

Research Article	Article History (23-007)	Received: 10 June 23	Revised: 13 Aug 23	Accepted: 18 Aug 23	Published: 27 Aug 23
------------------	--------------------------	----------------------	--------------------	---------------------	----------------------

GENETIC VARIABILITY IN ADVANCE LINES OF UPLAND COTTON FOR WITH IN BOLL YIELD COMPONENTS

Muhammad Talha Shafique¹, Muhammad Yasir Saleem¹, Abdul Ali Azam¹ and Muhammad Mubashir Asim^{*2}

¹Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan

²Department of Botany, University of Agriculture Faisalabad, Pakistan

*Corresponding author: mubashirasim1998@gmail.com

ABSTRACT

Cotton (*Gossypium hirsutum* L.) is an important fiber crop all over the world as well as in Pakistan. But the production of cotton crop is low due to biotic and abiotic factors. As boll is the basic determinant for yield in cotton crop, therefore a study on within boll yield parameters was carried out using 24 cotton bulk and 2 check varieties to check their variability for within boll components. The experiment was performed in the research area of the department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The genotypes were seeded in two replications following a randomized complete block design. Data were recorded at maturity for different traits including seed cotton yield, number of seeds per boll, boll weight, seed index, lint index, seed mass per boll, lint mass per boll, GOT%, seed volume, seed density, seed surface area and fiber related traits. Data were subjected to analysis of variance to check significance among different genotypes. Genotypes were significantly different. Basic statistical values like maximum or minimum value, standard error of mean and variance were calculated. Seed cotton yield, number of seeds per boll, boll weight, seed index, lint index, seed mass per boll, GOT %, seed volume, seed density, fiber length, fiber fineness and fiber strength showed high heritability with higher genetic advance. The genotype PB-132 performed best for most of the parameters including GOT %, lint index, lint mass per seed and seed density. The findings of the current study revealed the potential of different bulks of cotton for the development of high yielding varieties. This information may be used to devise breeding strategies to enhance cotton production and variety development.

Keywords: Seed Volume, Seed Density, Seed Index, Yield Components, Advance Lines.

Citation: Shafique MT, Saleem MY and Asim MM, 2023. Genetic variability in advance lines of upland cotton for with in boll yield components. Trends Biotech Plant Sci 1(1): 63-71. <https://doi.org/10.62460/TBPS/2023.003>

1. INTRODUCTION

Cotton (*Gossypium hirsutum* L.) has significant commercial importance as it provides fiber to the textile industry. It is the main fiber crop that supports the world's largest textile businesses, with an annual effect on the economy of at least \$0.6 trillion globally. The world's biggest textile industry is running on the basis of cotton fiber having an annual income impact of about \$599 billion worldwide (Ashraf et al. 2018). American cotton (*Gossypium hirsutum* L.), is a predominant cotton species mainly cultivated for its fiber in more than eighty countries in the world (Shahzad et al. 2019). Pakistan cotton yield have been reduced in the last few years due to many reasons. The main reason behind this low production is too many rains at sowing time, fluctuation in temperature, high temperature at flowering stage, late harvesting of wheat, delay cotton sowing, reduction in the area of cotton, improper use of production technology, insect pest attack especially CLCuV attack and lack of resistant varieties. The cotton breeding program needs genetic diversity in the germplasm that should be exploited to make improvements in the genetics of cotton crops. It helps us to select the parents with desirable attributes that may be crossed to bring broaden diversity in the germplasm. The evaluation of diversity in the yield-related attributes mainly helps us to develop a superior genotype that may be used in a future different breeding program (Rathinavel et al. 2017). In bulk population, every plant is different from all the remaining plants so therefore selection for the desirable traits is easier.

In any breeding program, the information of available genetic diversity in germplasm is required. The genetic diversity should be exploited to broaden the genetic base for crop improvement. It helps us to select parents with desirable characters that may be crossed to bring genetic diversity in the germplasm. The assessment of diversity in morphological characters mainly helps us to develop superior cultivars that may be used in different breeding programs (Rathinavel et al. 2017). The objective of cotton breeding is to provide high yielding varieties with better fiber quality. Because of its significance, plant breeders have been attracted to it in order to better its genetic

composition. As a result of these efforts, high yielding cultivars have been developed. Cotton's genetic architecture may be improved further; hence, cotton breeders are attempting to breed new types with high yield and higher fibre quality. SCY is a complicated property that results from the manifestation of its component qualities. As the world's population grows by the day, food output must expand to fulfil the demands of the textile industry. Cotton breeders benefit greatly from the genetic basis of yield contributing characteristics. Within-boll yield components are the most fundamental parameters influencing seed cotton and lint yield in cotton (*Gossypium hirsutum* L.). Because the boll serves as the foundation for seed cotton production, within-boll yield components may be the most important elements influencing cotton productivity on a per-unit-land-area basis. Before attempting to enhance a trait, it is vital to first understand the genetic mechanism that leads to its inheritance. Cotton yield is directly determined by SCY, seeds per boll, lint mass per boll, and GOT percent.

Utilization of available diversity in terms of morphological features is required to initiate a well-planned breeding program (Zada et al. 2013). BP, SCY, and lint yield are positively correlated with each other an increase in BP enhances SCY and lint production. The most important trait and the ultimate goal of the breeder for any crop is the yield. Yield is a quantitative trait which means multiple genes control it. Cotton yield is an inclusive trait, factors such as lint yield, lint %, LI, SI, SCY, boll number, boll size and BP affect the total yield. The main objective of this study is to evaluate the best performing lines based on within boll yield components.

2. MATERIALS AND METHODS

The data was composed of 24 advance cotton lines developed department of PBG. Cotton field area of the department of Plant Breeding and Genetics, was selected for experiment during the regular cotton planting season in 2021. Twenty-six genotypes were sown in a RCBD at the time of sowing, the recommended row to row distance (75cm) and plant to plant distance (30cm) were maintained. Proper agronomic practices were applied from sowing to picking like weeding, thinning, hoeing, proper irrigation and plant protection by using different pesticides as recommendations.

Ten plants of each line from each replication were chosen at random for data collection for the following traits.

2.1. Traits Evaluation

At the time of maturity 20 plants were selected from two replications. Ten from replication one and 10 from replication two. Ten effective bolls were picked from axial, terminal and middle part of the plant to study seed and lint related traits. Data were recorded from selected plants on the individual basis for the following parameters.

2.2. Seed cotton yield (g)

Total lint weight picked manually from one plant is described as SCY measured in grams (g). SCY per plant is calculated by electric balance. The calculated average for each genotype in each replication for further analysis.

2.3. Boll weight (g)

Weight of boll is measured in grams (g). It was calculated by dividing SCY obtained from one plant by its total number of picked bolls. Average data was calculated from each genotype in each replication.

$$BP = (\text{seed cotton yield}) / (\text{Total number of bolls})$$

2.4. Seed index (g)

100 seed weight was calculated with the help of electric balance for each plant in grams (g). Average data was calculated for each genotype in each replication.

2.5. Lint index (g)

LI is measured in grams (g) it is actually the weight of lint produced by 100 seeds. It was calculated by this formula.

$$LI = (\text{Seed index} \times \text{GOT \%}) / (100 - \text{GOT\%})$$

2.6. Seeds per boll

After ginning of 10 selected bolls, the collected seed were counted separately for each plant then divided by its total Number of bolls. Average data of seed per boll was calculated for each genotype.

$$\text{Seeds per boll} = (\text{Number of seeds after ginning}) / (\text{Number of bolls in sample})$$

2.7. Seed mas per boll

Seed mass per boll was obtained by dividing the seed weight of the sample by the number of bolls

2.8. Lint mass per boll

Lint mass per boll was obtained by dividing the lint weight of the sample by the number of bolls.

2.9. Ginning out-turn (%)

A single rolling electrical ginner was used to gin seed cotton after weighing it. Lint weight was recorded with the help of electric balance. Ginning outturn was calculated by using the following formula:

$$\text{GOT \%} = (\text{Sample lint weight}) / (\text{Seed cotton weight in sample}) \times 100$$

2.10. Seed Volume per 100 seeds (cm³)

Seed volume was found with the help of ethanol. Firstly, ethanol was filled in a flask and measure its volume. Then put 100 seeds into the ethanol-filled flask and measures the increased volume of ethanol with the help of measuring values that were put on the flask.

