton breeders (Farooq *et al*., 2014). In Pakistan, cotton yields have been stagnant since last two decades as compared to other cotton growing countries and need proper attention. Seed cotton yield mainly depends upon the relationship among yield and its contributing traits and environmental conditions. The ultimate objective of a cotton breeder is to develop high yielding cultivars, through different breeding techniques by utilizing the existing crop genetic resources. To achieve this aim, a breeder must exploit quantitatively based characters found in various genotypes. Due to complicated nature of yield, and due to interaction between genetic and environmental components, the genotypes with harmonious combination of desirable characters become difficult. Thus, for the development of promising genotypes, the cotton breeder is obliged to study breeding material regarding the nature and degree of association of yield with fiber quality traits and yield components under particular environmental conditions (Naveed *et al*., 2004).

Therefore, comprehensive knowledge about genetic potential of various cotton populations, extent of relation between yield and its components under diverse environmental conditions is vital for breeders to solve the yield problem successfully (Ahmad *et al*., 2008). Based on population means, mid-parent heterosis of F_2

suggested that less inbreeding depression exists for F_2 and F_3 populations and it is possible to select high yielding populations (Panni *et al*., 2012). Promising populations could be utilized either as F_2 hybrids or as a source population for further improvement through segregating generations, the average productivity of F_1 and F_2 hybrids could be best indicator (Khan *et al*., 2007).

Before initiating any cotton improvement program, information about the genetic potential of various genotypes, heritability and inheritance pattern of various characters and degree of association of yield with various morpho-yield traits is important for the breeders to handle the problem wisely and enhance the seed cotton and lint yields (Ahmad *et al*., 2008; Makhdoom *et al*., 2010). The desired plants selection is facilitated if some working knowledge about correlation between the traits is available. Further, the identification of the characters that influence the final productivity directly or indirectly is also helpful. Thus, correlation study has an important role in cotton plant improvement (Desalegn *et al*., 2009; Khan *et al*., 2010). Therefore, a research project was planned to quantify the genetic potential, heritability, inbreeding depression and correlation of yield with various yield contributing traits in F_3 populations and their parental genotypes of upland cotton.

MATERIALS AND METHODS

Plant materials and field procedure: Eight upland cotton parental genotypes i.e. SLH-284, CIM-446, CIM-473, CIM-496, CIM-499, CIM-506, CIM-544 and CIM-707 and their 56 F_3 populations (selection made in F_2 during 2010) were grown during crop season 2011 at The University of Agriculture, Peshawar, Pakistan. The experiment was laid out in a randomized complete block (RCB) design with three replications. Each genotype in each replication had four rows, five meters long and having 30 and 75 cm plants and rows spacing, respectively. Similarly, cultural practices and inputs including land preparation, sowing, fertilizer, irrigation, thinning and hoeing were carried out as per recommended package for cotton crop. Picking was made during the month of November on individual plant basis.

Traits measurement and statistical analysis: Data were recorded on days to first flowering, plant height, monopodia and sympodia per plant, bolls per sympodia and seed cotton yield per plant. Data were subjected to analysis of variance according to Steel *et al.* (1997). After getting the significant variations among genotypes performance for various parameters, the means for each trait were further separated and compared by using the least significant difference (LSD) test at 5% level of probability. Heritability (broad sense) and selection response were computed according to Breese (1972). Inbreeding depression estimates in F_3 populations was calculated according to Griffing (1950). The correlation of seed cotton yield with earliness, morphological and yield traits was worked out according to Kwon and Torrie (1964).

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant ($p \leq 0.01$) differences among F_3 populations and their parental lines for all the traits which revealed greater genetic variability among these populations (Table 1). Significant differences were reported among parental cultivars and their F_1 and F_2 populations for earliness, morphological and yield traits in upland cotton (Iqbal *et al*. 2003; Batool *et al*., 2010; Bibi *et al*., 2011a, b). Genetic variability was reported among various populations of upland cotton and was found useful for developing early maturing and high yielding cotton genotypes (Alishah *et al*., 2008; Shakeel *et al*., 2008).

Mean performance of F_3 populations and their parental cultivars: Days to first flowering ranged from 45.67 to 54.67 days in parental cultivars and 45.33 to 54.33 days in F_3 populations (Fig. 1). On average, parental cultivars (51.17 days) took more days to first flowering than F_3 populations (49.98 days). The F_3 population CIM-554 × CIM-506 showed minimum days to first flowering (45.33 days) and was similar in performance with six F_3 populations and one parental cultivar CIM-446 with same value (45.67 days). However, maximum days to first flowering were observed in the parental cultivar CIM-707 (54.67 days), and it was found equal with two other parental cultivars (CIM-506 and CIM-554) and nine F_3 populations ranging from 53.00 to 54.33 days. The remaining genotypes showed medium days to first flowering (47.33 to 52.67 days). Cotton breeders are mostly interested in earliness, which not only help in escaping the crop from pest attack but also vacate the land for timely cultivation of the following crop. Days to first flowering is more reliable measure for earliness than either blooming index or total flower count. Fewer the number of days taken to produce first flower, the earlier will be the boll setting and opening, hence genotype will have early maturity (Iqbal *et al*., 2006; Ahmad *et al*., 2008). Appearance of first flower depends on photoperiod and rate of plant growth, and was found highly associated with temperature in cotton (Sarwar *et al*., 2011). However, present results were in corroboration with past findings where significant differences among parental cultivars and their F_1 hybrids were observed for days to flowering in upland cotton (Batool *et al*., 2010; Bibi *et al*., 2011a, b). Genetic variability about earliness among parental lines and F_1 populations was useful to develop genotypes with early maturity in upland cotton (Iqbal *et al*., 2003).

