Jammu Kashmir J. Agri., 04 (02) 2024. 115-122
DOI: 10.56810/jkjagri.004.02.0161

Faculty of Agriculture, University of Poonch Rawalakot
Jammu Kashmir Journal of Agriculture
ISSN: 2958-3756 (Online), 2958-3748 (Print)
https://jkjagri.com/index.php/journal

SCREENING OF COTTON ADVANCED LINES ACROSS VARIOUS YEARS FOR FIBRE AND YIELD TRAITS

Liaquat Ali Bhutto, Babar Ali Shaikh

Agriculture Research Sindh, Tando Jam, Pakistan.

ABSTRACT

Cotton is a cash crop providing shelter and fiber around the globe. The superiority of the cotton crop lies in its fiber quality and yield performance. The present research was conducted in three consecutive years 2012, 2013, and 2014, respectively, to investigate the performance of various advanced cotton genotypes compared to local fiber and yield strength varieties. The experiment used a Randomized Complete Block Design with three replicates. Fiber quality and yield parameters were studied in this experiment. Significantly various years showed variability in the cotton advanced lines and performed very well in these consecutive years. Plant population and yield Kg/ha^{-1} exhibited significant results with $p<0.01$ and $p< 0.05$ probability level, while staple length and GOT% revealed non-significant. During 2012, TH-55/09 and TH-105/09 exhibited the maximum plant population compared to check varieties such as SINDH-1 and CRIS-134. However, TH-17/09 was observed to have the maximum plant population during 2013. During 2012 and 2014, GOT% exhibited greater in the genotype TH-17/09 (36.50% and 36.20%), respectively as compared to check varieties (SINDH-1 and CRIS-134). Similarly, the staple length was maximum in 2012, 2013, and 2014 in the genotype TH-17/09 (29.00, 29.30 and 29.00), respectively. Yield Kg/ha^{-1} observed to have variation in three years, TH-17/09 (4500) depicted higher yield as compared to other genotypes. However, TH-19/09, TH-55/09, and TH-55/09 proved to have greater yields also during 2012. Consequently, in the year 2013, the genotype TH-17/09 proved to have a higher yield of 5358.0 Kg/ha^{-1}. Almost all the genotypes performed very well though the yield Kg/ha^{-1} exhibited greater during 2013 than in other years. Correlation between yield and fiber characters revealed to have a significant positive relationship with each other. Hence, it is concluded that among the three consecutive years, the genotypes TH-17/09 performed best among the three years for fiber and quality traits.

Keywords: Plant Population, Got%, Fibre quality, Yield kg hectare^{-1}, Correlation.

Corresponding Author: Babar Ali Shaikh
Email: babarali987el@gmail.com

Article history
Received: June 10th, 2024
Revised: July 17th 2024
Accepted: July 23rd 2024

INTRODUCTION

Cotton is known as a “white gold” in cotton-productive countries, and it was grown over 33 million hectares in 2019 worldwide (Tarazi et al., 2019). Cotton is the prime natural fibre crop used in the textile industry, a source of edible oil, and cultivated in more than 80 countries/regions of the world (Li et al., 2019). Cotton (*Gossypium hirsutum* L.) is affiliated with the family *Malvaceae*, sub-family *hibiscaceae*, class Dicot, order Malva, and genus Gossypium. The genus *Gossypium* consists of 50 cultivated and wild species. Cotton is successfully planted as an annual crop in tropical and sub-tropical regions/areas of Pakistan. Cotton is chief an important fibre and cash crop and is also used as an oilseed crop in different countries of the world and uplifts the economic level of Pakistan (Riaz et al., 2013) numbers number of people grow the cotton crop and engage their fields for cotton crop. Cotton consumption is increasing day by day, corresponding to a tremendous increase in population around the globe (FAO, 2018). Pakistan is known to be an agricultural country and contributes the second most important crop with a significant role in its economy.

The production of cotton contributed 0.8% of the overall GDP and an additional 4.5% in agriculture value addition (Rehman et al., 2022). During the year 2018–2019, a decrease of 17.5% was seen with an overall production of 9

861 million bales versus 11 946 million bales in the year 2017–2018. Decreasing in cotton production was due to the decrease in incentives to the farmers compared to the previous year, leading to the shrinkage in cultivation area from 2,700 thousand to 2,373 thousand hectares (Economy Survey of Pakistan 2018–2019). There are many nations with a history of cotton germplasm production and cultivation such as China, Brazil, the United States, India and Pakistan (Robinson et al., 2007).