Seed Volume = *Ethanol Volume with 100 seed* – *Ethanol volume without 100 seed*

2.11. Seed surface area (cm²)

It was calculated in cm² by SI method. Seed volume per seed was converted to seed surface area by computing regression coefficient of the Hodson (1920) Table.

2.12. Seed density (g/cm³)

Seed density was found with the help of SI and seed volume.

Seed Density = *(SI)/(seed volume)*

2.13. Fiber length (mm)

Fiber length is measured in millimeters (mm) with the help of Uster HVI-900 S. A. Mean was value calculated for further analysis.

2.14. Fiber fineness (µg/inch)

A sample of lint weighing 5-10 g was put in a micronaire compartment using the HVI system for measuring fiber fineness. Micronaire test started automatically when sample weight was within the range and displayed on the testing screen. A compilation sample was emitted from the chamber by opening its lid. Average fiber fineness was recorded in this way for all the samples of each genotype for statistical analysis.

2.15. Fiber strength (g/tex)

The procedure for measuring fiber strength is the same as that of measuring staple length. A tuft of fiber was placed between two special clamps to determine the breaking strength.

2.16. Statistical analysis

The collected data was subjected to the analysis of variance. Mean plot of 24 cotton genotypes was plotted to display the mean values of each genotypes for different agronomic and fiber quality traits.

3. RESULTS AND DISCUSSION

Analysis of variance provides information about differences among the treatments whether they are significant, non-significant or highly significant. If data is non-significant then there is no need to further analyze this data because there are no significant differences among the genotypes. If data is significant or highly significant then data proceeds for the next analysis. The proportion of genotypic variance to the phenotypic variance is called heritability and it is represented as *h*. It is a considerable element in the selection of different parameters. It demonstrates how many differences in a given attribute are due to genetic variation. It studies the transfer of attributes from one generation to the next generation. It helps us to determine the superior genotypes from the different genetic populations.

3.1. Analysis of Variance

Analysis of variance manifested that the bulk population exhibited significant variation for all the attributes like BW, LI, SI, GOT (%), seeds boll⁻¹, FL, FF, FS, seed volume, seed density and SSA while SCY was highly significant (Table 1).

3.2. Seed cotton yield

Mean square results from analysis of variance depicted highly significant variation among genotypes for SCY per plant as shown in Table 1. Mean values pertaining to yield per plant depicted that highest mean values (170.65) was shown by PB-97 and lowest mean value (86.97) was observed in PB-129 (Fig. 1).

Higher phenotypic and genotypic variances were calculated for SCY. Genetic variance was much higher than environmental variance. It means that studied attribute is less influenced by the environment. PCV was a little higher than GCV indicating less environmental influence. Heritability response was maximum for selection which indicates that the selection of studied trait will be in our benefit (Table 2).

SCY is an important character which is of main concern for plant breeder. Genotypes having diverse germplasm with significant differences are beneficial for plant breeder for selection criteria of high yielding cultivars (Komala et al. 2018). High heritability with higher genetic advance was also reported by Kumar et al. (2019). Higher heritability with higher genetic advance percent of mean for SCY per plant is beneficial and there are chances of improvement of this trait for further breeding.

3.3. Seeds per Boll

Genotypes showed significant differences for the trait under evaluation according to Table 1. The range of variability among genotypes was observed from 35.50 to 24. Based on mean performance, maximum numbers of seeds per boll were depicted by PB-133 and lowest by PB-116 as shown in Fig. 2. The PC was higher than the GC

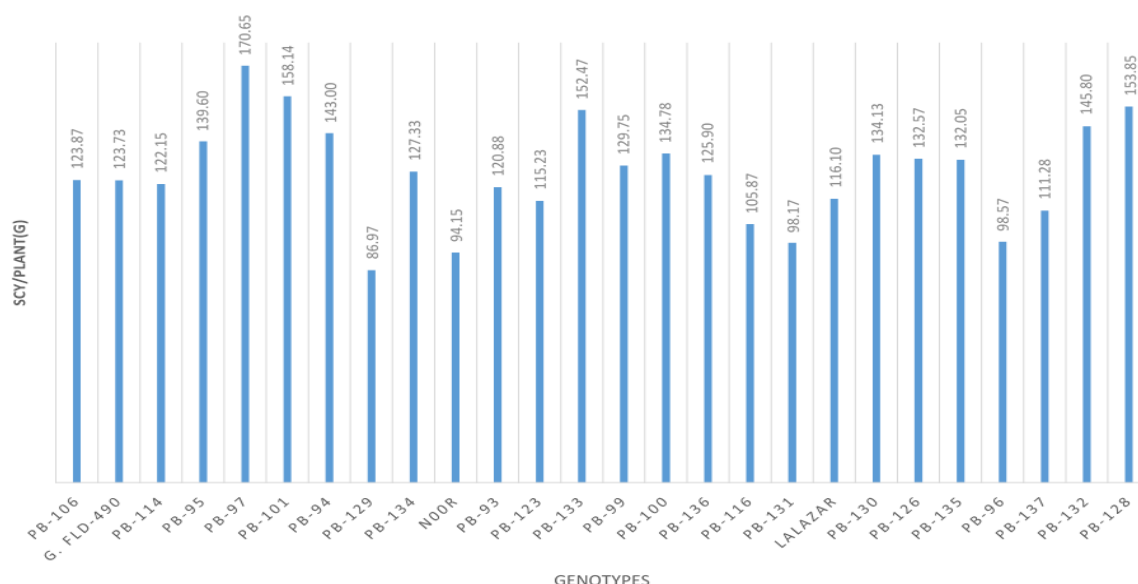


Fig. 1: Mean performances of 26 genotypes of cotton for seed cotton yield

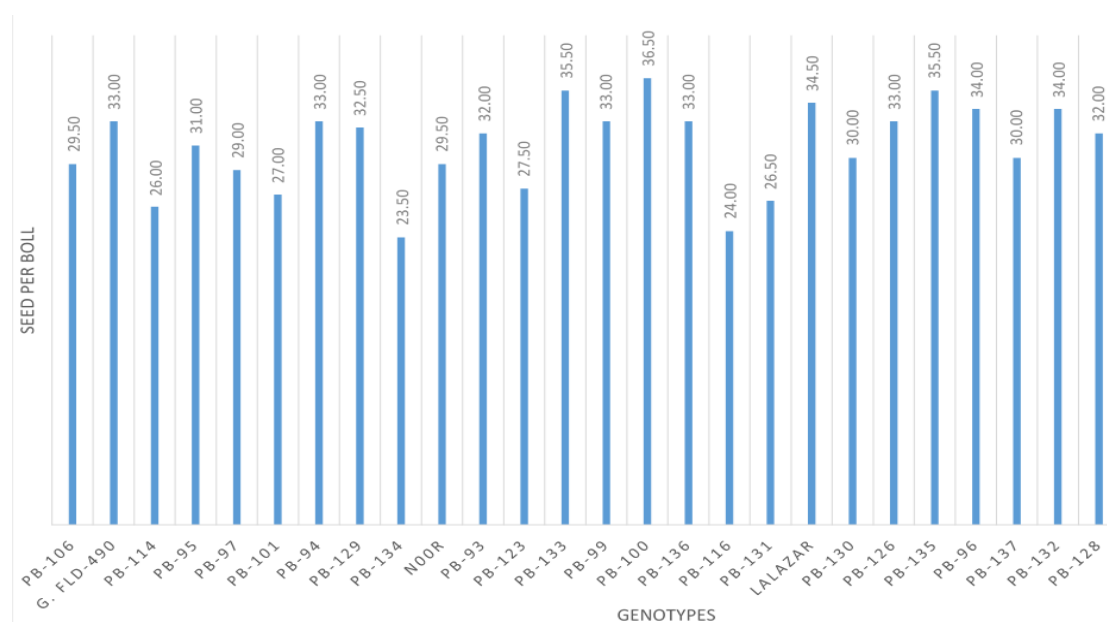


Fig. 2: Mean performances of 26 genotypes of cotton for seed per boll.