Plant height varied from 94.73 to 117.46 cm and 73.87 to 141.70 cm in parental cultivars and F_3 populations, respectively (Fig. 2). On average, parental cultivars (111.27 cm) obtained more plant height than F_3 populations (106.31 cm). The F_3 population CIM-506 × CIM-473 had less plant height (73.87 cm), however, it was found at par with thirteen other F_3 populations and one parental cultivar (CIM-473) ranging from 83.27 to 96.33 cm. The F_3 population CIM-445 × CIM446 (141.70 cm) revealed taller plants and it was found at par with seven other F_3 populations and one parental genotype (CIM-499) ranging from 119.70 to 137.10 cm. The remaining genotypes showed medium plant height ranging from 96.93 to 118.30 cm. Plant height is one of the important characters that play a useful role in managing seed cotton yield. Plant height has significant contribution in increasing fruiting branches and bolls per plant that leads to enhanced seed cotton yield if lodging did not occur. Greater genetic variability was observed for plant height among various cotton populations, with significant positive association with seed cotton yield in upland cotton (Hussain *et al*., 2000; Baloch *et al*., 2001; Naveed *et al*., 2004; Ahmad *et al*., 2008; Khan *et al*., 2009, 2010). However, negative correlation of plant height with bolls per plants and seed cotton yield had been reported in upland cotton (Elsiddig *et al*., 2007; Makhdoom *et al*., 2010; Panni *et al*., 2012), which might be due to lodging. The contrasting views might be due to different cotton populations used under diverse environmental conditions.

Monopodia per plant ranged from 0.47 to 1.80 in parental cultivars and 0.20 to 1.60 in F_3 populations (Fig. 3). On average, parental cultivars (0.87) showed more monopodia per plant than F_3 populations (0.83). The F_3 population CIM-446 × CIM-554 (0.20) exhibited minimum monopodia per plant, however, the said genotype was found similar in performance with five other F_3 populations with similar value (0.33) and SLH-284 × CIM-499 (0.40) and CIM-554 × CIM-707 (0.40). The parental cultivar CIM-506 (1.80) revealed maximum monopodia per plant and was at par with F_3 population CIM-506 × CIM-446 (1.60). The later genotype (CIM-506 × CIM-446) was also found similar in performance with three other F_3 populations i.e. CIM-506 × SLH-284, CIM-506 × CIM-707 and CIM-446 × CIM-506 ranging from 1.40 to 1.47 monopodia per plant. Remaining F_3 populations and parental genotypes revealed medium number of monopodia per plant. For vegetative branches, greater genetic variability was observed in upland cotton genotypes and vegetative branches played positive role in managing seed cotton yield (Iqbal *et al*., 2006; Ahmad *et al*., 2008). Salahuddin *et al.* (2010) observed significant mean differences in upland cotton genotypes for monopodia, and its positive correlation with seed cotton yield in upland cotton. However, some past studies did not support the present results and mentioned the variation for monopodia among various cotton populations but negative impact on seed cotton yield in upland cotton (Iqbal *et al*., 2003; Alishah *et al*., 2008; Batool *et al*., 2010). Therefore, the direct positive effect of monopodial branches could not be recognized in increased seed cotton yield in *G. hirsutum* L. (Rauf *et al*., 2004). The contradictory views might be due the different genetic background of cotton genotypes studied under diverse environmental conditions.

Sympodia per plant varied from 8.87 to 12.27 and 8.80 to 17.40 in parental cultivars and F_3 populations, respectively (Fig. 4). On average, parental cultivars (10.90) revealed less number of sympodia per plant than F_3 populations (12.79). The F_3 population CIM-473 × CIM-707 (17.40) showed maximum sympodia per plant; however, it was found at par in performance with five other F_3 populations ranging from 15.20 to 16.80. The F_3 population CIM-506 × CIM-473 (8.80) and cultivar CIM-446 (8.87) showed minimum number of sympodia per plant. Sympodia per plant play a key role in managing seed cotton yield through increased number of boll per plant. In past studies, greater genetic variability was reported among upland cotton genotypes for sympodia per plant and bolls per sympodia (Khan *et al*., 2009; Magadum *et al*., 2012). The findings of Satange *et al*. (2000) revealed that fruiting branches showed significant positive correlation with seed cotton yield in upland cotton.

Bolls per sympodia ranged from 1.00 to 1.34 and 1.13 to 2.28 in parental cultivars and F_3 populations, respectively (Fig. 5). On average, parental cultivars (1.22) exhibited less number of bolls per sympodia than F_3 populations (1.72). The F_3 population CIM-499 × CIM-506 (2.28) exhibited maximum bolls per sympodia; however, it was found similar with 13 other F_3 populations ranging from 1.86 to 2.18. Parental cultivar CIM-446 (1.00) showed least number of bolls per sympodia. However, the remaining genotypes showed medium number of bolls per sympodia. Boll per sympodia is an important yield component which manages the variation in seed cotton yield through increased number of bolls. Therefore, the said trait has significant positive impact on the seed cotton yield and the breeders should keep the said trait in mind while breeding for increased seed cotton yield. Past studies revealed that bolls per sympodia and bolls per plant have major role in yield protection, and during selection, such important characters should not be evaded (Djaboutou *et al*., 2005; Naveed *et al*., 2004; Iqbal *et al*., 2011). Present results revealed that parental cultivars and F_3 populations showed greater genetic variability for bolls per sympodia, and its positive correlation with seed cotton yield, which authenticated the findings of Khan *et al*. (2009). Larger genetic variability among various cotton genotypes was noticed for bolls per sympodia in upland cotton populations (Hassan *et al*., 2006; Khan *et al*., 2009).

However, Ahmad *et al*. (2008) noticed non-significant differences in the means values for bolls per sympodia. Significant positive correlation between bolls per sympodia and seed cotton yield was observed among various populations of upland cotton (Baloch, 2004; Ahmad *et al*., 2008). Contradictory findings between present and past findings might be due to varied genetic origin of cotton populations and the climatic conditions.