G. *arboreum* is indigenous to Pakistan and has culminated from G. *herbaceum* L. (Hutchinson, 1954). These types of species have been characterized by morphological, agronomical and physiological features showing tolerance against drought and insect/pest. Pakistan is one of the most significant countries of cotton production, exportation, and consumption in the world. Cotton is widely planted in several regions of Pakistan, including Punjab and Sindh provinces are the main growing belts, and Punjab is the main province in terms of the total cultivated area and the total production of cotton bales (Shuli et al., 2018). The relationship between both factors makes the difficult procedure for desirable cotton varieties. The knowledge of linkages between seed cotton yield and its allied traits supports breeders in obtaining the desirable genotypes.

To accomplish desirable cotton genotypes the correlation analysis provides good knowledge to visualize the consistent change which occurs in in one character and the proportional change that occurs in other parameters (Ahmad et al., 2008). The correlation mechanism governs cause and effect relation and direct and indirect effects of plant traits which provide the relative importance of each causal character to construct selection criteria to identify better early maturing combinations from segregating populations. Correlation study is an important distinction to breeders which yield characters that are related to each other. An increase in ginning outturn % may result in the reduction of staple length (Soomro et al., 2008).

MATERIALS AND METHODS

The present research/experiment was conducted during the consecutive Kharif season of 2012, 2013, and 2014 at the cotton section (Agriculture Research Institute) Tando Jam. The experimental design used Randomized Complete Block Design (RCBD) within Three Replication. The current research was conducted on six genotypes TH-17/09, TH-19/09, TH-55/09, TH-88/11, TH-96/09, TH-105/09 of cotton along with two check varieties SINDH-1, and CRIS-134. Observations were recorded of morphological characters, plant: pop/ha^{-1}, GOT%, staple length (mm), and yield Kg/ha^{-1}. The data was analysed by Gomez and Gomez (1984) using statistix 8.1. The least significant difference (LSD) was evaluated at a 5% probability level and correlation was estimated by Raghavrao (1983).

RESULTS

Cotton is a wide crop grown for fibre and shelter purposes. The present research investigated different cotton advance lines for various quantitative and qualitative characters. The results revealed significant differences among most of the characters. Plant population depicted significant results for years, genotypes, and interaction at $p<0.01$ probability level. GOT% and staple length were observed to have non-significant results for years, genotypes, and interaction. Besides yield Kg/ha^{-1} depicted significant results at $p<0.05$ probability level. These results showed that there is no variation between GOT% and staple length.

Mean Performance

Significant results were obtained for plant population year-wise for 2012, 2013, and 2014. The plant population showed maximum mean performance for various genotypes and different years. During the year 2012, the genotypes TH-55/09 (51209) and TH-105/09 (49525) exhibited maximum plant population compared to check varieties as SINDH-1(49491) and CRIS-134 (49408) and minimum performance TH-19/09 (48710) was found in these genotypes. Similarly, during the year 2013, most of the genotypes showed similar performance, however, TH-17/09 (47060) was revealed to have the maximum plant population during this year. Consequently, in 2014 all the genotypes showed similar results as compared to check varieties. GOT% showed variation during three consecutive years among genotypes. During the year 2012, greater GOT% was observed in the genotypes TH-17/09 (36.500) and TH-96/09 (36.020), respectively. Similarly, in 2013 GOT% was observed greater in TH-88/11 (38.200) and TH-96/09 (37.900). However, in 2014, TH-17/09 exhibited a greater GOT% of (36.500%). Staple length was revealed to have significant variation towards three consecutive years. Maximum staple length in 2012 was found in the genotype TH-17/09 (29.00). Consequently, TH-17/09 and TH-55/09 (29.30 and 29.00) showed maximum staple length during 2013. During 2014, the staple length was greater in the genotype TH-17/09 (29.00). Yield is a complex character responsible for many quantitative traits. During 2012, the yield performed with significant variability. The genotype TH-17/09 (4500) was observed to have maximum yield as compared to other genotypes. However, TH-19/09 (4000) and TH-55/09 (4038) proved to have greater yields also during this year. Similarly, in 2013 the yield Kg/ha^{-1} varied significantly. Maximum yield was observed in the genotype TH-17/09 as (5358) Kg/ha^{-1}. While other genotypes during 2014 performed maximum yield TH-17/09 (4825) and remaining obtained similar yields. There was also not much difference in the year 2014, among the genotypes for this trait. However, almost all the genotypes performed very well as having high yield Kg/ha^{-1}. The yield Kg/ha^{-1} exhibited greater during 2013 as compared to other years. However, GOT% was also found to be higher in the years 2013 and 2014. These characters are correlated with each other by having more yield and GOT% (Figure 1-4).