Table 1: Mean square values for different agronomic and fiber quality traits in cotton

SOV	DF	SCY (g)	SPB	BW (g)	GOT (%)	SMPB (g)	LMPB (g)	SI (g)	LI (g)	FS (g/tex)	FF (μg/inch)	FL (mm)	SV (g/cm ³)	SSA (cm ²)	SD (g/cm ³)
Replication I	84.99	24.92	1.14	1.72	0.28	0.04	1.05	0.99	2.08	0.013	0.0008	0.3	0.00007	0.005	
Genotypes	25	834.39**	25.1**	0.14*	3.88**	0.04**	0.02**	0.3**	0.3**	8.97**	0.13**	1.09**	4.39**	0.015**	0.04**
Error	25	59.53	1.92	0.006	1.53	0.011	0.006	0.07	0.11	0.85	0.037	0.2	0.35	0.003	0.0006

for a seed per boll while the genotypic variance was higher than the environmental variance. PCV and GCV displayed almost similar trends indicating less environmental influence. Heritability was higher with moderate GA % of the mean (Table 2). Highly significant mean square results of analysis of variance for a number of several among different genotypes were revealed by Tyagi et al. (2014). For number of seeds per boll (Nawaz et al. 2019).

3.4. Bolls per plant

Mean square results from investigation of variance depicted highly significant variation among genotypes for BP per plant (Table 1). Mean square values for BP per plant were ranged from 4.41 to 3.56. The highest mean values were depicted by genotype PB-116 and the lowest by PB-100 as shown in Fig. 3. Higher phenotypic and genotypic variances were calculated for BP as compared to environmental variance. It means trait has the potential of improvement and this can be done by selection. PCV was little higher than GCV indicating less environmental influence. Heritability in broad sense was higher with maximum response to selection which indicates that selection of studied trait could be done (Table 2). Genotypes showed diverse significant results which predict about the

importance of this trait for further experiments with respect to yield components. Variability among genotypes should be exploited to get beneficial results (Naik et al. 2016; Kumbhar et al. 2020). PCV was one percent higher than GCV which shows less environmental impacts on genotypes. Heritability in broad sense was higher with a higher selection response.

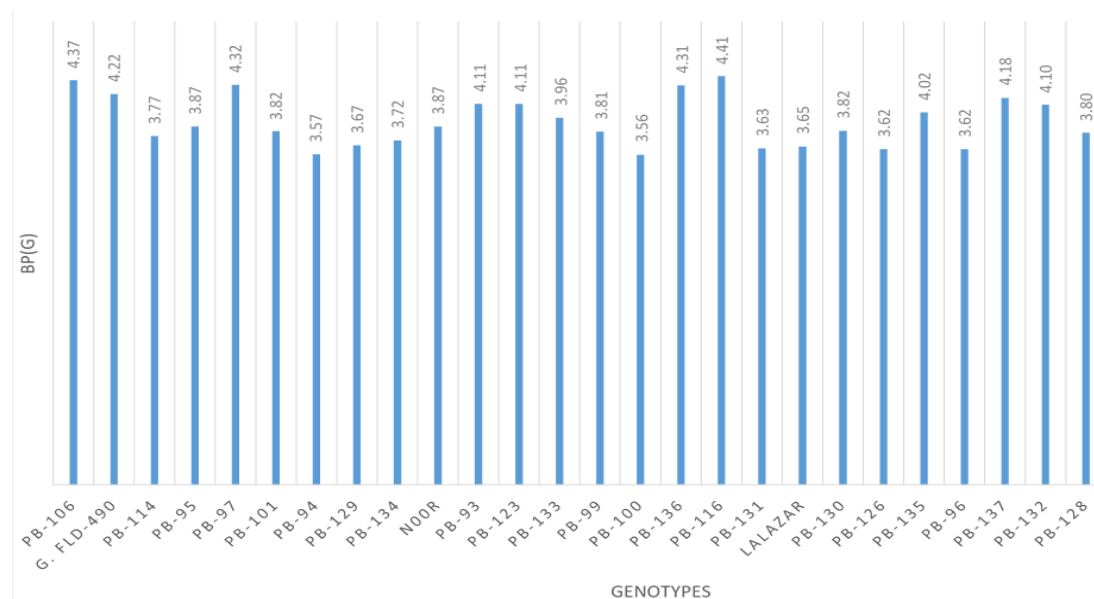


Fig. 3: Mean performances of 26 genotypes of cotton for bolls per plant.

Table 2: Estimation of Genetic variability and heritability of cotton genotypes for different agronomic and fiber quality traits in cotton

SOV	SCY (g)	SPB	BW (g)	GOT (%)	SMPB (g)	LMPB (g)	SI (g)	LI (g)	FS (g/tex)	FF (μg/inch)	FL (mm)	SV (g/cm ³)	SSA (cm ²)	SD (g/cm ³)
Observation	26	26	26	26	26	26	26	26	26	26	26	26	26	26
Maximum	170.65	35.5	4.41	44.98	1.64	1.64	7.15	5.85	31.95	4.85	30.62	11.5	1.79	1.19
Minimum	86.97	24	3.56	38.4	1.04	1.04	5.7	3.89	23.75	3.91	27.45	6	1.39	0.51
Mean	126.81	2.75	3.982	41.69	1.34	1.34	6.42	4.87	27.85	4.38	29.04	8.75	1.59	0.85
SE	5.46	0.98	0.0558	0.87	0.077	0.06	0.19	0.23	0.65	0.14	0.31	0.41	0.03	0.01
Phenotypic Variance	451.46	13.54	0.0748	2.7	0.028	0.02	0.19	0.19	4.91	0.08	0.64	2.36	0.008	0.0216
Genotypic Variance	391.93	11.62	0.0686	1.17	0.016	0.01	0.12	0.08	4.06	0.04	0.45	2.02	0.006	0.021
Environmental Variance	59.53	1.92	0.0062	1.53	0.012	0.01	0.07	0.11	0.85	0.04	0.19	0.34	0.002	0.0006
Genotypic coefficient variation	15.61	11.01	6.683	2.55	9.49	7.87	5.39	6.25	7.12	5	2.35	16.07	7.39	19.57
Phenotypic Coefficient Variation	16.76	11.88	6.98	3.86	12.39	10.3	6.85	9.58	7.83	6.63	2.81	17.4	8.93	19.87
Heritability (Broad Sense)%	86.8147	85.79	91.68	43.49	58.64	58.47	62.15	42.53	82.72	56.84	69.54	85.32	68.64	97.02
Genetic Advance % of mean	29.96%	21.00%	13.18%	3.46%	14.97%	12.40%	8.80%	8.39%	13.34%	7.76%	4.03%	30.58%	12.62%	39.72%

3.5. Ginning out turn (GOT%).

Ginning out - turn contribute directly to yield as it is calculated by using lint weight. ANOVA demonstrated significant results for GOT as the genotypes were genetically different (Table 1). PB-132 displayed maximum value 44.98 for GOT % whereas least value 38.40 was observed by PB-95. Remaining varieties showed moderate values. Range of mean values shows that there is a lot of variability among germplasm for this trait and can use for future breeding program (Fig. 4). For GOT % Phenotypic variance was higher than genotypic variance with very low environmental variance which means that it was less influenced by environment. PCV was bit higher as compared to GCV. For this trait moderate heritability with low GA% of mean was observed (Table 2). Significant differences among studied genotypes for lint percentage were reported by Jarwar et al. (2019).

3.6. Seed Mass per boll

Means square results from exploration of variance depicted significant variation among genotypes for seed mass per boll (Table 1). Mean performances of genotypes for studied trait were ranged from 1.04 -1.64 as shown in Fig. 5.

Higher phenotypic variance and genotypic variances were observed. GCV was higher than ECV indicating less environmental influence. PCV was little higher than GCV indicating less environmental influence. For seed mass

per boll moderate heritability (58.64) with moderate GA% of mean (14.97) was observed which indicates that selection of studied trait could be done (Table 2).

