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# Genetic Assessment of Oil Contributing Traits in Upland Cotton

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## Abstract

Cotton is the most important fiber as well as oil crop around the globe and plays a vital role in the economy of Pakistan. Present research work was planned to evaluate 5 parents along with their 20 hybrids of upland cotton for oil content and oil contributing traits in a complete diallel fashion in randomized complete block design with three replications. Genetic variance, phenotypic variance, environmental variance, heritability and correlation was estimated for various morphological traits. Results revealed that parent AA-802 and exhibited good performance for sympodial branches per plant, number of bolls per plant, boll weight, ginning outturn (GOT) seed index, lint index and seed cotton yield. Whereas, C-26 identified as better performer exclusively for plant height, sympodial branches per plant, seed index and oil contents. Cross SB-149 × C-26 showed significant response for seed cotton yield, sympodial branches per plant, boll weight, number of bolls per plant, plant height, seed index, lint index, seed cotton yield and oil contents. SB-149 × AA-802 presented better results for the traits namely, sympodial branches per plant, boll weight, GOT, seed index and seed cotton yield. High heritability estimate was recorded in boll weight, number of bolls per plant, GOT, oil contents while moderate heritability was estimated in seed cotton yield, lint index and seed index. Low heritability was estimated in plant height and sympodial branches. These identified parents and hybrids could be used in future breeding programs to overcome the oil-related problems in upland cotton.

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## Introduction

Cotton (*Gossypium hirsutum* L.) is the most important fiber crop. It is the second-largest source of vegetable oil worldwide (Alishah *et al.*, 2008). It contributes 4.1% in agricultural value addition and 0.8% in GDP of Pakistan (ESP, 2019-2020). Cotton seeds oil is cholesterol-free and entitled as "Heart oil". Cotton contributes 60-70% in total edible oil production in Pakistan and 4% in the world's vegetable oil production (Munawar and Malik, 2013). Cotton is regarded as one of the important conventional oilseed crops with the potential to bridge the existing gap between the supply and domestic demand for vegetable oil (Sekhar and Rao, 2011). It is considered as 5$^{th}$ oilseed crop after soybean, canola, sunflower and palm and 2$^{nd}$ best source of plant protein after soybean. Cottonseed oil, a by-product of cottonseed, is a valuable source of edible oil due to the presence of 15-20% oil (Sawan *et al.*, 2006). But in Pakistan, oilseed crops meet only 30% of the country's demand, with the remaining 70% still imported from other countries in the form of palm oil and soybean oil. Therefore, due to the crop's undisputed economic importance, the stable production of quality cotton and increased oil content is vital in the national interest.

In this context, awareness among growers, millers, and exporters is mandatory for improving and maintaining cotton standards to compete in the international market.

Various researchers analyzed in detail about seed traits, but very little work was reported against the genetics of cottonseed oil percentage. Whereas, cotton genotypes behaved significantly different for oil percentage (Ashokkumar and Ravikesavan, 2013). The seed index presented a positive and direct relationship with oil contents (Munawar and Malik, 2013). Oil contents were positively correlated with protein and seed cotton yield (Ahmad and Azhar, 2000). Selection based on seed cotton yield, bolls per plant and boll weight could be helpful for the breeders to develop genotypes with high oil contents (Qayyum *et al.*, 2010). In cotton, within-boll yield related traits are influenced by alterations in plant density (Bednarz *et al.*, 2007). The existence of genetic variation within a species for certain traits is a pre-requisite for the development of new genotypes (Azhar and Naeem, 2008). The first step for an effective breeding program is the selection of appropriate parents. Then, the mating design used to study the correlation analysis leads to the identification of parents with additive and non-additive genetic effects for particular characteristics. These techniques help for the identification of potential parents in hybridization and breeding programs (MURTHY and Chamundeswari, 2006). The identification of suitable parents and cross combinations also lead to exploit heterosis. Cotton crop has a slight genetic base, that's why it is essential to develop new hybrids with higher heterotic performance. Heterosis and recombination breeding in cotton is highly amenable.

In cotton breeding programs, heterosis substantially remained as one of the significant key factors in plant growth and development (Ranganatha *et al.*, 2013; Choudhary *et al.*, 2016). The present study was carried out to find the relative effects of heterosis, genetic potential, variability, heritability and correlation in upland cotton for oil associated traits.