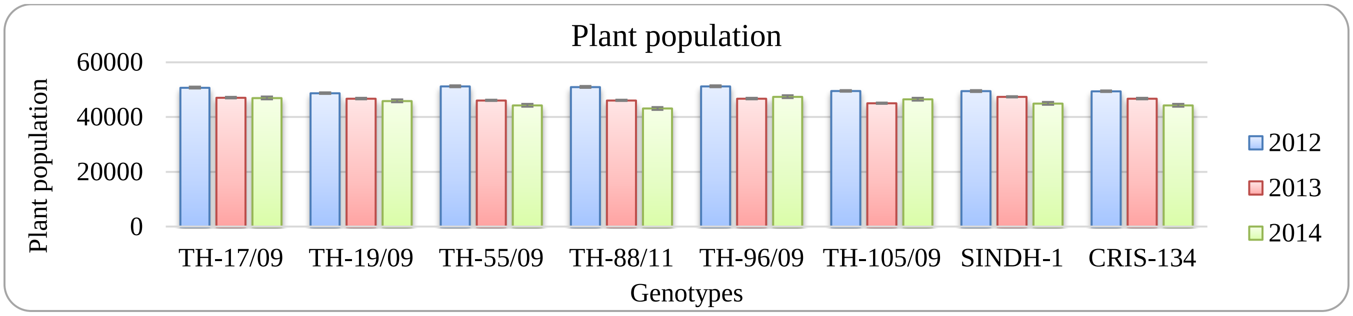

Figure 1. Performance of advanced genotypes in various years for plant population.

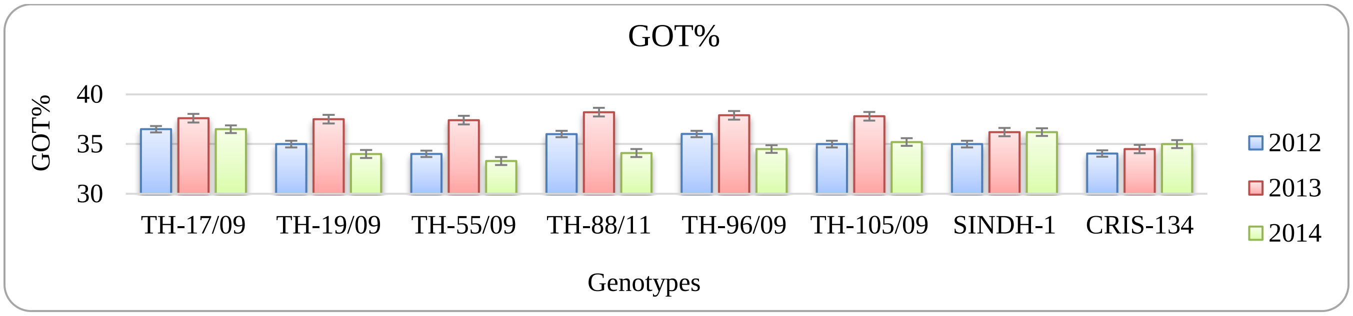

Figure 2. Performance of advanced genotypes in various years for GOT%.