3.7. Lint mass per boll

Mean square results from an investigation of variance depicted highly significant variation among genotypes for lint mass per boll (Table 1). On the basis of the performance of mean values genotypes ranged from 1.04 to 1.64 as shown in Fig. 6. ECV was much higher than genotypic GCV which indicates greater environmental influence than genotypic variability. Heritability estimates were also observed medium with medium GA percent of mean which shows that this trait is not beneficial for future breeding programs and would show non - significant association (Table 2). PCV was higher than GCV. GCV was much higher than ECV (Riaz et al. 2019).

3.8. Seed index

The results revealed that genotypes were significantly different for the studied trait as shown in Table 1. Mean performance of genotypes for SI ranged from 5.7 to 7.15. Maximum values were depicted by PB-132 and PB-99 while Minimum by PB-97 (Fig. 7) SI displayed higher phenotypic variance as compared to genotypic variance. PCV was a bit higher than GCV indicating less influence from the environment. For SI, higher heritability estimates (62.15) were observed with higher genetic advance 8.8 % of the mean (Table 2). The genotypic variance was much higher as compared to environmental variance. It means this trait is less influenced by the environment. For SI, high ha assessments with high GA were observed by Shar et al. (2017).

3.9. Lint index

Mean square results from the exploration of variance depicted highly substantial variation among genotypes for LI (Table 1). Maximum values (5.85) for LI were noted for PB-132 and minimum values (3.89) for PB-97 (Fig. 8). Low Phenotypic (0.19) and genotypic variances (0.08) were calculated for the SI. PCV was a bit higher than GCV indicating less environmental influence. The genotypic variance was higher as compared to the environmental variance this means the studied attribute can be improved by selection (Table 2). Genotypes were genetically different for the studied trait. Improvement of the yield traits will help in the enhancement of yield (Shar et al. 2017). For LI, a higher heritability estimate with higher GA % was observed Reddy et al. (2019). Results indicate that the studied trait is beneficial for a future breeding program.

3.10. Fiber Strength

Fiber Strength means square results from an investigation of variance depicted highly significant variation among genotypes for fiber strength (Table 1). On the basis of the performance of mean values genotypes ranged from 31.95 to 23.75 as shown in Fig. 9. The GV was much higher than the EV which indicates low environmental. Heritability estimates were also observed high with medium GA percent of mean which shows that this trait is beneficial for future breeding programs (Table 2).

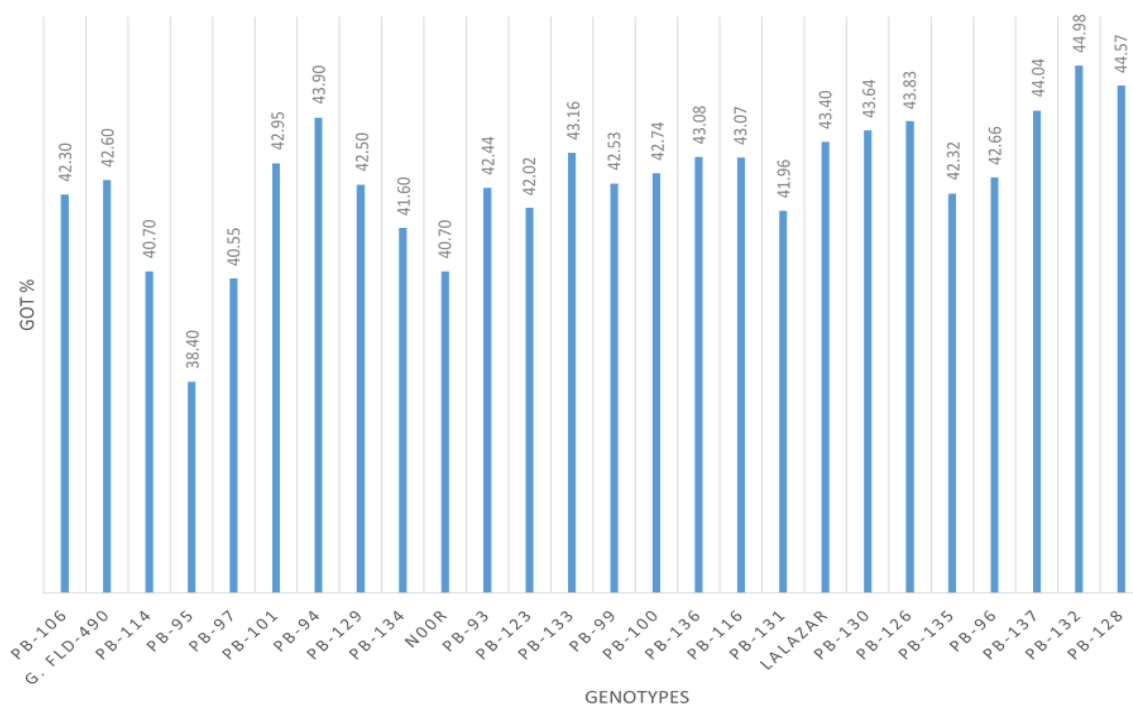


Fig. 4: Mean performances of 26 genotypes of cotton for GOT%.

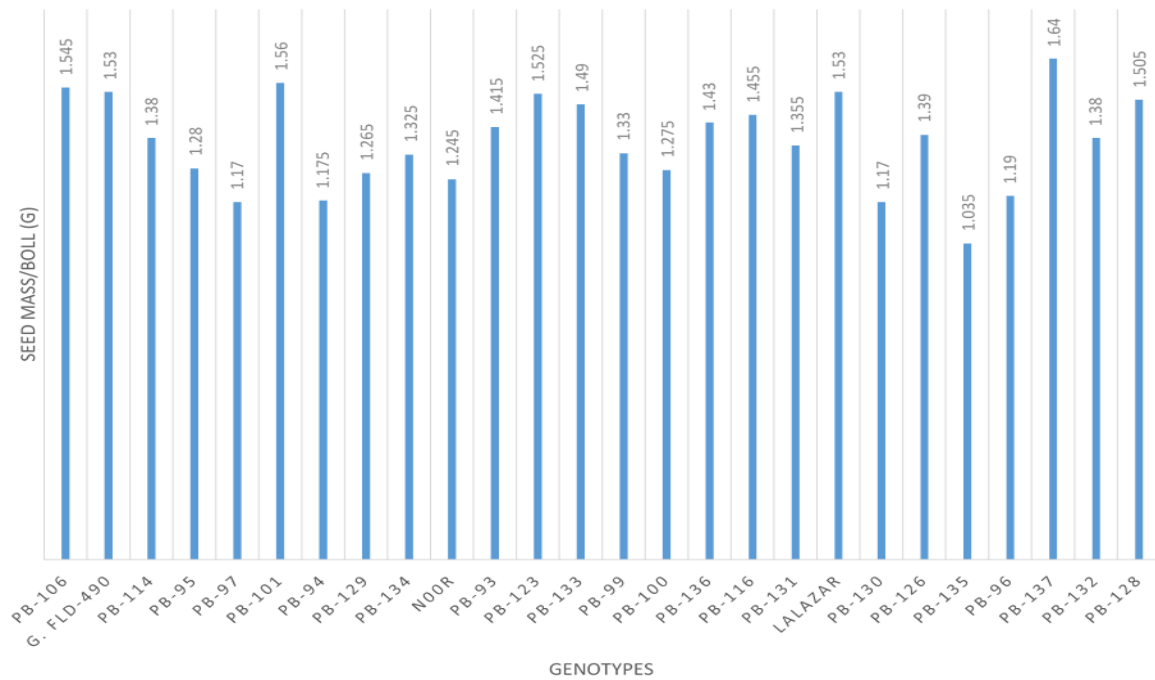


Fig. 5: Mean performances of 26 genotypes of cotton for seed per boll.

3.11. Fiber Fineness

The results revealed that genotypes were significantly different for the studied trait as shown in Table 1. Mean performance of genotypes for fiber fineness ranged from 4.85-to 3.91. Maximum values were depicted by PB-96 while Minimum by PB-95 (Fig. 10) Fiber Fineness displayed higher phenotypic variance as compared to genotypic variance. PCV was a bit higher than GCV indicating less influence from the environment. For Fiber Fineness, medium heritability estimates (56.85) were observed with a low genetic advance mean (7.76) % (Table 2). The genotypic variance was similar to environmental variance. It means this trait is highly influenced by the environment.