## Material and methods

The present experiment was conducted in the glasshouse and experimental area in of Department of Plant Breeding and Genetics, University of Agriculture, (latitude 31°25ˈN, longitude 73°09ˈE and altitude 184.4 m from sea level) Faisalabad. Five varieties of *Gossypium hirsutum* L. were used as parents collected from the gene pool of Cotton Research Group, Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. In 2018, the plant material was developed by crossing five genetically diverse upland cotton varieties, namely AA-802, C-26, AGC-2, SB-149 and VH-282 according to complete diallel fashion in earthen pots in the glasshouse with sand to soil ratio (1:2). The optimal growing conditions, *i.e.*, temperature (25~35°C) light intensity (25,000~30,000 lux) and humidity (44~49%) was maintained for germination and growth of the plants in glasshouse. All of the agronomic practices were applied to obtain a healthy plant population. After germination, thinning was practiced by keeping 1 healthy seedling at two leaves stage in each pot. At the time of bud formation, these five genotypes were self-pollinated as well as crossed in all possible combinations to produce $F_1$ hybrids (Table 1). All of the precautionary measures were followed to avoid the mixing of genetic material.

$F_0$ seeds of five parents along with their 20 hybrids were planted in 2019 to get $F_1$ population. The experiment was conducted according to a randomized complete block design with three replications. Each replication contained 25 rows of twenty-five families. There were 10 plants for each family in each row. Plant to plant and row to row distance was kept 30 cm and 75 cm respectively. At the time of maturity, the data was collected on the following traits from five guarded plants from each row.

*Plant height*

The height of five selected plants were taken in centimeters from the first cotyledonary node to epical bud using meter rod. Then the average height was calculated for statistical analysis.

*Number of sympodial branches per plant*

The fruit-bearing branches were counted from the selected plants then averaged.

*Number of bolls per plant*

Number of bolls per plant was counted at the time of picking and the average number was calculated for each entry in three replications from each family for biometrical analysis.

*Boll weight*

The boll weight of individual plants was calculated by dividing the total seed cotton yield from a plant by the total number of bolls picked.

$$\text{Boll weight} = \frac{\text{Weight of seed cotton yield}}{\text{Number of bolls from plant}}$$

*Seed cotton yield per plant*

Mature bolls of selected plants were picked, and seed cotton was collected and weighed in grams with the help of electronic balance. For each plant, the total seed cotton yield was recorded.

The average seed cotton yield per plant for each genotype was calculated in each replication for further analysis.

*Ginning outturn (GOT)*

Dry and clean samples of seed cotton were weighed and ginned individually with single roller electrical gin available in the ginning lab of the department.

The lint obtained from each sample was weighed and lint % was calculated by the following formula.

$$\text{GOT \%} = \frac{\text{Weight of lint in a sample}}{\text{weight of seed cotton in sample}} \times 100$$

*Seed index*

Seed index refers to the weight of 100 seeds in grams. After ginning, disease-free 100 cotton seeds were taken from each sample and weighed in grams using electrical balance. The average seed index for three replications of each family was calculated.

*Lint index*

Lint index refers to the weight of lint obtained from 100 seeds in grams. It is calculated by using the following formula.

$$\text{Lint index} = \frac{\text{Seed index} \times \text{GOT}}{100 - \text{GOT}}$$

*Oil contents*

The oil contents in the sample of cotton seed were estimated by using a Soxhlet apparatus. It is calculated by using the following formula:

$$\text{Oil Contents \%} = \frac{S1 - S2}{S1} \times 100$$

Where: S1: Weight of cotton seeds before extraction

S2: Weight of cotton seeds after extraction

*Statistical analysis*

The mean data of traits and Pearson's correlation (r) coefficient was calculated from $F_1$ population following the method described by Steel *et al.* (1997) using the statistical software Minitab 17. Genetic, environmental and phenotypic variances and broad-sense heritability were further estimated from ANOVA mean square for each trait according to Burton (1951).

**Results**

The analysis of variance (ANOVA) indicated the presence of significant differences among parents and hybrids for all of the characters namely plant height, number of sympodial branches per plant, seed cotton yield per plant, number of bolls per plant, seed index, boll weight, lint index, GOT and oil contents among all the genotypes (Table 2).

