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# PHENOTYPIC CORRELATION AND HERITABILITY ESTIMATES IN BT AND NON-BT COTTON GENOTYPES

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**ABSTRACT**
*The field experiment was conducted at Sindh Agriculture University Tandojam during 2016-2017 to assess phenotypic correlations and heritability estimates in Bt and non-Bt cotton genotypes. The experiment was laid out in a Randomized Complete Block Design with four replications. The material was consisted of eight upland cotton genotypes viz. CRIS-129, BT-3701, FH-901, FH-142, MS-370, Sindh-1, NIA-ufaq and S.G.A-1. The observations were recorded on plant height plant$^{-1}$ (cm), sympodial branches plant$^{-1}$, bolls plant$^{-1}$, boll weight (g), ginning outturn percentage, seed index (g), seed cotton yield plant$^{-1}$ (g) and staple length (mm). Analysis of variance showed significant differences among the genotypes for all traits studied except seed index, which was non-significant. The phenotypic correlations indicated that characters such as plant height, sympodial branches plant$^{-1}$, number of bolls, ginning outturn % were positively associated with yield. The results further revealed high heritability ( $h^2$b.s.) for plant height, sympodial branches plant$^{-1}$, bolls plant$^{-1}$, boll weight, ginning outturn %, yield plant$^{-1}$ and staple length, whereas low heritability was observed only for seed index. Promising genotypes can be used for hybridization programs in order to isolate useful recombinants in the segregating generations.*
***Keywords:*** *Phenotypic correlation, broad sense heritability, Bt cotton, seed cotton yield*

## INTRODUCTION

The correlation coefficient quantifies the relationship between yield-related traits and fiber quality. Phenotypic correlation between different plant characters exists as reported by earlier researchers [1, 2, 3, 4, 5]. The observation on correlation by [6], stated that sympodial branches, boll weight, and number of bolls were significantly and positively associated with yield plant$^{-1}$. Hence, selection with these characters will eventually enhance the chances to improve yield production. Thus, knowledge about the nature of gene action, mean performance of genotypes, extent of relationship between yield and various agronomic characters is indispensable for breeders to successfully increase seed cotton yield [7]. Correlation determines the power of association between two variables. High correlation indicates that two characters are highly associated whilst stumpy correlation suggests that two characters are poorly correlated. Thus, correlation coefficient deals with the extent of association between several plant traits and finds-out the component traits which may be used as selection criteria for the enhancement of yield and fiber quality traits [6]. The correlation analysis reflects the correlated response of particular character with counterpart traits thus provides a good index to predict the corresponding change which occurs in one character due to proportionate change in the other [8]. Hence, coefficient is a measure of strength of association between different traits. If two traits are positively correlated, then one trait can be improved indirectly by improving the other trait [9].

Heritability is genetic statistics which is used in breeding and genetics studies that estimates as how much variation in a phenotypic trait is attributable to genetic and environmental factors. Hence, heritability determines the extent of transmissibility of characters from parents to their progenies [10]. [11], studied heritability of different traits in *Gossypium hirsutum* L. and reported that genetic variance was much greater than the environmental variances. They calculated higher broad sense heritability estimates were calculated for seed index (77.0%), lint index (96.0 %), lint% (96.0%) and seed cotton yield (98.0%). [12], noted that the overall performance of a genotype has always changed due to environment, however greater the heritability, the easier will be the selection procedure and higher will be progress towards selection. The success of any cotton programme largely depends on the choice and exploitation of potential parental cultivars for hybridization and selection [13]. It is very important that genetic diversity, available in both cultivated and its wild progenitors may be thoroughly utilized to create new genetic complexes for higher yield and resistance to different types of stresses in cotton [14]. The science of plant breeding has a documented history in cotton improvement so as to meet the requirement of producers and processors. To meet fiber necessities of the world`s growing population, a significant improvement in cotton production has been universally realized [15]. It is still desirable for plant breeders to know the extent of relationship between yield and its various components which may facilitate them in selecting plants with desirable characteristics. Expression of various traits often changes due to breeding material and environment for evaluation. Therefore the information of character association between the traits themselves and with the yield is important for the breeding material subjected to selection for developing high yielding genotypes [8]. The Bt toxin gene has been incorporated into cotton making cotton to create its own insecticidal effect. In many regions, the major insect in commercial cotton is lepidopteron larvae, which are killed by the Bt protein when they feed on it. This toxic material eliminates the application of broad-spectrum insecticides [16].