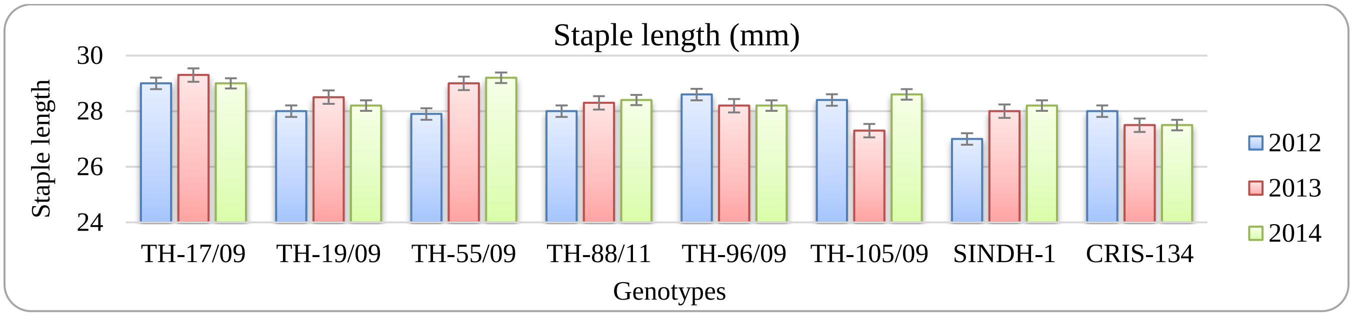

Figure 3. Performance of advanced genotypes in various years for staple length.

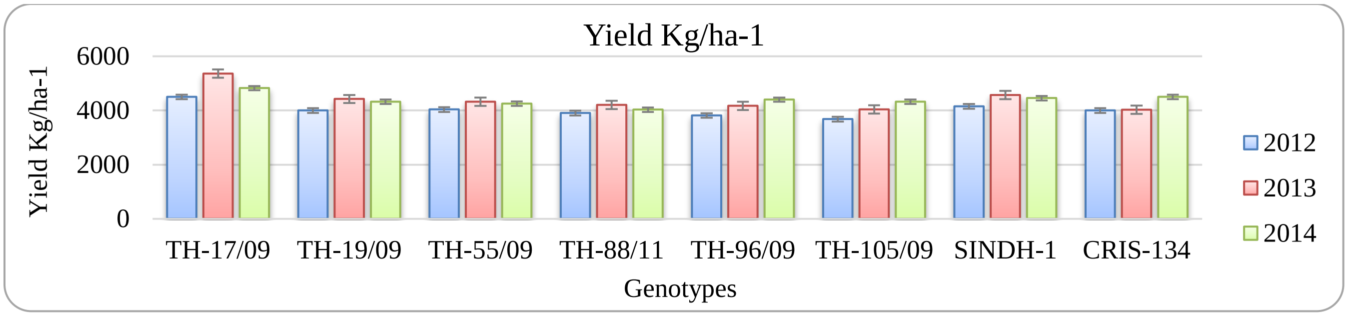

Figure 4. Performance of advanced genotypes in various years for yield Kg hectare^{-1}.

Correlation between Quality and Quantity Parameters

The correlation between various quantitative and qualitative characters depicted a significant association with yield Kg/ha^{-1}. Plant population was observed to have a positive and significant association with yield Kg/ha^{-1} (r=0.145**), respectively. Similarly, GOT% also showed a significant and positive relationship with yield kg ha^{-1} (r=0.498**). Also, staple length depicted a positive and significant correlation with yield kg ha^{-1} (r=0.498**) (Figure 5).

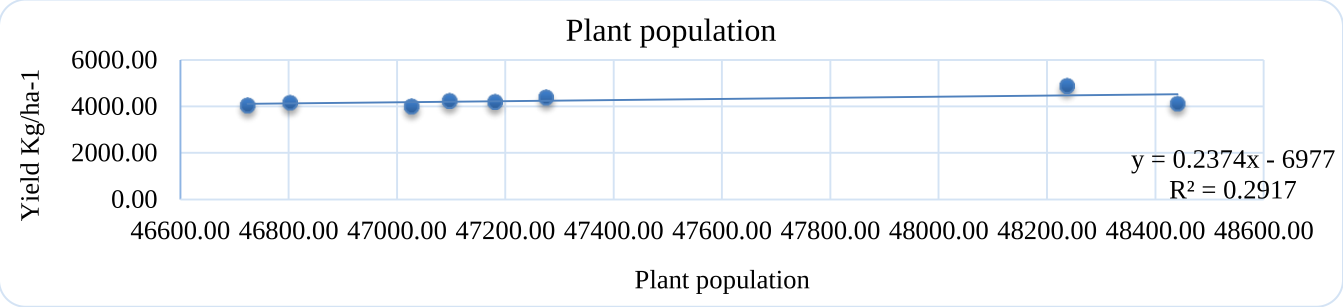

Figure 5. Correlation between Plant population vs Yield Kg/ha^{-1}.