**Table 1.** List of upland cotton parents along with their $F_1$ hybrid.

| Parents | Direct crosses | Indirect crosses |
|---|---|---|
| AA-802 | AA802 × C-26 | C-26 × AA-802 |
| | AA-802 × SB-149 | SB-149 × AA-802 |
| C-26 | AA802 × AGC-2 | SB-149 × C-26 |
| | AA802 × VH282 | AGC-2 × AA-802 |
| SB-149 | C-26 × SB-149 | AGC-2 × C-26 |
| | C-26 × AGC-2 | AGC-2 × SB149 |
| AGC-2 | C-26 × VH-282 | VH-282 × AA-802 |
| | SB-149 × AGC-2 | VH-282 × C-26 |
| VH-282 | SB-149 × VH-282 | VH-282 × SB-149 |
| | AGC-2 × VH-282 | VH-282 × AGC-2 |

*Mean values*

Average comparisons of all the genotypes for plant height were given in Table 3 and Fig. 1. The genotype C-26 exhibited maximum plant height of 82 cm as compared to AGC-2 which gained 60.3 cm height. The hybrids C-26 × SB-149 showed a maximum plant height of 89.2 cm while AA-802 × AGC-2 presented a minimum value of 57.3 cm. Similarly, sympodial branches ranged between 13 and 20. The genotype SB-149 and C-26 presented the maximum number of sympodial branches per plant while minimum showed by AGC-2. Among hybrids SB-149 × AA-802, 21 branches were expressed as the highest value whereas AA-802 × AGC-2 exhibited 13 minimum number of sympodial branches per plant.

The variety AGC-2 showed 28 number of bolls per plant while SB-149 presented 14. Among hybrids, the highest 30 number of bolls presented by VH-282 × AGC-2 and 10 by VH-282 × SB-149.

**Table 2.** Analysis of variance for boll weight in upland cotton.

| SOV | DF | PH | SB | NOB | BW | GOT | SI | LI | SCY | OC |
|---|---|---|---|---|---|---|---|---|---|---|
| Rep | 1 | 350 | 25.9 | 0.32 | 0.01 | 1.09 | 0.02 | 0.94 | 11.4 | 0.05 |
| Gen | 24 | 134.765** | 8.263** | 105.838** | 0.437** | 17.356** | 0.285** | 1.251** | 69.231** | 6.075** |
| Err | 24 | 64.5 | 3.75 | 8.28 | 0.02 | 2.44 | 0.1 | 0.25 | 12.3 | 0.96 |
| Tot | 49 | | | | | | | | | |

Where, N.S= non-significant,* = P > 0.05, ** =P > 0.01, Plant height (PH), Sympodial branches (SB), Number of bolls per plant (B/P), Boll weight (BW), Ginning outturn (GOT), Seed index (SI), Lint index (LI), Seed cotton yield (SCY), Oil contents (OC).

The genotype AGC-2 showed a maximum boll weight of 3.29 while VH-282 presented minimum estimates of 2.05. Among crosses, AA-802 × VH282 (3.48) showed maximum while C-26 × AA-802 (2.06) displayed minimum boll weight. The genotype VH-282 (44.05) showed maximum GOT while C-26 (38.59) presented minimum GOT. Among combinations, VH-282 × AA-802 (45.20) displayed maximum GOT and C-26 × VH-282 (34.97) exhibited minimum value for this particular trait. The genotype

AA-802 displayed maximum value (7.6) whereas SB-149 exhibited minimum estimates (6.4) for seed index. Among crosses, AA-802 × AGC-2 showed maximum seed index while VH-282 × AGC-2 presented a minimum seed index. The genotype SB-149 showed maximum value (7.36) for the lint index while C-26 exhibited minimum value (4.55). VH-282 × SB-149 (7.32) presented maximum lint index whereas SB-149 × VH-282 (4.73) displayed minimum value. The genotype AGC-2 showed a maximum seed cotton yield of 32.26 whereas SB-149 presented a minimum value of 17.15 for seed cotton yield. The hybrid SB-149 × C-26 (33.43) showed maximum while AGC-2 × C-26 displayed the least value seed cotton yield per plant. The genotype C-26 showed a maximum percentage of 16.39 for this particular character whereas AGC-2 presented a minimum 15.01%. The hybrid C-26 × AGC-2 displayed a maximum 17.16% for oil contents while cross AGC-2 × VH-282 displayed a minimum value of 11.08%.