Seed cotton yield per plant ranged from 38.32 to 72.00 g and 41.14 to 93.68 g in parental cultivars and F_3 populations, respectively (Fig. 6). On average, parental cultivars (62.83 g) showed less seed cotton yield than F_3 populations (69.60 g). The F_3 population CIM-707 × CIM-554 (93.68 g) showed maximum seed cotton yield per plant. However, it was followed by eight other F_3 populations (SLH-284 × CIM-473, SLH-284 × CIM-446, CIM-473 × CIM-496, CIM-496 × CIM-446, CIM-506 × SLH-284, CIM-554 × CIM-506, CIM-554 × CIM-707 and CIM-707 × CIM-506) ranging from 83.44 to 86.41 g. The minimum seed cotton yield per plant was exhibited by parental cultivar CIM-446 (38.32 g). Seed cotton yield is the ultimate goal of breeders, which is mainly dependent on bolls per plant and boll weight. In the present study, seed cotton yield was positively correlated with yield contributing traits. Taller plant with more sympodia increased seed cotton yield if logging did not occur (Khan *et al*., 2003). Yield is complex polygenic character, and its inheritance has been characterized as the most vary, showing low to high heritability and selection response (Magadum *et al*., 2012).

Parental cultivars CIM-496, SLH-284, CIM-554 and CIM-707, and their F_3 populations i.e. CIM-506 × SLH-284, CIM-707 × CIM-554, CIM-473 × CIM-496, SLH-284 × CIM-707, SLH-284 × CIM-473 and CIM-473 × CIM-707 showed best performance for sympodia per plant, bolls per sympodia and seed cotton yield. The above promising F_3 populations also showed negative values for inbreeding depression by indicating stability and performed better then F_2 populations even after segregation, and these genotypes can be further studied for enhancement in seed cotton and lint yields.

Inbreeding depression: For days to flowering, 37 F_3 populations revealed inbreeding depression ranging from 0.60 to 10.50% (Fig. 7). However, highest inbreeding depression was found in F_3 population CIM-499 × SLH-284 (10.50%), while least in two F_3 populations i.e. CIM-506 × CIM-554 and CIM-707 × CIM-496 with same value (0.60%). Some of the F_3 populations revealed negative values for inbreeding depression ranging from -0.62 to -2.64%, means these populations performed better than their F_2 populations even after segregation. Inbreeding depression estimates were found negative and highly significant for days to 50% flowering, first fruiting per plant and days to 50% maturity (Abdalla, 2007; Abd-El-Haleem *et al*., 2010). Higher magnitude of heterosis and inbreeding depression was detected for majority of the traits including days to first flower in the two cotton crosses (Esmail, 2007).

For plant height, 46 F_3 populations revealed inbreeding depression ranging from 0.09 to 36.36% (Fig. 8). However, maximum inbreeding depression was observed in F_3 population CIM-506 × CIM-473 (36.36%) followed by CIM-496 × CIM-506 (28.09%). Least inbreeding depression was revealed by F_3 population CIM-554 × CIM-473 (0.09%). In present studies, the F_3 populations CIM-446 × CIM-473 showed maximum negative value (-44.50%) for inbreeding depression followed by CIM-554 × CIM-506 (-10.66%) which connote that these populations maintain their stability and performed better than F_2 populations even after segregation. The F_2 populations revealed inbreeding depression for plant height and was maximum in best performing hybrids (Khan *et al*., 2007). In F_2 populations, the significant inbreeding depression was observed for plant height and yield contributing traits (Khan, 2011; Panni *et al*., 2012).

For monopodia per plant, maximum inbreeding depression (83.33%) was observed in F_3 population CIM-446 × CIM-554, while the minimum value was exhibited by SLH-284 × CIM-473 (6.45%) (Fig. 9). However, some F_3 populations showed negative values for inbreeding depression ranging from -4.72 to -263.63%, which might be due to their stability. The highest negative value for inbreeding depression was shown by CIM-473 × CIM-554 (-263.63%) while the lowest negative value was observed in F_3 population CIM-473 × CIM-496 (-4.72%). Soomro *et al*. (2010) observed 100% inbreeding depression in five out of ten F_2 direct crosses, while in case of reciprocals, 50% crosses showed inbreeding depression, while remaining F_2 populations revealed no inbreeding depression for vegetative branches in upland cotton. In past studies, greater genetic variability and inbreeding depression were exhibited by various cotton populations for monopodia in upland cotton (Iqbal *et al*., 2006; Ahmad *et al*., 2008).

For sympodia per plant, 49 F_3 populations revealed inbreeding depression; however, the highest inbreeding depression was enunciated by F_3 population CIM-446 × CIM-554 (56.74%) (Fig. 10). Minimum inbreeding depression was exhibited by F_3 population CIM-473 × CIM-499 (1.14%). The remaining seven F_3 populations showed negative values for inbreeding depression ranging from -3.50 to -42.62%. Significant inbreeding depression for sympodial branches was observed in some segregating populations of upland cotton (Khan, 2011; Panni *et al*., 2012). Greater variability and inbreeding depression were reported among upland cotton genotypes for sympodia per plant (Khan *et al*., 2009; Magadum *et al*., 2012).

According to inbreeding depression, three F_3 populations (CIM-473 × CIM-446, CIM-473 × CIM-707, CIM-496 × CIM-449) revealed inbreeding depression for bolls per sympodia ranging from 7.71 to 15.30% (Fig. 11). However, for bolls per sympodia, maximum inbreeding depression was found in F_3 population CIM-473 × CIM-707 (15.30%) followed by CIM-496 × CIM-499 (11.13%) while the lowest value (7.71%) was observed in CIM-473 × CIM-446. The remaining F_3 populations exhibited negative values for inbreeding depression ranging from -0.19 to -66.83%, signifying their stability and better performance even after segregation. Inbreeding depression was negative and highly significant for yield contributing traits i.e. boll weight and boll number (Abdalla, 2007; Esmail, 2007; Abd-El-Haleem *et al*., 2010).

For seed cotton yield, 27 F_3 populations revealed inbreeding depression ranging from 0.52 to 44.14% (Fig. 12). Maximum inbreeding depression was revealed by F_3 population CIM-707 × CIM-554 (44.14%), while minimum was exhibited by CIM-506 × CIM-496 (0.52%). In F_3 populations, the abrupt drop in yield traits was due to inbreeding depression, and Basamma *et al*. (2009) and Soomro *et al*. (2012) reported significant inbreeding depression for yield and yield contributing traits in F_2 and F_3 populations of upland cotton. The promising F_3 populations also showed negative values for inbreeding depression, and authenticated stability and better performance than F_2 populations even after segregation which could be further studied for enhancement in seed cotton and lint yields.