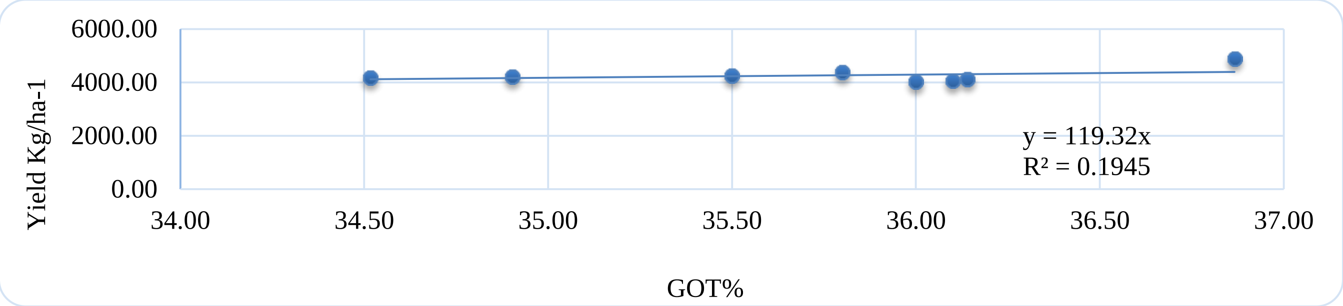

Figure 6. Correlation between GOT% vs Yield Kg/ha^{-1}.

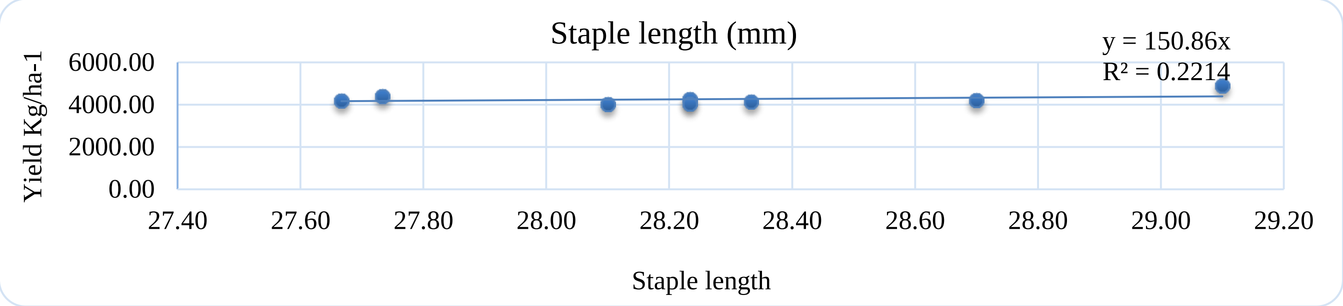

Figure 7. Correlation between Staple vs Yield Kg/ha^{-1}.

DISCUSSION

Cotton is an important fibre crop for humans and animals, providing shelter and meals (Shahzad et al., 2019). This crop evolved for fine thread by maintaining staple length, fibre fineness, and GOT% of the crop species (Li et al., 2019). The present research was conducted for quality and quantitative characteristics such as plant population, GOT%, staple length and Yield Kg/ha^{-1}. Various years as 2012, 2013, and 2014 were studied for these traits and compared their significant variation towards yield performance and quality characters. The analysis of variance depicted that plant population was significant for p<0.01 for years, genotypes, and interaction. GOT% and staple length showed non-significant results for years, genotypes, and interaction. However, yield Kg/ha^{-1} was revealed to have significance at p<0.05 probability level. These results agreement with (Rehman et al., 2022; Sahito et al., 2016b) showed that all the growth and yield components of cotton were significantly (P < 0.01) affected by varieties and years except for monopodial branches and staple length.

Plant population exhibited variable significant differences among the genotypes in various years as 2012, 2013, and 2014. It seems that during 2012 TH-17/09, TH-55/09, TH-88/11 and TH/96/09 depicted more plant population as compared to check variety. In the years 2013 and 2014, the genotypes showed almost similar plant populations in the genotypes. These results are in agreement with (Monisha, 2018) who also exhibited a greater plant population in cotton. GOT% was obtained greater in the year 2013 in which almost all the genotypes showed more GOT% as compared to check variety SINDH-1 and CRIS-134. However, for GOT%, the genotype TH-88/11 obtained has maximum GOT% as compared to other genotypes during the year 2013. Rehman et al. (2022) also obtained more GOT% in newly evolved genotypes. Monicashree and Balu (2018), observed that GOT had a positive linkage with plant height, the number of sympodial branches per plant and the yield of seed cotton.