**Table 3.** Mean values of the parents and hybrids for plant height, sympodial branches per plant, number of bolls per plant, boll weight, ginning outturn, seed index, lint index, seed cotton yield and oil contents in *G. hirsutum* L.

| | Genotypes | PH | SB | NOB | BW | GOT | SI | LI | SCY | OC |
|---|---|---|---|---|---|---|---|---|---|---|
| Parents | AA-802 | 65.9 | 16 | 21 | 3.1 | 42.51 | 7.6 | 5.38 | 23.10 | 15.88 |
| | SB-149 | 74.4 | 17 | 14 | 2.40 | 40.17 | 6.4 | 7.36 | 17.15 | 16.06 |
| | AGC-2 | 60.3 | 13 | 28 | 3.29 | 43.16 | 7.3 | 5.54 | 32.26 | 15.01 |
| | C-26 | 82 | 17 | 18 | 2.64 | 38.59 | 7.2 | 4.55 | 21.33 | 16.39 |
| | VH-282 | 67.8 | 16 | 27 | 2.05 | 44.05 | 6.7 | 4.87 | 30.37 | 15.83 |
| Hybrids | AA-802 × SB-149 | 66.1 | 16 | 12 | 2.73 | 36.96 | 6.4 | 6.26 | 14.85 | 11.35 |
| | AA-802 × AGC-2 | 57.3 | 13 | 27 | 3.23 | 43.99 | 7.7 | 5.29 | 23.02 | 14.73 |
| | AA-802 × C-26 | 65.7 | 18 | 14 | 2.25 | 37.36 | 6.7 | 6.50 | 17.88 | 16.34 |
| | AA-802 × VH-282 | 62.8 | 15 | 28 | 3.48 | 44.19 | 7.3 | 5.45 | 20.40 | 13.86 |
| | SB-149 × AA-802 | 73.4 | 20 | 25 | 3.27 | 43.64 | 7.2 | 4.99 | 32.28 | 16.35 |
| | SB-149 × AGC-2 | 67.1 | 18 | 11 | 2.3 | 38.79 | 6.7 | 6.4 | 17.40 | 15.68 |
| | SB-149 × C-26 | 76.9 | 20 | 28 | 3.4 | 42.7 | 7.1 | 5.19 | 33.43 | 17.03 |
| | SB-149 × VH-282 | 77.5 | 16 | 14 | 2.54 | 39.23 | 6.6 | 4.73 | 26.60 | 13.15 |
| | AGC-2 × AA-802 | 73.9 | 17 | 14 | 2.3 | 43.42 | 6.6 | 5.60 | 21.86 | 15.58 |
| | AGC-2 × SB-149 | 63.6 | 16 | 26 | 3.47 | 39.83 | 6.8 | 5.03 | 17.28 | 12.91 |
| | AGC-2 × C-26 | 67.2 | 15 | 12 | 2.45 | 44.78 | 7.1 | 5.99 | 14.00 | 16.33 |
| | AGC-2 × VH-282 | 68.0 | 15 | 26 | 3.36 | 40.64 | 7.1 | 4.83 | 28.28 | 11.08 |
| | C-26 × AGC-2 | 79 | 19 | 27 | 2.56 | 43.17 | 6.8 | 5.21 | 22.10 | 17.16 |
| | C-26 × AA-802 | 79.3 | 20 | 13 | 2.06 | 37.61 | 6.7 | 5.15 | 24.30 | 15.15 |
| | C-26 × SB-149 | 89.2 | 19 | 25 | 2.56 | 43.32 | 7.1 | 5.44 | 28.40 | 15.15 |
| | C-26 × VH-282 | 84.6 | 19 | 12 | 2.73 | 34.97 | 7.3 | 5.03 | 22.90 | 15.73 |
| | VH-282 × SB-149 | 66.5 | 16 | 10 | 2.45 | 37.39 | 7.1 | 7.32 | 23.20 | 13.02 |
| | VH-282 × AA-802 | 62.1 | 15 | 29 | 2.26 | 45.20 | 6.5 | 5.09 | 30.45 | 12.97 |
| | VH-282 × C-26 | 61 | 16 | 11 | 2.41 | 39 | 7.3 | 6.90 | 15.92 | 16.09 |
| | VH-282 × AGC2 | 69.5 | 17 | 30 | 2.38 | 43.24 | 6.3 | 5.09 | 29.47 | 13.79 |