Heritability: Heritability is of greater interest to the plant breeders which primarily measures the value of selection for characters in various types of progenies and serves as an index of transmissibility. There is a direct relationship between heritability and response to selection which is referred as genetic progress. The expected response to selection is also called genetic gain. Higher heritability coupled with high genetic gain offers the most effective condition for selection in upland cotton. Genotypic and phenotypic coefficients of variations, heritability and selection response have been used to assess the magnitude of different variances in cotton populations. A wide range of variability was observed for various traits among eight parental cultivars and their 56 F_3 populations (Table 2) as is evident from genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Genetic variability revealed that the GCV and PCV values were comparatively high for bolls per sympodia (108.82 and 206.26%), monopodia per plant (96.93 and 103.90%), moderate for sympodia per plant (16.22 and 22.56%), days to first flowering (11.59 and 12.23%), while low for plant height (2.01 and 3.55%) and seed cotton yield (12.50 and 23.95%). The comparable magnitudes of GCV and PCV values indicated that genotypes had played greater role rather than environment indicating less influence of environment on majority of these traits. However, for bolls per sympodia the PCV value was double than GCV. The PCV measures total variation and if significantly greater than GCV, indicates some degree of environmental influence and selection for improvement of such trait sometimes might be misleading.

Present results revealed that heritability ranged from 0.27 to 0.90 for various traits (Table 2). However, high heritability was recorded for days to first flowering (0.90) and monopodia per plant (0.87), moderate for sympodia per plant (0.56), and low for seed cotton yield, bolls per sympodia and plant height ranging from 0.27 to 0.32. Past findings reported high heritability for days to flowering and earliness traits in upland cotton (Joshi *et al*., 2006). Present results revealed that selection response values for various traits were ranging from 0.12 # (bolls per sympodia) to 7.69 cm (plant height). High heritability accompanied with high genetic gain indicates that most likely the heritability is due to additive gene effects and selection might be effective in upland cotton (Dahiphale *et al.*, 2015). Desirable estimates of heritability and genetic gain were reported for plant height, vegetative and fruiting branches, bolls per sympodia and seed cotton yield in upland cotton populations (Ahmad *et al*., 2008; Soomro *et al.*, 2008). Significant genetic variability among cultivars, and high heritability with desirable selection response were reported for various traits i.e. monopodia and sympodia, plant height, bolls per plant, boll weight, lint and seed cotton yields in *G. hirsutum* L. (Efrem *et al.*, 2010; Bolek *et al.*, 2010; Elango *et al.*, 2012). Therefore, it is of great importance for the cotton breeders to know the genetic variability and heritability of important traits to improve the seed cotton yield effectively.

Correlation: Seed cotton yield revealed highly significant positive correlation with morphological and yield traits while non-significant positive with days to flowering (Table 3). Significant positive association between plant height and seed cotton yield was reported in upland cotton populations (Ahmad *et al*., 2008; Khan *et al*., 2009, 2010). However, negative correlation of plant height with bolls per plant and seed cotton yield had been reported in some upland cotton populations (Elsiddig *et al*., 2007; Makhdoom *et al*., 2010; Panni *et al*., 2012) which might be due to lodging of cotton plants in worse environmental conditions. Positive correlation was observed between vegetative branches and seed cotton yield (Salahuddin *et al*., 2010). However, Alishah *et al*. (2008) and Batool *et al*. (2010) observed negative correlation between monopodia and seed cotton yield in upland cotton. Positive correlation of sympodia per plant with seed cotton yield was reported by Kaliyaperumal and Rajasekaran (2010). Present results were supported by findings of Annapurve *et al.* (2006) who suggested that selection based on sympodia per plant would help to increase cotton yields. However, past findings revealed very low direct effect of sympodia on seed cotton yield, but recorded its high and indirect effects of fruiting branches via boll weight while positive direct effect through boll number (Ahuja *et al.*, 2006; Salahuddin *et al.*, 2010). Significant positive correlation between bolls per sympodia and seed cotton yield was reported among various populations of upland cotton (Ahmad *et al.*, 2008; Khan *et al.*, 2009). Contradictions in present and past findings might be due to varied genetic makeup of the cotton genotypes and the environment in which studied.

Table 1. Mean squares and coefficient of variability (CV) for various traits in upland cotton.

Parameters	**Mean squares**			**CV (%)**
	Replications	**Genotypes**	**Error**	
Days to first flowering	0.297	23.921**	0.868	1.86
Plant height	2171.984	483.010**	200.299	13.24
Monopodia plant^{-1}	0.076	0.338**	0.016	15.31
Sympodia plant^{-1}	24.881	9.249**	1.906	10.66
Bolls sympodia^{-1}	0.050	0.151**	0.070	15.34
Seed cotton yield plant^{-1}	2281.387	447.706**	50.956	10.38

* Degrees of freedom (d.f.) for replications, genotypes and error were 2, 63 and 126, respectively.

Table 2. Genetic, environmental and phenotypic variances, heritability (bs), GCV, PCV and selection response for various traits in parental cultivars of upland cotton and their F_3 populations.

Traits	Σ^2g	σ^2e	σ^2p	h^2	GCV (%)	PCV (%)	Re
Days to first flowering	7.68	0.87	8.55	0.90	11.59	12.23	3.68 days
Plant height	94.24	200.30	294.54	0.32	2.01	3.55	7.69 cm
Monopodia plant^{-1}	0.11	0.02	0.12	0.87	96.93	103.90	0.43 #
Sympodia plant^{-1}	2.45	1.91	4.35	0.56	16.92	22.56	1.64 #
Bolls sympodia^{-1}	0.03	0.07	0.10	0.28	108.82	206.26	0.12 #
Seed cotton yield plant^{-1}	78.92	210.96	289.87	0.27	12.50	23.95	6.49 g

σ^2g: Genetic variance, σ^2e: Environmental variance, σ^2p: Phenotypic variance, h^2: Heritability (bs), GCV: coefficient of variance, PCV: Phenotypic coefficient of variance, Re: Selection response

Table 3. Correlation of seed cotton yield with various traits in parental cultivars of upland cotton and their F_3 populations.