**Materials and Methods**

Current research was conducted at Experimental farm, Department of Plant Breeding and Genetics, Faculty of Crop Production, Sindh Agriculture University Tandojam so as to work-out correlation and broad sense heritability for various yield and fibre traits of eight upland cotton (*Gossypium hirsutum* L) genotypes. The genotypes included were: CRIS-129, BT-3701, FH-901, FH-142, MS-370, Sindh-1, NIA-ufaq, and S.G.A-1. The experiment was carried-out in a randomized complete block design (RCBD) with four replications. The observations were taken on ten randomly tagged plants from each genotype per replication. Thus, characters of forty plants were recorded. The characters studied were; plant height (cm), number of sympodial branches plan$^{-1}$, bolls plant$^{-1}$, boll weight (g), ginning outturn percentage (GOT%), seed index (g), seed cotton yield plant$^{-1}$ (g) and staple length (mm). All the cultural practices and inputs were adopted as recommended for healthy growth of the crop. The data were analyzed according to statistical technique developed by [17] through Statistix 8.1 computer software for determining variability amongst the varieties for various traits. Whereas, means were compared by using the least significant difference (L.S.D.) test at 5% probability level. The broad sense heritability ($h^2$) was estimated according to procedures adopted by [18] while correlations were determined according to formula developed by [19].

## Results and Discussion

Plant breeding uses the natural and artificial hybridization techniques to create heritable variations and novel combinations of alleles in plants and thereby identify plants with useful properties. That goal of plant breeding is to develop crop varieties which produce unique and superior characters of economic importance. Plant breeders employ a number of improve the genetic composition of the crop plants and a successful strategy is dependent on heritability of yield and fiber characters of cotton plant.

## Analysis of variance and mean performance

The analysis of variance indicated that varieties performed variably for most of the traits like plant height, sympodial branches, number of bolls, boll weight, fibre length, ginning outturn % and yield plant$^{-1}$. Such results indicated that the studied material is useful as genetic resources for variety development programmes. Similar results have been reported by Baloch [6] who also observed significant differences (P ≤0.05) among the varieties for all the studied traits. Hence, such promising cultivars can further be exploited in various breeding programs to improve different quantitative and qualitative characters in cotton genotype. Baloch [12] studied correlation and heritability for seed cotton yield and fiber quality traits in *Gossypium hirsutum* L. cultivars. Their analysis of variance suggested highly significant differences among the genotypes for studied traits which were highly variable and heritable also.

The mean performance of genotypes in present study revealed that FH-901 produced the tallest plants measuring 154.05 cm, while Sindh-1 recorded shortest plants (103.53 cm). Reta and Fowler [20] suggested that cultivars with reduced plant height, shorter branches, modified leaves and combination of these characters grown in high plant densities and in narrow-row system could be good alternative to increase seed

**Table 1. Mean squares from analysis of variance for various yield and fiber traits in upland cotton genotypes**

| S.O.V. | D.F | Plant height | Sympodial Branches Plant$^{-1}$ | Bolls plant$^{1-}$ | Boll weight | Staple length | G.O.T% | Seed cotton yield plant$^{-1}$ | Seed index |
|---|---|---|---|---|---|---|---|---|---|
| Replication | 3 | 3.53 | 0.22 | 0.57 | 0.007 | 0.094 | 1.178 | 23.83 | 0.279 |
| Genotypes | 7 | 1487.95** | 76.21** | 217.16** | 0.058** | 3.065** | 15.485** | 2959.59** | 0.509 |
| Error | 21 | 3.62 | 1.10 | 1.711 | 0.016 | 0.417 | 2.320 | 87.49 | 0.239 |

** = Significant at 1% probability

**Table 2. Mean performance of upland cotton genotypes for yield and fiber traits**

| Genotypes | Plant height (cm) | Sympodial branches plant$^{-1}$ | Bolls plant$^{-1}$ | Boll weight (g) | Staple length (mm) | G.O.T% | Seed cotton yield plant$^{-1}$ | Seed index (g) |
|---|---|---|---|---|---|---|---|---|
| CRIS-129 | 107.93 | 22.70 | 48.75 | 3.30 | 26.37 | 36.78 | 160.90 | 6.48 |
| BT-3701 | 131.95 | 32.60 | 51.90 | 3.10 | 27.85 | 41.72 | 160.95 | 6.72 |
| FH-901 | 154.05 | 32.10 | 52.55 | 3.30 | 28.02 | 37.12 | 176.25 | 6.60 |
| FH-142 | 153.53 | 28.90 | 61.87 | 3.37 | 28.45 | 38.07 | 208.70 | 7.18 |
| MS-370 | 126.63 | 26.07 | 43.65 | 3.42 | 28.97 | 38.07 | 149.52 | 6.52 |
| Sindh-1 | 103.03 | 22.97 | 62.07 | 3.12 | 29.07 | 36.97 | 145.25 | 6.82 |
| NIA-ufaq | 143.95 | 33.42 | 61.52 | 3.37 | 28.80 | 35.72 | 207.63 | 5.92 |
| Average | 130.50 | 29.34 | 55.54 | 3.29 | 28.26 | 37.47 | 177.14 | 6.58 |
| LSD (5%) | 2.79 | 1.54 | 1.92 | 0.18 | 13.75 | 2.24 | 0.72 | 0.95 |