*Genetic variance, phenotypic variance, environmental variance and Heritability*

Plant height exhibited genetic variance 35.14, phenotypic variance 99.62 and environmental variance 64.47. Consequently, the heritability estimation was 35% (Table 4). For sympodial branches, genotypic, environmental and phenotypic variance were 2.25, 3.75 and 6.00, respectively with heritability estimation of 35%. The number of bolls per plant exhibited highest genotypic variance 48.78, while environmental variance and phenotypic variance were 8.27, and 57.05 respectively and broad-sense heritability was 85%. Genotypic, environmental, phenotypic variances and heritability for boll weight were 0.206, 0.024, 0.231 and 89% respectively. For GOT, genotypic, phenotypic, environmental variance and heritability were 7.45, 9.89, 2.44, and 75% respectively. The genetic variance for the seed index was 0.094, the phenotypic variance was 0.190 and the environmental variance was 0.095 while heritability estimate was 49%. The genetic, environmental and phenotypic variances were 0.500, 0.250 and 0.750, respectively and heritability estimate for lint index was 66%.

**Table 4.** Genetic, environmental and phenotypic variances and heritability plant height, sympodial branches, number of bolls per plant, boll weight, ginning outturn, seed index, lint index, seed cotton yield and oil contents in upland cotton.

| Parameters | Vg | Ve | Vp | $h^2$ |
|---|---|---|---|---|
| PH | 35.14 | 64.47 | 99.62 | 0.35 |
| SB | 2.25 | 3.75 | 6.00 | 0.37 |
| NOB | 48.78 | 8.27 | 57.05 | 0.85 |
| BW | 0.206 | 0.024 | 0.231 | 0.89 |
| GOT | 7.457 | 2.441 | 9.899 | 0.75 |
| SI | 0.094 | 0.095 | 0.190 | 0.49 |
| LI | 0.500 | 0.250 | 0.750 | 0.66 |
| SCY | 28.44 | 12.34 | 40.78 | 0.69 |
| OC | 2.560 | 0.955 | 3.515 | 0.72 |

The genetic variances (28.44) for seed cotton yield were found greater than the environmental variances (12.34) which revealed that this trait was less affected by environmental factors. Thus, genetic variance played an important role in the inheritance of seed cotton yield. The heritability recorded for seed cotton yield was 69%. Oil content contributed genotypic, environmental variance and phenotypic variance with 2.56, 0.95 and 3.51 respectively with a heritability estimate of 72%.

*Correlation*

Correlation analysis provides useful information to plant breeders about the relationship among various quantitative traits. It helps the plant breeders to develop appropriate selection criteria for the improvement of quality and yield. The presence of correlation between two traits indicates the genetic influence among them. The correlation matrix among various traits in five parental lines and 20 combinations was estimated to explore breeding material (Table 5). Correlation coefficients for plant height revealed that this trait had a positive association with the number of sympodial branches per plant, the number of bolls per plant, boll weight, GOT and seed cotton yield per plant. Correlation analysis also revealed that sympodial branches per plant had a positive correlation with boll weight, the number of bolls per plant, seed cotton yield per plant, GOT and plant height. The number of bolls per plant showed a positive correlation with plant height, GOT, sympodial branches per plant and seed cotton yield per plant. The association between bolls per plant and boll weight was negative. Correlation analysis revealed that boll weight had a positive association with seed index, GOT, lint index and seed cotton yield per plant. Correlation studies for GOT revealed that it had a positive correlation with seed cotton yield per plant, sympodial branches per plant, number of bolls per plant, boll weight and plant height. Correlation studies revealed a negative correlation of seed index with GOT. Correlation coefficients for lint index revealed that it had a positive association with GOT, seed cotton yield, boll weight and seed index. Seed cotton yield had a positive correlation with all the traits under study except oil contents and seed index.

Whilst oil contents showed a positive association with the number of sympodial branches per plant, the number of bolls per plant, boll weight and seed index while it had a negative relationship with seed cotton yield per plant.

**Table 5.** Correlation matrix among plant height, sympodial branches, number of bolls per plant, boll weight, ginning outturn, seed index, lint index, seed cotton yield and oil contents in upland cotton.

| Traits | PH | SB | NOB | BW | GOT | SI | LI | SCY |
|---|---|---|---|---|---|---|---|---|
| SB | 0.736** | | | | | | | |
| B/P | 0.319** | 0.288* | | | | | | |
| BW | 0.257** | 0.168** | -0.508** | | | | | |
| GOT | 0.026 N.S | 0.018 N.S | 0.009 ** | 0.065 ** | | | | |
| SI | 0.006 N.S | 0.013 N.S | -0.102 ** | 0.164** | -0.181** | | | |
| LI | -0.010 N.S | -0.003 N.S | -0.070 N.S | 0.144 ** | 0.876** | 0.203** | | |
| SCY | 0.162** | 0.138 N.S | 0.071** | 0.205** | 0.695** | -0.111 N.S | 0.600** | |
| OC | 0.343* | 0.405** | 0.006* | 0.133** | -0.090 N.S | 0.070** | -0.070 N.S | -0.019 |

* = P > 0.05, **= P > 0.01, N.S=non-significant.