Parameters	**Correlation (r) with seed cotton Yield plant^{-1}**
Days to first flowering	0.008^{NS}
Plant height	0.567**
Monopodia plant^{-1}	0.201**
Sympodia plant^{-1}	0.543**
Bolls sympodia^{-1}	0.626**

** = Significant at $p \leq 0.01$, NS = Non-significant.

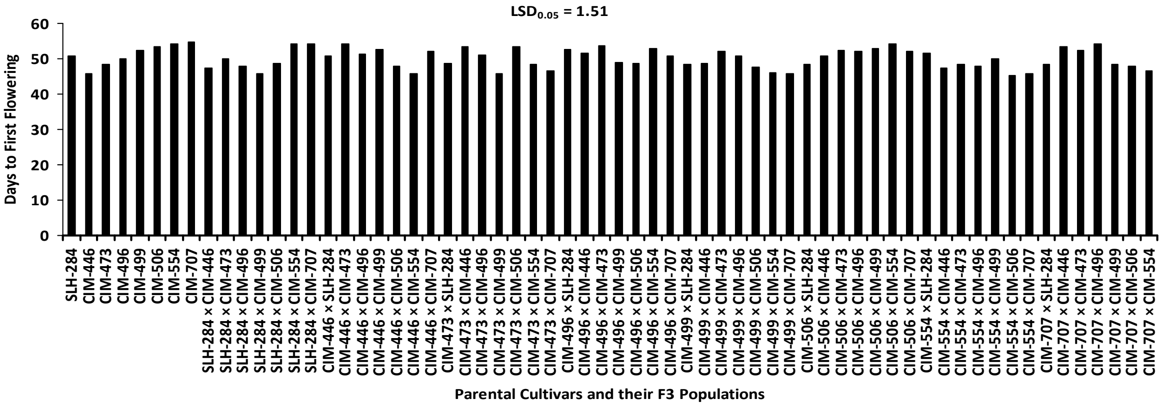

Fig. 1. Mean performance of parental cultivars of upland cotton and their F_3 populations for days to first flowering.

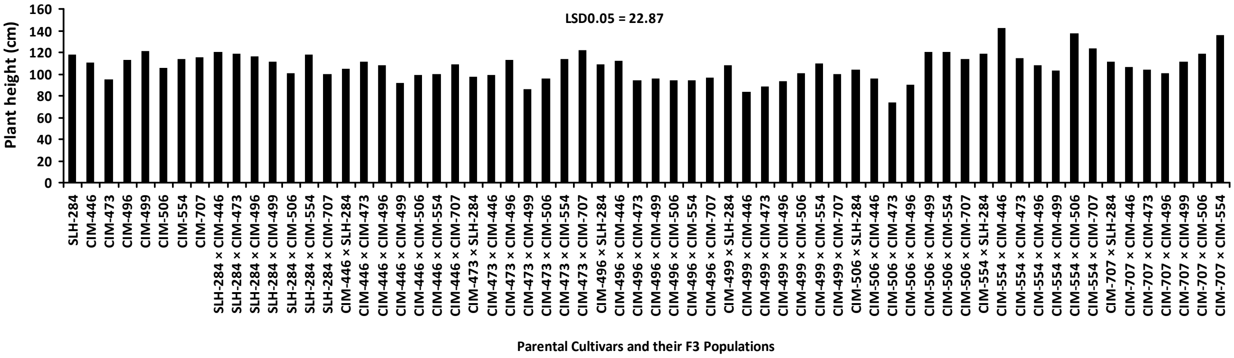

Fig. 2. Mean performance of parental cultivars of upland cotton and their F3 populations for plant height.

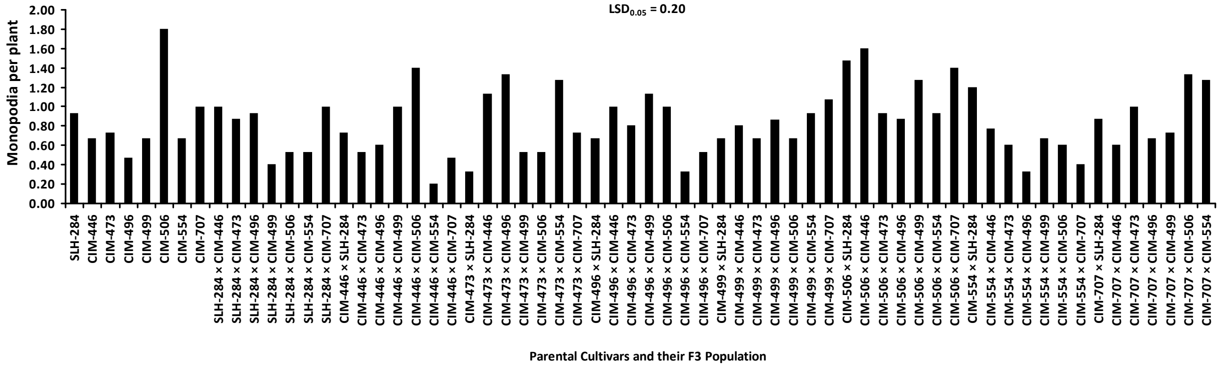

Fig. 3. Mean performance of parental cultivars of upland cotton and their F3 populations for monopodia per plant.