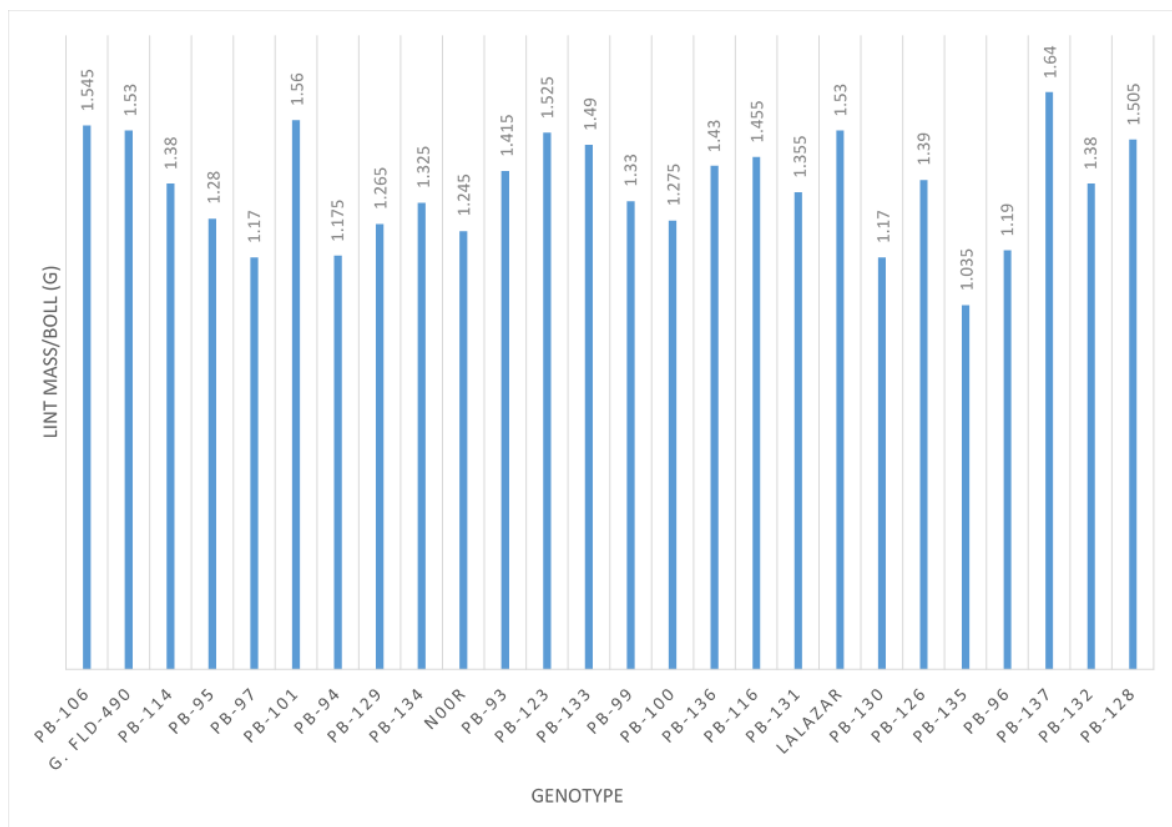


Fig. 6: Mean performances of 26 genotypes of cotton for seed per boll.

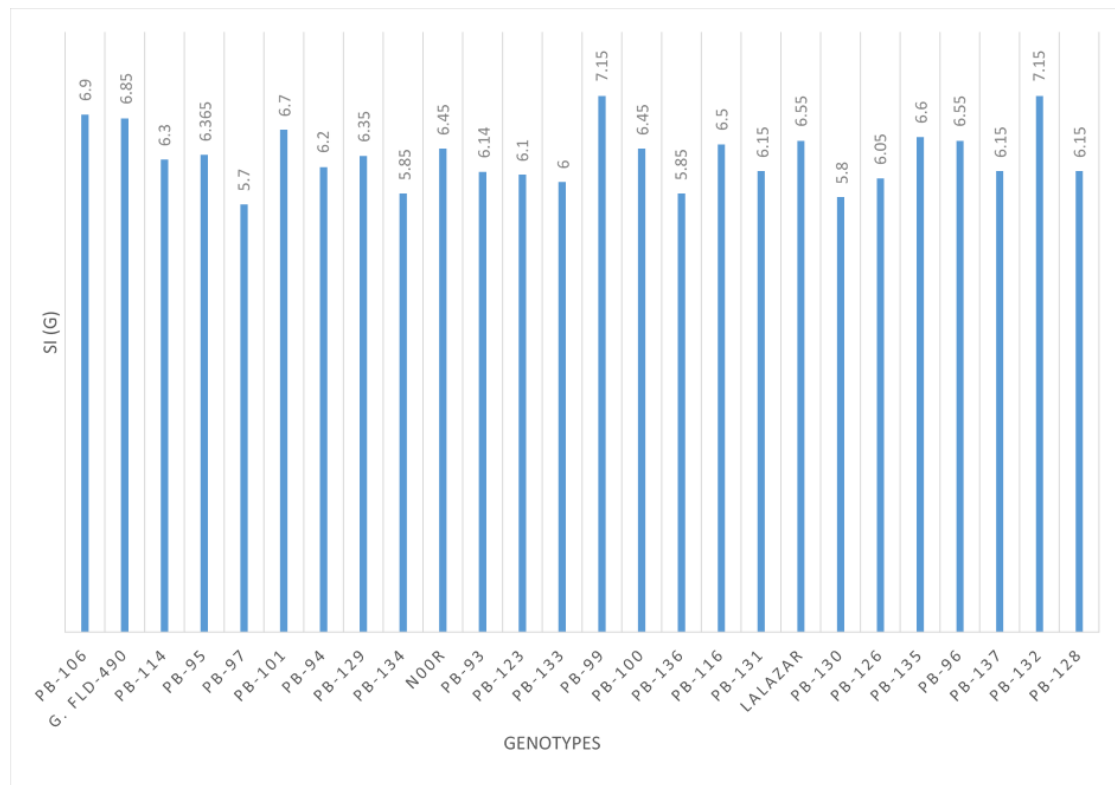


Fig. 7: Mean performances of 26 genotypes of cotton for SI.

3.12. Fiber Length

Fiber Length Mean square results from an investigation of variance depicted highly significant variation among genotypes for fiber length (Table 1). On the performance basis of mean values genotypes ranged from 30.62 to 27.45 as shown in Fig. 11. The GV was much higher than the genotypic Environmental variance which indicates low environmental influence than genotypic variability. Heritability estimates were also observed high with low GA percent of mean which shows that this trait is not beneficial for future breeding programs (Table 2).