** = Significant at 1% probability

cotton yield. In case of sympodial branches$^{-1}$, NIA-ufaq produced the highest number of branches (33.42) followed by BT-3701 (32.60), and lowest number of sympodial branches plant$^{-1}$

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were counted in CRIS-129 (22.70). The maximum bolls plant$^{-1}$ was recorded in Sindh-1 (62.07) followed by FH-142 (61.87) yet minimum bolls plant$^{-1}$ were obtained from MS-370 (43.65). The maximum boll weight was weighed by M.S-370 (3.42g) closely followed by FH-142 and NIA-ufaq which produced bolls of similar weight (3.37g), while smaller bolls were obtained from BT-3701 (3.10g). Makhdom [21] stated that average boll weight is the main yield component which plays a prime role in improving seed cotton yield. The longest staple length was measured by Sindh-1 (29.07mm) while shortest staple length was obtained from CRIS-129 (26.37mm). The highest lint % was ginned by BT-3701 (41.72%) nevertheless the lowest ginning outturn was given by NIA-ufaq (34.72 %/). The FH-142 gave higher seed index (7.18g) and next maximum by Sindh-1 (6.82 g), while NIA-ufaq gave the lower seed index (5.92g). The genotype FH-142 produced maximum seed cotton yield plant$^{-1}$ (208.70g) followed by NIA-ufaq (207.63 g), while minimum seed cotton yield plant$^{-1}$ was recorded by sindh-1 (145.25g).

**Correlation Coefficient (r)**

The correlation coefficient was worked-out between eight yield and fiber quality characters. Plant height displayed significant and affirmative association with sympodial branches (r =0.79**), bolls plant$^{-1}$ (r =0.54**), boll weight (r =0.31*) and seed cotton yield plant$^{-1}$ (r =0.57**). The positive and significant relationship of sympodial branches with bolls plant$^{-1}$ (r=0.40*) and yield plant$^{-1}$ (r =0.36*) was also recorded. The correlations of bolls per plant with seed cotton yield per plant (r =0.95**) were also highly significant and positive in direction. The boll weight was positively correlated with seed cotton yield per plant (r=0.52**) but negatively correlated with GOT % (r=-0.40*). The seed cotton yield was positively correlated with plant height$^{-1}$, sympodial branches, number of bolls and boll weight. The ginning outturn percentage expressed highly significant and positive association and GOT % (r=0.35*). The only significant but negative correlation was established between boll weight and GOT% in the present studies. Similar to our findings, Baloch [22] observed that sympodial branches plant$^{-1}$, boll weight and bolls plant$^{-1}$ expressed significant and positive associations with seed cotton yield plant$^{-1}$. Thus, indirect selection based on these traits will ultimately enhance the chance to increase seed cotton yield per plant.

**Table 3. Correlation coefficient (r) between yield and fiber characters**

**,* = Significant at 1 and 5% probability levels respectively

| Characters | Plant height | Sympodial branches plant$^{-1}$ | Bolls plant$^{-1}$ | Boll weight | Seed cotton yield plant$^{-1}$ | G.O.T% | Seed index | Staple length |
|---|---|---|---|---|---|---|---|---|
| Plant height | | | | | | | | |
| Sympodial Branches plant$^{-1}$ | 0.79** | | | | | | | |
| Bolls plant$^{-1}$ | 0.54** | 0.40* | | | | | | |
| Boll weight | 0.31* | 0.02 | 0.25 | | | | | |
| Seed cotton yield plant$^{-1}$ | 0.57** | 0.36* | 0.95** | 0.52** | | | | |
| G.O.T% | 0.08 | 0.28 | - 0.25 | - 0.40* | 0.35* | | | |
| Seed index | - 0.05 | - 0.25 | - 0.10 | - 0.16 | - 0.14 | 0.06 | | |
| Staple length | 0.15 | 0.12 | 0.10 | - 0.04 | 0.07 | - 0.06 | -0.04 | |