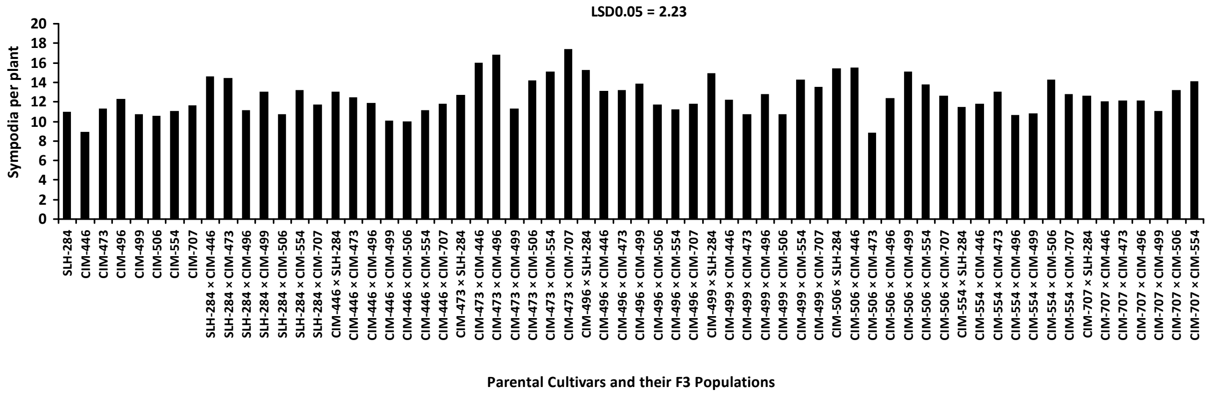

Fig. 4. Mean performance of parental cultivars of upland cotton and their F3 populations for sympodia per plant.

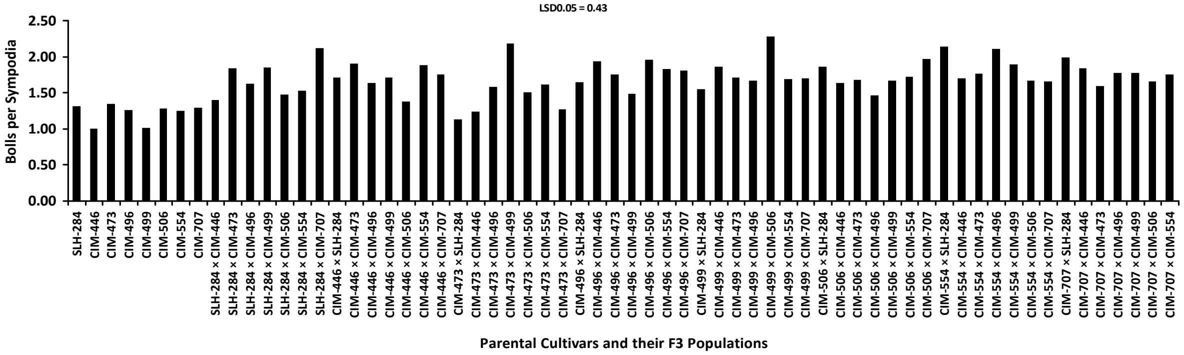

Fig. 5. Mean performance of parental cultivars of upland cotton and their F3 populations for bolls per sympodia.

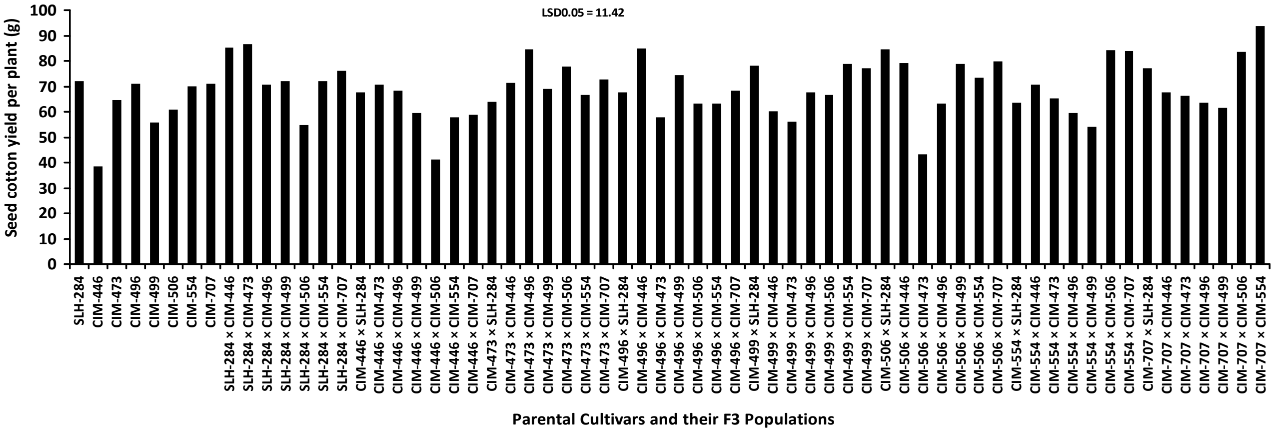

Fig. 6. Mean performance of parental cultivars of upland cotton and their F_3 populations for seed cotton yield per plant.

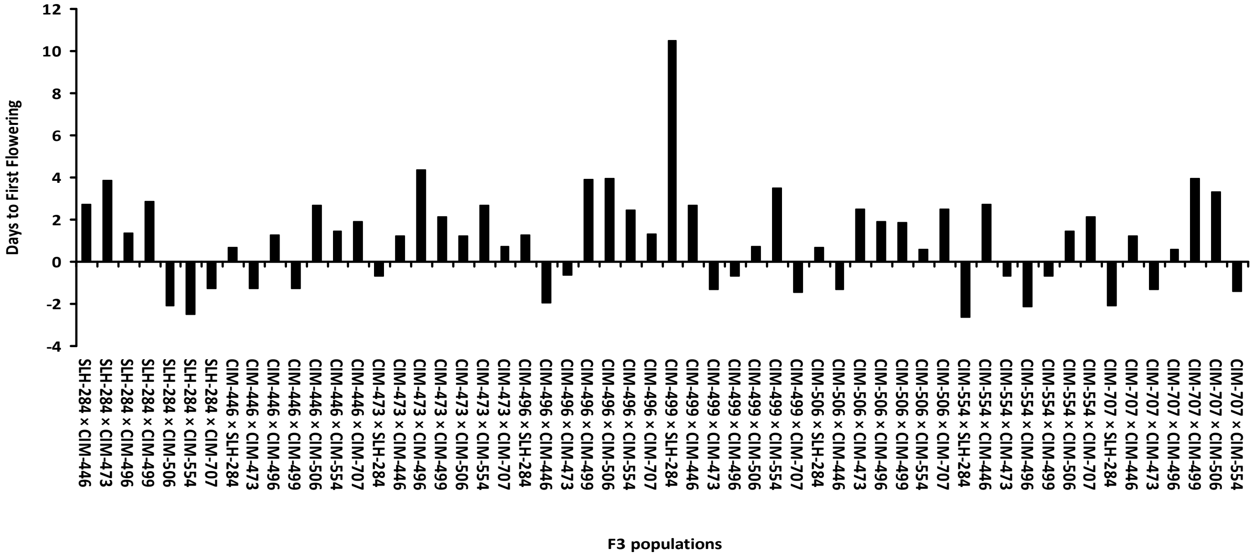

Fig. 7. Inbreeding depression in F_3 populations of upland cotton for days to first flowering.