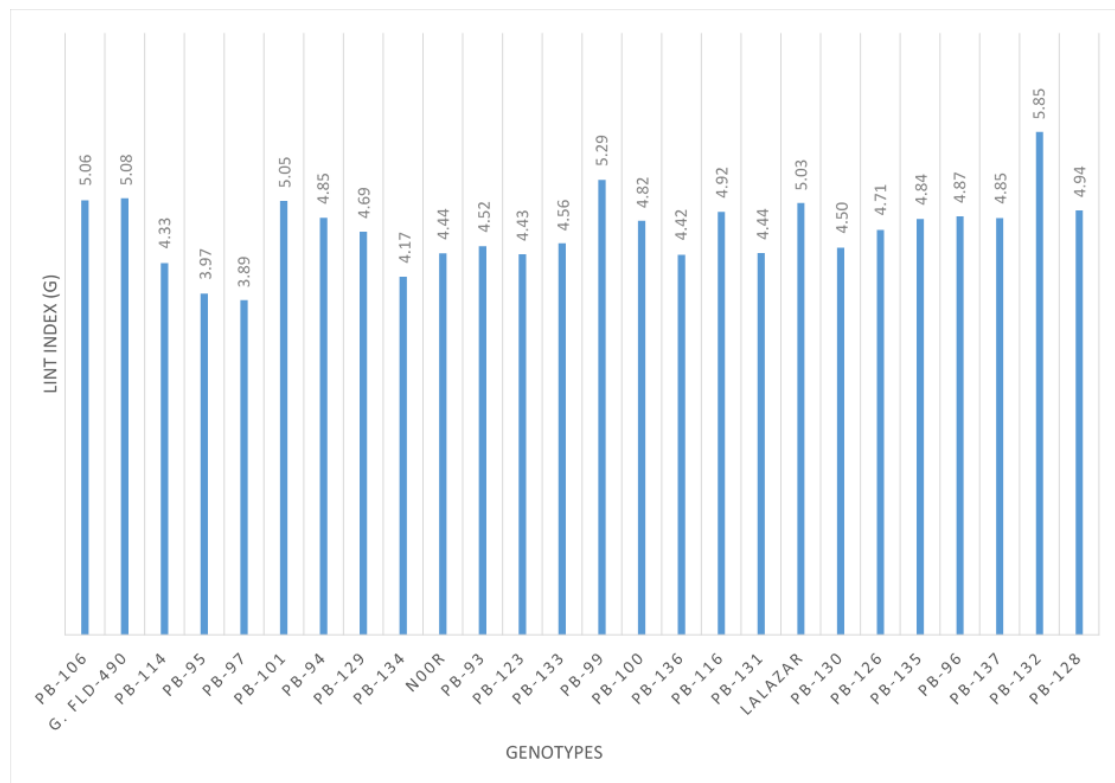


Fig. 8: Mean performances of 26 genotypes of cotton for lint index

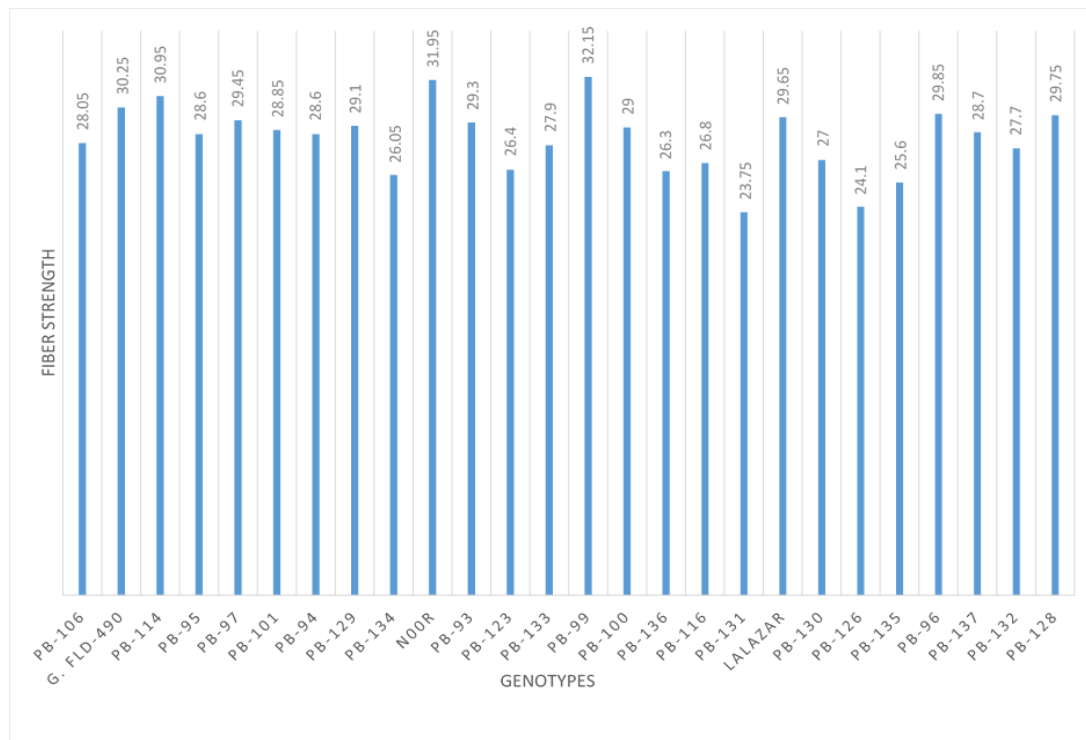


Fig. 9: Mean performances of 26 genotypes of cotton for fiber strength

3.13. Seed Volume

Mean square results from the investigation of variance depicted highly significant variation between genotypes for seed volume (Table 2). Mean square values for seed volume ranged from 6.00 to 11.50. The highest mean values were depicted by genotype PB-134 and the lowest by PB-132 as shown in Fig. 12. Phenotypic and genotypic variances were calculated high for seed volume as compared to environmental variance. PCV was a little higher than GCV indicating less environmental influence. Heritability in the broad sense was higher with maximum response to selection which indicates that selection of studied trait could be done (Table 2). Genotypes showed diverse significant results which predict the importance of this trait for further experiments with respect to yield components.