**Discussion**

In the present study, 5 parents along with their 20 crosses exhibited significant differences among parents and hybrids for all of the characters namely plant height, number of sympodial branches per plant, seed cotton yield per plant, number of bolls per plant, seed index, boll weight, lint index, GOT and oil contents among all the genotypes. The genetic variance was less than phenotypic variance and environmental variance for plant height with 35% heritability.

The genetic variance was less than the environmental variance which indicated that plant height was less influence by genetic components as compared to environmental components. Meena and Meena (2017) and Ahmad *et al.* (2008) reported varied values for plant height. Killi *et al.* (2005), Ahmad *et al.* (2011) and Ullah *et al.* (2015) reported 20%, 81% and 87% broad-sense heritability for plant height, respectively. Environmental variance for number sympodial branches per plant was little more than genetic variance which designated that this trait was little influenced by genetic variance. Killi *et al.* (2005), Mustafa *et al.* (2007) and Ahmad *et al.* (2014) reported almost similar results for sympodial branches per plant.

The genotypic variance of the number of bolls per plant was six times greater than the environmental variance hence it is influenced by genetic components as compared to environmental components. Soomro *et al.* (2005) observed similar findings for this trait. Ahmad *et al.* (2011), Abbas *et al.* (2013), Vineela *et al.* (2013), Reddy and Sarma (2014) and Ullah *et al.* (2015) reported 88%, 77%, 57%, 64% and 90% broad-sense heritability for the number of bolls per plant, respectively. Present findings revealed that the inheritance of boll weight was nine times more affected by genetic variance than an environmental variance. Krishnarao and Mary (1990) and Afiah and Ghoneim (2000) reported that boll weight is more affected by genetic variance than environmental variance. Desalegn *et al.* (2009) reported 62% broad-sense heritability for this trait. Bibi *et al.* (2011), Ranganatha *et al.* (2013) and Reddy and Sarma (2014) reported 71%, 78% and 44% broad-sense heritability, respectively. Similar findings were observed for GOT and subsequently supported by Cook and El-Zik (1993), Joshi *et al.* (2006), Rasheed *et al.* (2009) and Choudki *et al.* (2013). Genetic variance for seed index was approximately equal to environmental variance which depicted that the seed index was equally controlled by environmental and genetic components. Dani (1991) and Suinaga *et al.* (2006) reported varied values for seed index whereas Iqbal *et al.* (2015) observed 97%, Killi *et al.* (2005) reported 6% and Bibi *et al.* (2011) found 71% heritability. Genetic variance for oil contents also revealed more contribution of genetic variance with 72% heritability. Hassan *et al.* (2005) found significant variability for cottonseed oil also Khan *et al.* (2010) reported 87% broad-sense heritability for cottonseed oil.