Staple length was observed greater among the genotypes during the year 2014 with improved lines of cotton as compared to check varieties (SINDH1 and CRIS-134). During the year 2014, TH-17/09 and TH-55/09 attained larger staple lengths of 29cm, though other genotypes/lines proved to have greater staple lengths of 28cm as compared to check varieties. Similarly, in 2013, the genotypes TH-17/09 and TH-55/09 were found to have more staple length of 29 cm and exhibited 29 cm in 2012 (TH-17/09), respectively. These results showed that these lines performed incredibly very well in the case of staple length, GOT% and Yield Kg/ha^{-1} and may be suggested for further selection programs. Sahito et al. (2016a) claimed that staple length could vary from variety to variety and different seasons and growing conditions of cultivars.

Yield/hectare was declared to have a positive response during the years 2013 and 2014 having high yields among advance lines. Almost all the genotypes performed very well. However, it was found that the TH-17/09 genotype profoundly performed better among the genotypes during 2012 and 2013. This may be due to good characters depicted in the genotypes during different years of selection. Such genotypes can be useful for engaging farmers for yield and profit towards thread marketing and other businesses through high-yield cotton genotypes. Yield was contributed greater in various genotypes as dependent on fibre and quality parameters (Rehman et al., 2022).

The correlation analysis between various quantitative and qualitative parameters depicted a significant and positive correlation with yield Kg/ha^{-1}. Association analysis revealed that seed cotton yield had a significant positive correlation with GOT, staple length and fibre strength (Rehman et al., 2022). Investigations revealed the association and inheritance for various quantitative and fibre-related parameters of American cotton (Haq et al., 2017).

Hence, it has been overviewed from the results that the genotype TH-17/09 displayed positive characteristics towards quality and yield. This genotype may be useful for farmers as well as industrial companies for thread and cloth making. It would be fruitful if we would bring good quality cotton genotypes for yield and fibre.

CONCLUSION

During 2012 and 2013, the genotypes TH-55/09 and TH-105/09 exhibited greater plant population and staple length. Similarly, TH-17/09 was observed to have more plant population, GOT% and staple length yield kg^{-1} during 2013. TH-17/09 also performed well for yield kg/hectare during 2014. It is recommended that the TH-17/09 genotype will be able to enhance more plant population ha^{-1}, GOT%, staple length (mm) yield kg ha^{-1} for the next generation or experimental trial for researchers in the field.

CONFLICT OF INTEREST

The authors declare that there is no conflict in the publication of this article.

AUTHOR’S CONTRIBUTION

All the authors contributed equally in the manuscript.

REFERENCES

Ahmad, W., Khan, N., Khalil, M., Parveen, A., Saeed, M., Shah, S., 2008. Genetic variability and correlation analysis in upland cotton. Sarhad Journal of Agriculture 24, 573-580.

FAO, 2018. A global repository for harmonised individual quantitative food consumption studies. Food and Agriculture Organisation.

Gomez, K.A., Gomez, A.A., 1984. Statistical Procedures for Agricultural Research. John Wiley and Sons.

Haq, A., Khan, N., Raza, H., Gul, S., Akbar, S., Khan, S., Muhammad, S., Ali, M., Khan, H., Khan, S., 2017. Genetic attributes of F3 populations and their parental lines in upland cotton. Journal of Animal and Plant Sciences 27, 655-666.

Hutchinson, J.B., 1954. New evidence on the origin of the old world cottons. Heridity 8, 225–241.

Li, X., Shahzad, K., Guo, L., Qi, T., Zhang, X., Wang, H., Tang, H., Qiao, X., Zhang, J., Wu, J., 2019. Using yield quantitative trait locus targeted SSR markers to study the relationship between genetic distance and yield heterosis in upland cotton (*Gossypium hirsutum*). Plant Breeding 138, 105-113.

Monicashree, C., Balu, P.A., 2018. Association and path analysis studies of yield and fibre quality traits in intraspecific hybrids of upland cotton (*Gossypium hirsutum* L.). Research Journal of Agricultural Sciences 9, 1101-1106.

Monisha, K., 2018. Genetic variability and correlation studies in upland cotton (*Gossypium hirsutum* L.). Electronic Journal of Plant Breeding 9, 1053-1059.