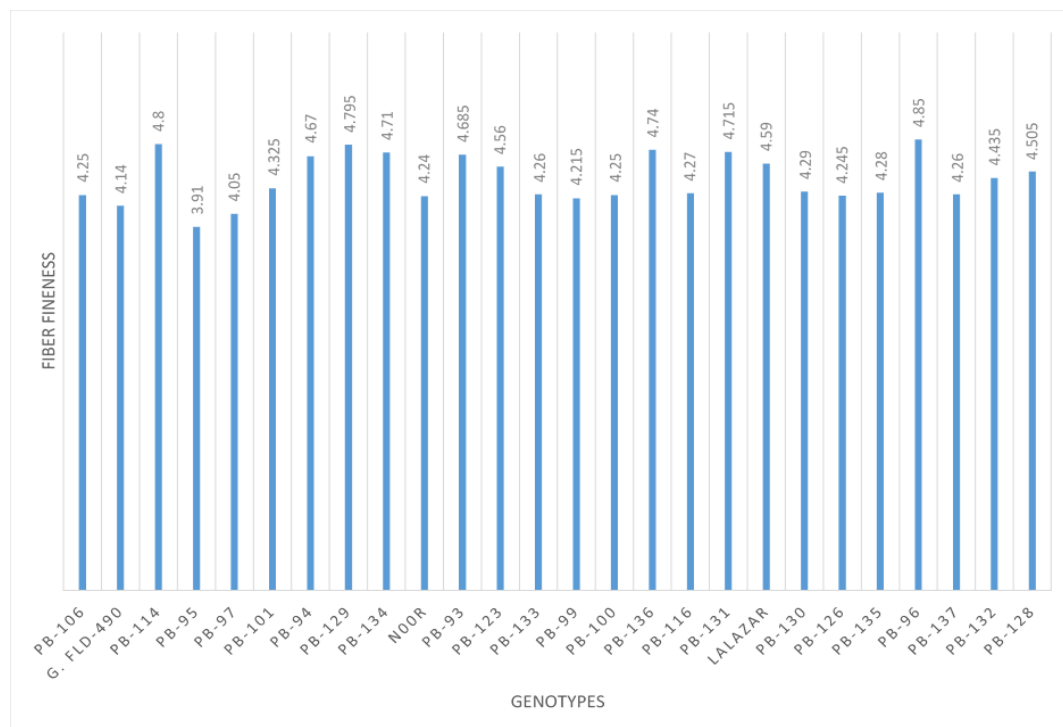


Fig. 10: Mean performances of 26 genotypes of cotton for fiber fineness

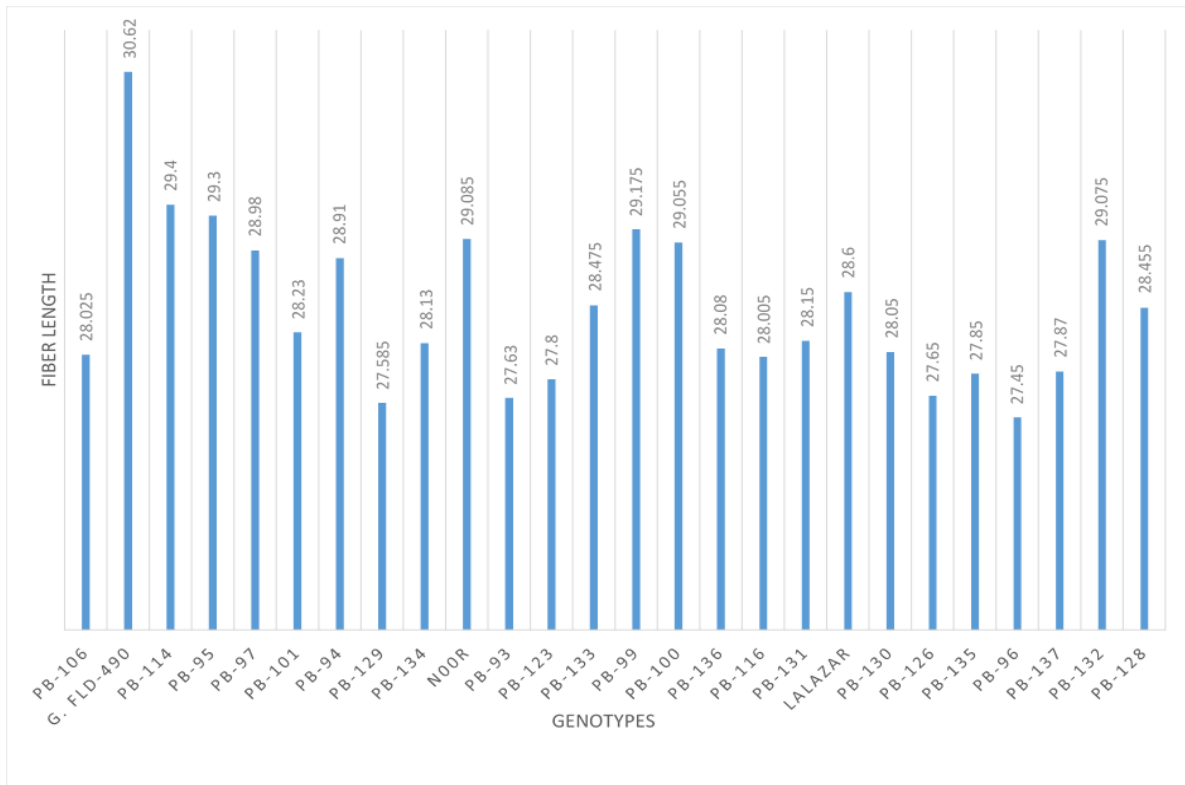


Fig. 11: Mean performances of 26 genotypes of cotton for fiber length

3.14. Seed Surface Area

Means square results from an investigation of anova value depicted significant variation among genotypes for seed surface area (Table 1). On the basis of the performance of mean values genotypes ranged from 1.39 to 1.79 as shown in Fig. 13. The GV was higher than the Environmental variance which indicates a low environmental effect on this trait. Heritability estimates were also showed high with a moderate genetic advance percent of mean which shows that this trait is beneficial for future breeding programs (Table 2).

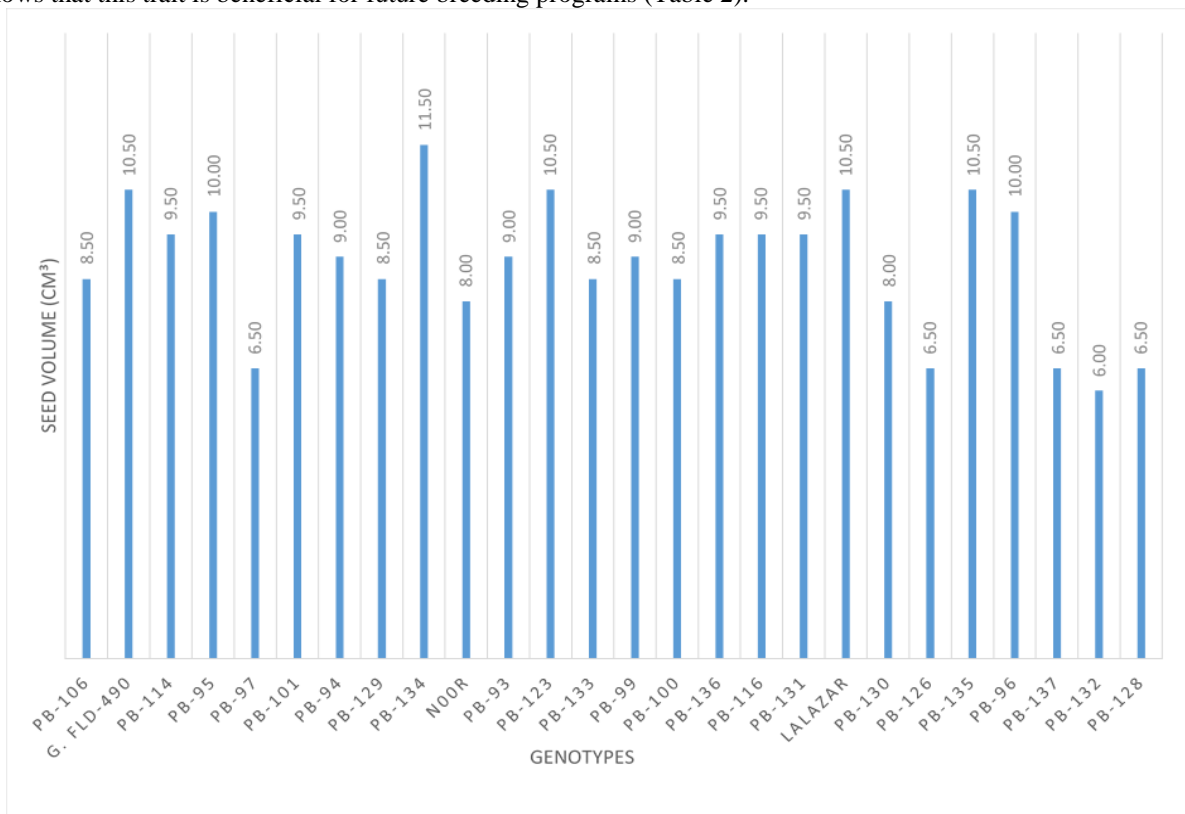


Fig. 12: Mean performances of 26 genotypes of cotton for seed per boll.

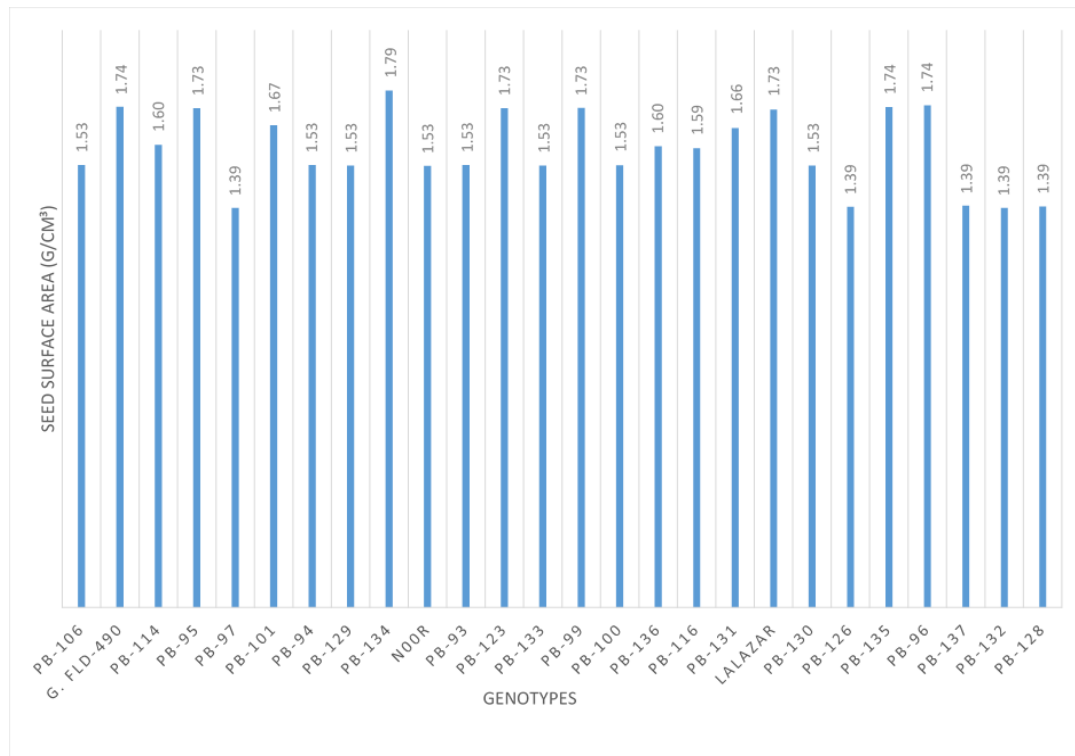


Fig. 13: Mean performances among 26 genotypes of cotton for seed surface area.