**Heritability estimates**

Heritability estimates measure the fraction of phenotype variability that is attributable to genetic variation Raj [23]. Heritability estimates ($h^2$) in broad sense was calculated from genetic ($\sigma^2$g), phenotypic ($\sigma^2$p) and environment ($\sigma^2$e) variances for various traits. Heritability estimates are helpful in deciding the characters to be considered while making selection. In present studies, high heritability in broad sense was recorded for plant height, sympodial branches, number of bolls, boll weight, ginning outturn %, yield plant$^{-1}$ and staple length, whereas low heritability was found for only seed index. Nizamani [24] studied character associations and heritability estimates for yield and fiber traits in promising cotton genotypes. High heritability values in their studies for various traits indicated that the variation observed in plant traits was mainly under genetic control and less influenced by

**Table 4. Heritability estimates in broad sense for various traits in upland cotton**

| Characters | Genotypic variance ($\delta^2g$) | Phenotypic variance ($\delta^2p$) | Environmental variance ($\delta^2e$) | Heritability % (b.s.) |
|---|---|---|---|---|
| Plant height | 1484.33 | 1488.85 | 0.905 | 99.69% |
| Sympodial plant$^{-1}$ | 75.11 | 76.485 | 0.275 | 89.20% |
| Bolls plant$^{-1}$ | 215.44 | 217.587 | 0.42 | 99.01% |
| Boll weight | 0.042 | 0.062 | 0.004 | 67.74% |
| Ginning outturn (%/) | 13.165 | 16.065 | 0.58 | 81.94% |
| Seed index | 0.27 | 0.568 | 0.059 | 47.53% |
| Seed cotton yield plant$^{-1}$ | 2871.51 | 2981.46 | 21.87 | 96.30% |
| Staple length | 2.648 | 3.169 | 0.104 | 83.55% |

the environmental conditions. Such results suggested the involvement of additive genes for the expression of those traits. Hence, the improvement of traits under study can be made through direct phenotypic selection of single plants. Our findings results are in conformity as reported by Abbas [25], Dhivya [1] and Farooq [26].

## Conclusion

The results of present study indicated the presence of genetic diversity among the upland cotton varieties for different yield and fiber traits. Correlation coefficients showed significant and positive association of major yield traits with seed cotton yield. Highest heritability was found in almost all the characters. Promising parents can be used for hybridization programs in order to isolate useful recombinants in the segregating generations.

## REFERENCES

1. Dhivya R, Amalabalu P, Pushpa R and Kavithamani D (2014). Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.) Afr. J. Plant Sci., 8(1): 1-5.
2. Shakeel A, Talib I, Saeed RA, Ziaf K, and Saleem MF (2015). Genetic diversity among upland cotton genotypes for quality and yield related traits. Pak. J. Agri. Sci., 52 (1): 73-77.
3. Abdullah M, Numan M, Shafique MS, Shakoor A, .Rehman S, and Ahmed MI (2016). Genetic variability and interrelationship of various agronomic traits using correlation and path analysis in cotton (*Gossypium hirsutum* L.) Academia. J. Agri Res 4(6): 315-318.
4. Gopi TJS, and Patil BR (2017). Genetic variability and heritability study in $F_2$ segregation of desi cotton yield and its component traits. Int. Curr. Microbiol. app. Sci., 6(9): 2679-2684.
5. Khan M.I, Haq HA, Kali mullah, Arshad M, Majid A (2017). Genetic diversity and correlation studies for cotton leaf curl disease (CLuD) fiber and yield related attributes in exotic lines. American. J. plant. Sci., 8: 615-624.
6. Baloch M, Baloch AW, M.K. Baloch, Mallano IA, Baloch AM, Baloch NJ, Abro S (2015). Association and heritability analysis for yield and fiber traits in promising genotypes of cotton (*Gossypium hirsutum* L.). J. (Sci. Ser.). 47 (2): 303-306.
7. Ahmad W, Khan N, Khalil MR, Parveen A, Umm-E-Aiman, Samiullah MS and S.A. Shah SA (2008). Genetic variability and correlation analysis in upland cotton. J. Agri. 24: 4.
8. Salahuddin S, Abro S, Rehman A and Iqbal K (2010). Correlation analysis of seed cotton yield with some quantitative traits in upland cotton (*Gossypium hirsutum* L.) Pak. J. Bot., 42(6): 3799-3805.