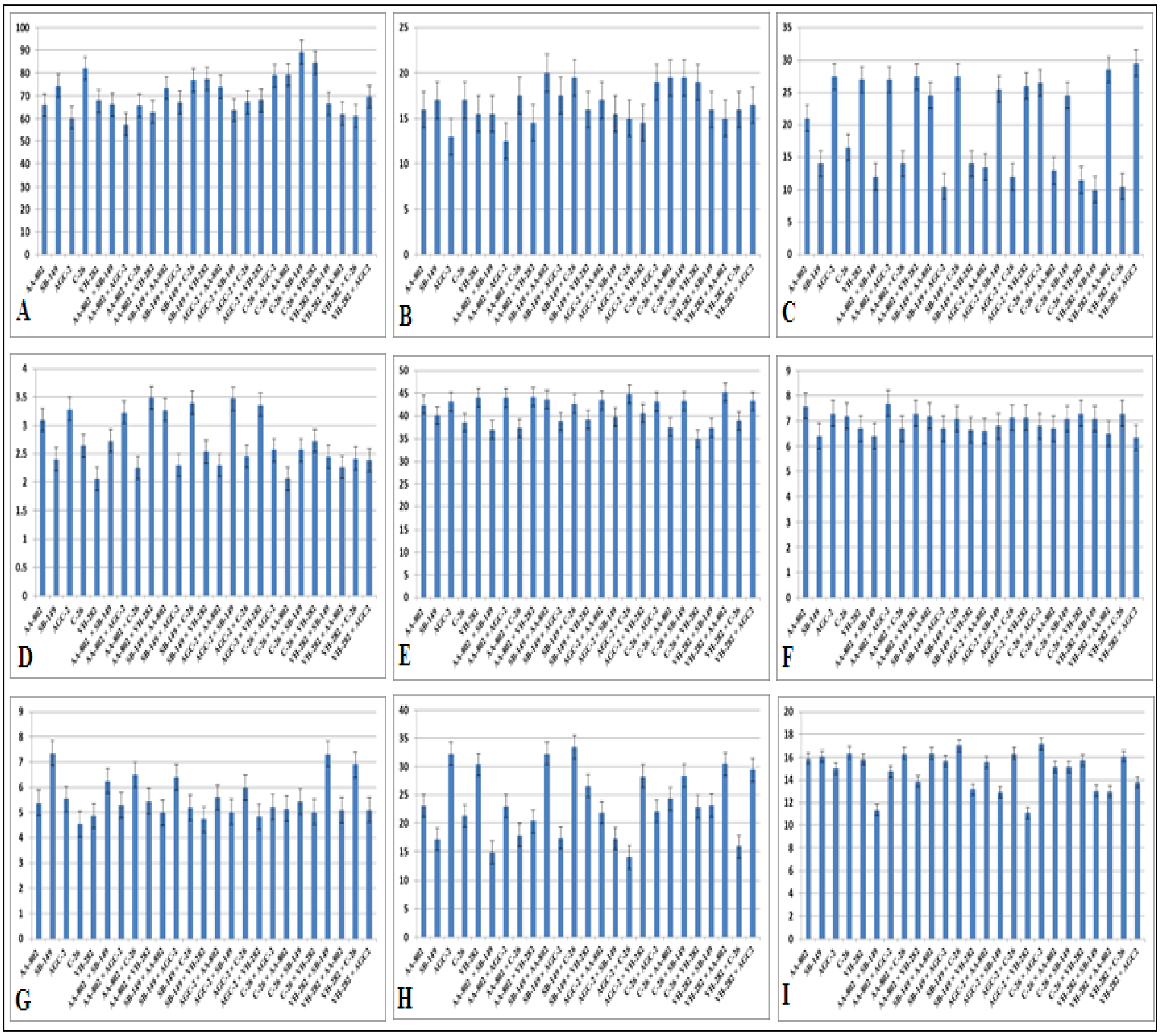


**Fig. 1.** Average performance of parents and hybrids for (A) Plant height (B) Sympodial branches (C) Number of bolls per plant (D) Boll weight (E) GOT (F) Seed index (G) Lint index (H) Seed cotton (I) Oil contents in *G. hirsutum*.

Correlation coefficients for plant height revealed positive association sympodial branches per plant, the number of bolls per plant, boll weight, GOT and seed cotton yield per plant. Mustafa *et al.* (2007) and Baloch *et al.* (2014) concluded that the number of sympodial branches per plant had a positive association with plant height. Khan *et al.* (2009), Abbas *et al.* (2015) and Rehman *et al.* (2014) reported a positive association of plant height with the number of bolls per plant whereas Ranjan *et al.* (2014) reported a positive correlation of plant height with boll weight and Al-Bayaty (2005) reported a positive association of plant height with GOT. Other researchers including Pujer *et al.* (2014), Baloch *et al.* (2014) and Khan *et al.* (2009) concluded that plant height had a positive correlation with seed cotton yield. Sympodial branches per plant exhibited a positive correlation with boll weight, the number of bolls per plant, seed cotton yield per plant, GOT and plant height. Alkuddsi *et al.* (2013) and Shar *et al.* (2017) examined the positive association of sympodial branches per plant with the number of bolls per plant. Afiah and Ghoneim (2000) and Baloch *et al.* (2015) reported a positive correlation of seed cotton yield with several sympodial branches per plant. Chattha *et al.* (2013) and Farooq *et al.* (2013) reported that sympodial branches had a positive association with GOT. The number of bolls per plant showed positive correlation with plant height, GOT, sympodial branches per plant and seed cotton yield per plant.