3.15. Seed density

Mean square results from the investigation of variance depicted highly significant variation among genotypes for seed density (Table 1). Mean square values for seed density ranged from 1.19 to 0.51. The highest mean values were depicted by genotype PB-132 and the lowest by PB-134 as shown in Fig. 14. Phenotypic and genotypic variances were calculated low for seed density as compared to environmental variance. PCV was a little higher than GCV indicating less environmental influence. Heritability in the broad sense was higher with maximum response to selection which indicates that selection of studied trait could be done (Table 2). Genotypes showed diverse significant results which predict the importance of this trait for further experiments with respect to yield components.

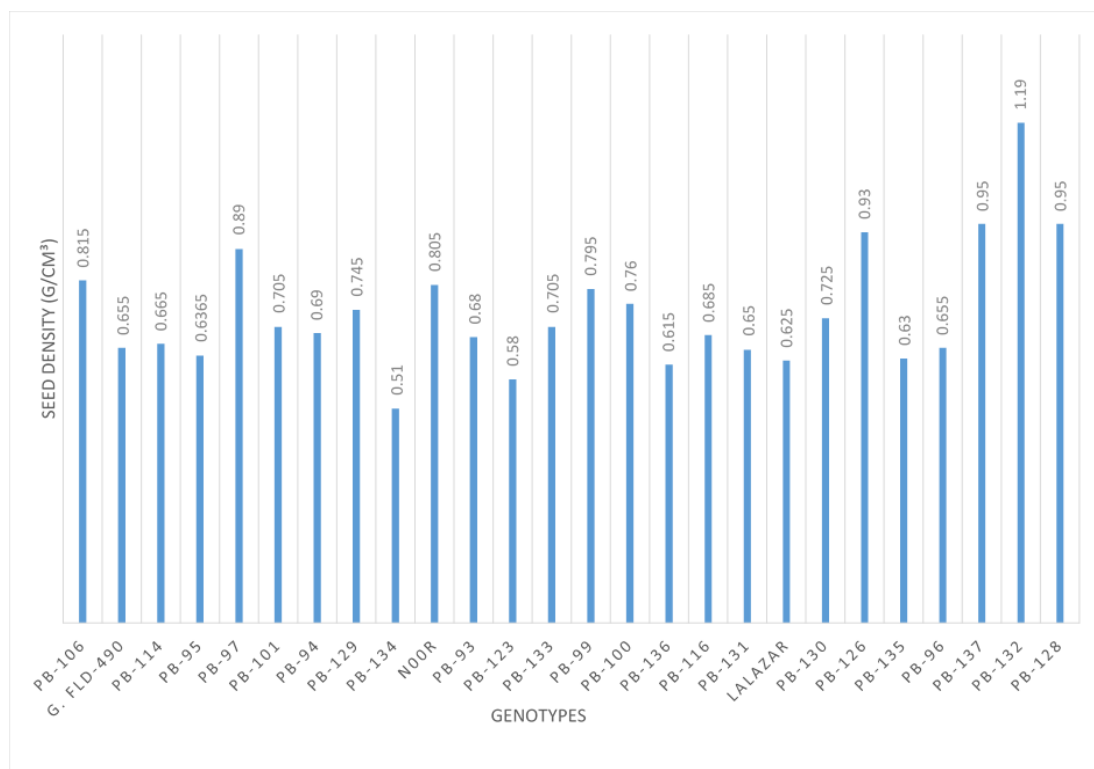


Fig. 14: Mean performances of 26 genotypes of cotton for seed density

Conclusion

The seed cotton yield, number of seeds per boll, boll weight, seed index, lint index, seed mass per boll, GOT %, seed volume, seed density, fiber length, fiber fineness, and fiber strength were highly heritable with high genetic advance. The genotype PB-132 had the best GOT %, lint index, mass per seed, and seed density. The current study showed that varied cotton bulks can produce high-yielding cultivars. This knowledge can improve cotton productivity and variety development through breeding.

REFERENCES

- Ashraf, I., Zuo, D., Wang, Q., Malik, W., Zhang, Y., Abid, M. A. and Song, G. (2018). Recent insights into cotton functional genomics: progress and future perspectives. *Plant Biotechnology Journal*, 16(3), 699-713.
- Jarwar, A. H., Wang, X., Iqbal, M. S., Sarfraz, Z., Wang, L., Ma, Q. and Shuli, F. I. P. I. B. (2019). Genetic divergence on the basis of principal component, correlation and cluster analysis of yield and quality traits in cotton cultivars. *Pakistan Journal Botony*, 51(3), 1143-1148.
- Komala, M., Ganesan, N. M. and Kumar, M. (2018). Genetic variability, heritability and correlation analysis in F2 populations of ratoon upland cotton hybrids. *International Journal of Agriculture, Environment and Biotechnology*, 11(6), 815-827.
- Kumar, C. P. S., Raju, S., Rajan, R. E. B., Muraleedharan, A. and Sujii, D. B. (2019). Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). *Plant Archives*, 19(1), 934-937.
- Kumbhar, Z. M., Jatoi, W. A., Sootaher, I. K., Baloch, M. I., Gadahi, A. A., Menghwar, K. K. and Kachi, M. (2020). Studies on correlation and heritability estimates in upland cotton (*Gossypium hirsutum* L.) genotypes under the agro-climatic conditions of Tandojam, Sindh, Pakistan. *Pure Appl Biology*, 2020; 9 (4): 2272-8.
- Naik, B. M., Satish, Y. and Babu, D. R. (2016). Genetic diversity analysis in American cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*, 7(4), 1002-1006.
- Nawaz, B., Sattar, S. and Malik, T. A. (2019). Genetic analysis of yield components and fiber quality parameters in upland cotton. *International Multidisciplinary Research Journal*, 9(9), 13-19.
- Rathinavel, K., Kavitha, H. and Priyadharshini, C. (2017). Assessment of genetic variability and correlation analysis of seed and seed cotton yield attributing traits of tetraploid cotton genotypes (*G. hirsutum* L.). *Electronic Journal of Plant Breeding*, 8(4), 1275-1283.
- Reddy, K. R., Koti, S., Davidonis, G. H. and Reddy, V. R. (2004). Interactive effects of carbon dioxide and nitrogen nutrition on cotton growth, development, yield and fiber quality. *Agronomy Journal*, 96(4), 1148-1157.
- Riaz, B., Saeed, A., Fiaz, S. and Riaz, A. (2019). Genetic diversity among Bt cotton (*Gossypium hirsutum* L.) germplasm assessed through morphological and within boll yield attributes. *Journal of Animal and Plant Sciences*, 29(1), 226-231.
- Shahzad, K., Li, X., Qi, T., Guo, L., Tang, H., Zhang, X. and Wu, J. (2019). Genetic analysis of yield and fiber quality traits in upland cotton (*Gossypium hirsutum* L.) cultivated in different ecological regions of China. *Journal of Cotton Research*, 2(1), 1-11.
- Shar, T., Baloch, M. I., Arain, M. A., Jatoi, W. A. and Lochi, R. (2017). Phenotypic associations, regression coefficients and heritability estimates for quantitative and fiber quality traits in upland cotton genotypes. *Pakistan Journal of Agriculture, Agricultural Engineering and Veterinary Sciences*, 33(2), 142-152.
- Tyagi, P., Bowman, D. T., Bourland, F. M., Edmisten, K., Campbell, B. T., Fraser, D. E. and Kuraparthi, V. (2014). Components of hybrid vigor in upland cotton (*Gossypium hirsutum* L.) and their relationship with environment. *Euphytica*, 195, 117-127.
- Zada, M., Zakir, N., Rabbani, M. A. and Shinwari, Z. K. (2013). Assessment of genetic variation in Ethiopian mustard (*Brassica carinata* A. Braun) germplasm using multivariate techniques. *Pakistan Journal Botony*, 45(S1), 583-593.