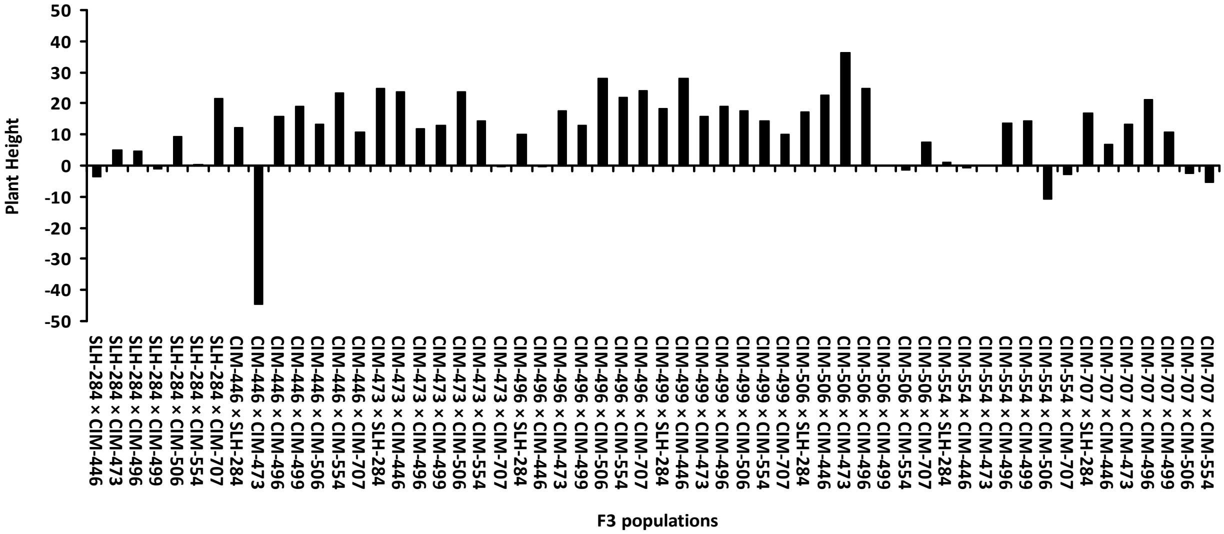

Fig. 8. Inbreeding depression in F_3 populations of upland cotton for plant height.

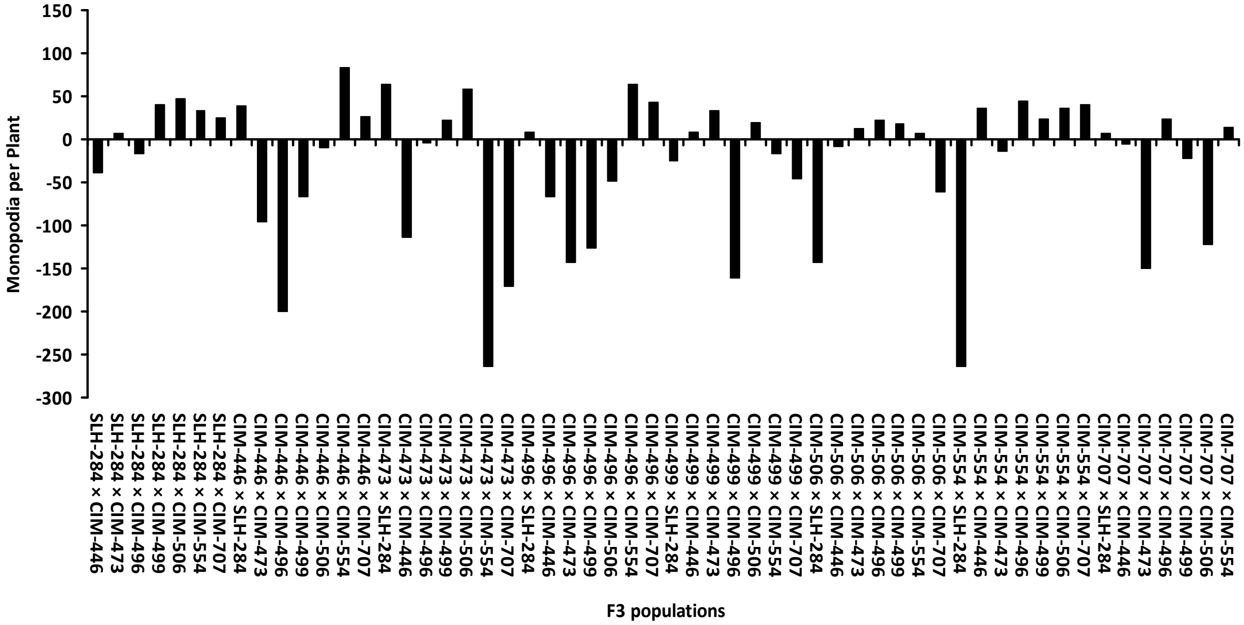

Fig. 9. Inbreeding depression in F_3 populations of upland cotton for monopodia per plant.