The association between bolls per plant and boll weight was negative. Tayade *et al.* (2011) and Khan (2014) reported a negative correlation between boll weight and bolls per plant. Shar *et al.* (2017) reported that the number of bolls per plant had a positive correlation with seed cotton yield and Al-Bayaty (2005) reported a positive correlation of boll number with plant height whereas Farooq *et al.* (2015) discussed the positive association of the number of bolls per plant with GOT. Boll weight had a positive association with seed index, GOT, lint index and seed cotton yield per plant. Kumari *et al.* (2011) reported that boll weight had a positive correlation with seed cotton yield and Choudhary *et al.* (2016) found a positive association of boll weight with seed index. Whilst Ahmad and Azhar (2000) reported a strong association of boll weight with GOT. Xu *et al.* (2005) and Punitha *et al.* (2013) reported a positive association of boll weight with lint index. The correlation studies indicated that any improvement in boll weight may have a positive effect on plant yield. GOT showed a positive correlation with seed cotton yield per plant, sympodial branches per plant, number of bolls per plant, boll weight and plant height while the negative association with seed index. Pujer *et al.* (2014) reported positive correlation of GOT with yield of seed cotton. Killi *et al.* (2005) found that GOT had positive relationship with number of sympodial branches per plant. Wadeyar and Kajjidoni (2015) reported negative association of GOT with seed index while Feiyu *et al.* (2012) reported positive association of GOT with number of bolls per plant. Chao-zhu *et al.* (2008) estimated positive association of GOT with boll weight and Al-Bayaty (2005) reported positive relationship between plant height and GOT. The seed index exhibited a negative correlation with GOT. Similar findings were reported by Karademir *et al.* (2009), and Ahmad *et al.* (2016). Lint index had a positive association with GOT, seed cotton yield, boll weight and seed index. Ahmad *et al.* (2016) revealed that the lint index had a positive association with GOT. Rao and Gopinath (2013), and Rajamani *et al.* (2013) reported a positive association of seed cotton yield with lint index. Punitha *et al.* (2013) reported that lint index and boll weight correlated positively. Alkuddsi *et al.* (2013) reported a positive correlation of lint index with GOT and seed index and Ahmad *et al.* (2016) reported a positive correlation of lint index with seed index and yield of seed cotton.

Seed cotton yield presented a positive correlation with all the traits under study except oil contents and seed index. And these findings were supported by Srinivas *et al.* (2015), Baloch *et al.* (2015), Abdullah *et al.* (2016), Ranjan *et al.* (2014), Salahuddin *et al.* (2010), Farooq *et al.* (2014), El-Kady *et al.* (2015), Latif *et al.* (2015) and BABU *et al.* (2017).

Oil contents showed a positive association with the number of sympodial branches per plant, number of bolls per plant, boll weight and seed index while it had a negative relationship with seed cotton yield per plant. Mishra and Satpute (2007) reported a negative correlation between oil contents and seed cotton yield per plant. Chaudhari *et al.* (2017) also found a positive association between the yield of seed cotton and oil contents. Ashokkumar and Ravikesavan (2010) found that cottonseed oil correlated positively with sympodial branches per plant, number of bolls per plant, boll weight and seed index whereas it showed a negative relationship with a yield of seed cotton. Qayyum *et al.* (2010) and Munawar and Malik (2013) reported the same findings.

**Conclusion**

Parents AA-802 exhibited good performance for sympodial branches per plant, number of bolls, boll weight, GOT seed index, lint index and seed cotton yield. Whereas, C-26 identified as better performer exclusively for plant height, sympodial branches per plant, seed index and oil contents. Cross SB-149 × C-26 showed significant response against seed cotton yield, sympodial branches per plant, boll weight, number of bolls per plant, plant height, seed index, lint index, seed cotton yield and oil contents. SB-149 × AA-802 presented better results for the traits namely, sympodial branches per plant, boll weight, GOT, seed index and seed cotton yield. Whilst C-26 × AGC-2 identified as best performer for the traits *i.e.*, plant height, number of bolls per plant, GOT, lint index and oil contents. These identified parents and hybrids could be used in future breeding programs to overcome oil-related problems. It is also suggested that this information must be substantiated by another genetic experiment that may involve a reasonable number of cotton genotypes, evaluated under diverse environments to enhance oil contents of existing commercial cultivars and to develop new cultivars with improved oil content for cotton-growing areas.

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