9. Hussain S, Nawab NN, Ali MA, Hussain A, Nawaz MA and Malik TA (2010). Evaluation of performance, genetic divergence and character association of some polygenic traits in upland cotton. J. Agric. Social Sci., 6: 79-82.
10. Baloch MJ and Baloch QB (2004). Plant character in relation to earliness in cotton (*Gossypium hirsutum* L.) Proc. Pakistan Acad. Sci., 41: 103-108.
11. Khan NU, Marwat KB, Hassan G, Farhatullah, Batool S, Makhdoom K, Ahmad W and Khan HU (2010). Genetic variation and heritability for cotton seed, fiber and oil traits in *Gossypium hirsutum* L. Pak. J. Bot., 42(1): 615-625.
12. Baloch M.J, Kumar C, Jatoi WA and Rind IH (2014). Phenotypic correlation and regression analysis of yield and fiber traits in upland cotton (*Gossypium hirsutum* L.). Pak. J. Agri., Eng. Vet. Sci., 30(2): 135-146.
13. Raza H, Khan NU, Khan SA, Gui S, Latif A, Hussain I, Khan J, Raza S and Baloch M (2016). Genetic variability and correlation studies in $F_4$ populations of upland cotton. The J. Animal and Plant Sci., 26 (4): 1048-1055.
14. Sanghera GS, Kashyap SC, Rana V and Parray GA (2014). Agro-morphological and genetic diversity among elite wheat genotypes grown under Kashmir conditions. Int. J. Curr. Res., 6(8): 7735-7740.
15. Farooq J, Anwer M, Riaz M, Farooq A, Mahmood A, Shahid MTH, Rafiq M and Ilahi F (2014). Correlation and path coefficient analysis of earliness, fiber quality and yield contributing traits in cotton (*Gossypium hirsutum* L.) The J. Animal and Plant sci., 14(3): 781-790.
16. Abid M, Ashfaq M, Quddus MA, Tahir MA and Fatima N (2011). A resource use efficiency analysis of small BT cotton farmers in Punjab, Pakistan. Pak. J. Agri. Sci., 48: 75-81.
17. Gomez KA and Gomez AA (1984). Statistics for Agriculture Research (2 eds.), P: 680. Willy, New York, USA.
18. Baloch M.J, Kakar MS, Jatoi WA and Veesar NF (2010). Identification of potential $F_2$ populations from intraspecific crosses of upland cotton. Pak. J. Sci. Ind. Res., 53 (3):1515-157.
19. Raghavrao D (1983). Design of Expriments Statistical Techniques in Agriculture and Biological Research. Oxford and IBH Publishing Company, New Delhi.
20. Reta-Sanchez D and Fowler JL (2002). Canopy light environment and yield of narrow row cotton as affected by canopy architecture. Agronomy J., 94: 1317-1323.
21. Makhdoom K, Khan NU, Sundas B, Bibi Z, Farhatullah, Khan S, Mohammad F, Hussain D, Raziuddin, Sajjad M and Khan N (2010). Genetic aptitude and correlation studies in (*Gossypium hirsutum* L). Pak. J. Bot., 42(3): 2011-2017.
22. Baloch M, Baloch AW, Baloch MK, Mallano IA, Baloch AM, Baloch NJ, Abro S (2015). Association and heritability analysis for yield and fiber traits in promising genotypes of cotton (*Gossypium hirsutum* L.). J. (Sci. Ser.). 47 (2): 303-306.
23. Raj A, Ougenaarden V and Alexander A. 2008. Nature or chance stochastic gene expression and its consequences. Cell, 135(2): 216-226.
24. Nizamani F, Baloch MJ, Buriro M, Nizamani GS, Nizamani MR and Baloch IA (2017). Genetic distance, heritability and correlation analysis for yield and fiber quality traits in upland cotton. Pak. J. Biotech. 14 (1): 29-36.
25. Abbas HG, Mahmood A and Ali Q (2013). Genetic variability, heritability, genetic advance and correlation studies in cotton (*Gossypium hirsutum* L.). Int. Res. J. Microbiol., 4(6): 156-161.
26. Farooq J, Anwar M, Riaz M, Mahmood A, Farooq A, Iqbal MS and Iqbal MS (2013) Association and path analysis of earliness yield and fiber related traits under cotton leaf curl virus (CLCuV) intensive conditions in G. *hirsutum* L. Plant Knowledge J. 2 (1): 43-50.