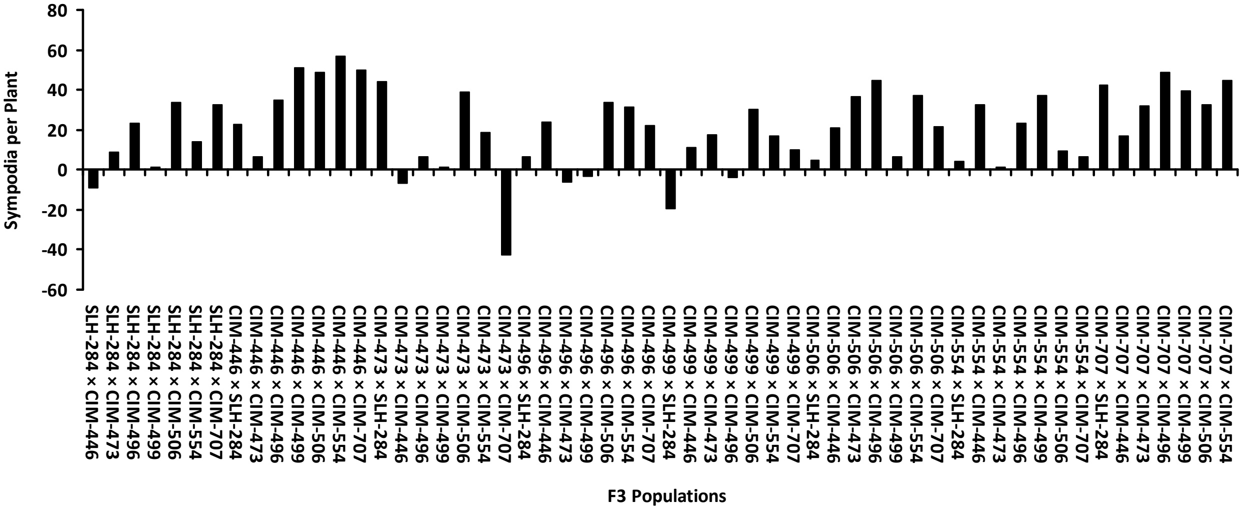

Fig. 10. Inbreeding depression in F_3 populations of upland cotton for sympodia per plant.

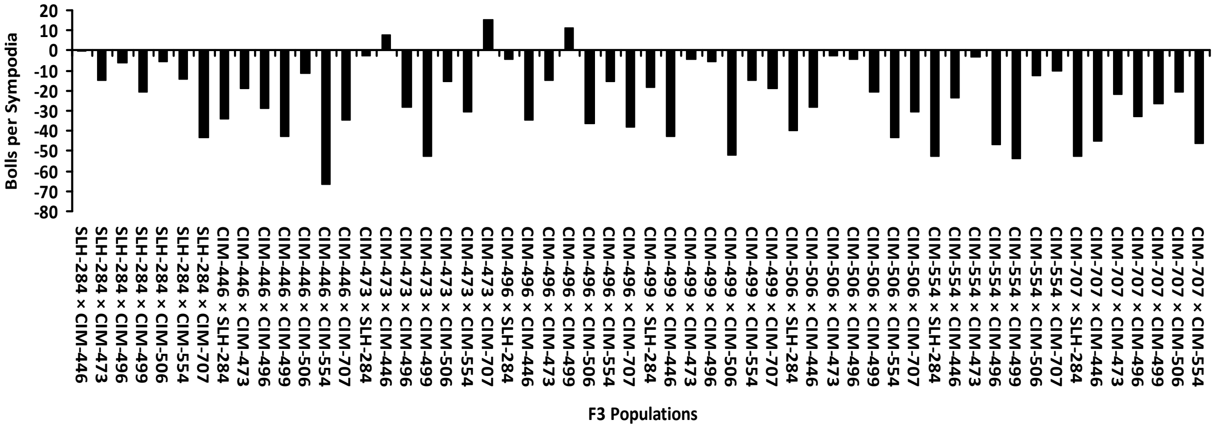

Fig. 11. Inbreeding depression in F_3 populations of upland cotton for bolls per sympodia.

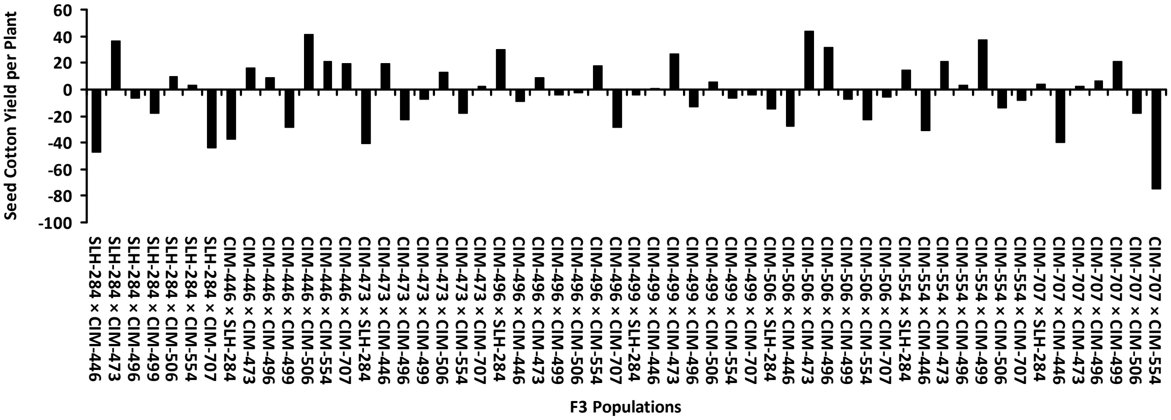

Fig. 12. Inbreeding depression in F$_3$ populations of upland cotton for seed cotton yield per plant.

Conclusions: Highly significant mean differences were observed among the parental lines and F$_3$ populations for all the characters. On average, the F$_3$ populations showed best performance than parental cultivars for yield contributing traits and eventually increased seed cotton yield. Some of the F$_3$ populations revealed negative values for inbreeding depression by transgressing their F$_2$ populations in performance. The PCV and GCV values were comparable for almost all the traits which revealed greater role of genotypes and less involvement of environment. Heritabilities (broad sense) were low to high with desirable selection response for all the traits. Seed cotton yield had significant positive correlation with all the traits. F3 population i.e., CIM-506 × SLH-284, CIM-707 × CIM-554, CIM-473 × CIM-496, SLH-284 × CIM-707, SLH-284 × CIM-473 and CIM-473 × CIM-707 revealed maximum seed cotton yield; and therefore, these populations can be used in future breeding programs to enhance the seed cotton and lint yields.

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