Raghavrao, D., 1983. Design of Experiment Statistical Techniques in Agricultural and Biological Research. Oxford and IBM Publishing Company, New Delhi, India.

Rehman, H., Farooq, U., Bhutta, M., Ahmad, S., Akram, M., Shahid, M., Hussnain, H., Shahid, M., Iqbal, M., Raza, A., 2022. Genetic variability and performance of cotton (*Gossypium hirsutum* L.) genotypes for yield related agro-morphologic and fiber quality traits under water deficit natural environment. Sarhad Journal of Agriculture 38, 657-668.

Riaz, M., Farooq, J., Sakhawat, G., Mahmood, A., Sadiq, M., Yaseen, M., 2013. Genotypic variability for root/shoot parameters under water stress in some advanced lines of cotton (*Gossypium hirsutum* L.). Genetics and Molecular Research 12, 552-561.

Robinson, A., Bell, A., Dighe, N., Menz, M., Nichols, R., Stelly, D., 2007. Introgression of resistance to nematode Rotylenchulus reniformis into upland cotton (*Gossypium hirsutum*) from *Gossypium longicalyx*. Crop Science 47, 1865-1877.

Sahito, J.H., Gao, S., Nie, Z., Abro, S., Channa, S.A., Wahocho, N.A., 2016a. Correlation analysis of yield and fiber traits in upland cotton (*Gossypium hirsutum* L.). American-Eurasian Journal of Agricultural and Environmental Sciences 16, 1358-1361.

Sahito, J.H., Gao, S., Rao, S.H., Abro, S., Channa, S.A., Baloch, A.W., Wahocho, N.A., 2016b. Association of quantitative traits in upland cotton (*Gossypium hirstum* L.). Journal of Applied Environmental and Biological Sciences 6, 8-12.

Shahzad, K., Li, X., Qi, T., Guo, L., Tang, H., Zhang, X., Wang, H., Zhang, M., Zhang, B., Qiao, X., 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, 1-11.

Shuli, F., Jarwar, A.H., Wang, X., Wang, L., Ma, Q., 2018. Overview of the cotton in Pakistan and its future prospects. Pakistan Journal of Agricultural Research 31, 396.

Soomro, Z., Larik, A., Khan, N., Baloch, M., Mari, S., Memon, S., Panhwar, N., 2008. Genetic variability studies on quantitative traits in upland cotton. Sarhad Journal of Agriculture 24, 202-205.

Tarazi, R., Jimenez, J.L.S., Vaslin, M.F., 2019. Biotechnological solutions for major cotton (*Gossypium hirsutum*) pathogens and pests. Biotechnology Research and Innovation 3, 19-26.

DOI: 10.56810/jkjagri.004.02.0161

Appendix

Table 1. Combined analysis of variance among qualitative and quantitative traits.

Source of variation	DF	Plant pop/ha	GOT%	Staple length (mm)	Yield kg/ha
Replication	3	4020.08	215.522	35.3686	1424614
Years	2	5343553**	48.624^{NS}	0.7200^{NS}	1517049*
Genotypes	7	4920679**	6.657^{NS}	2.6760^{NS}	950559*
Year x Genotypes	14	4936733**	3.746^{NS}	0.8495^{NS}	124599^{NS}
Pooled error	69	2440.52	64.592	56.7663	493479

**,*= Significant at P<0.01 and P<0.05probability level, ns. = Non-significant

Table 2. Mean performance of Interaction between years and genotypes among various quantitative and qualitative characters for plant population.

GENOTYPES	YEAR-WISE MEAN PERFORMANCE FOR PLANT POPULATION		
	2012	2013	2014
TH-17/09	50704	47060	46945
TH-19/09	48710	46724	45857
TH-55/09	51209	46057	44275
TH-88/11	50955	46057	43160
TH-96/09	51207	46724	47392
TH-105/09	49525	45059	46497
SINDH-1	49491	47392	44942
CRIS-134	49408	46724	44275
Average	44802.3333	41534.4	40595.2
LSD 5%	Year=24.638	Genotypes=40.234	Year x Genotypes=69.688

**,*= Significant at P<0.01 and P<0.05probability level, ns. = Non-significant

Table 3. Mean performance of Interaction between years and genotypes among various quantitative and qualitative characters for GOT%.

GENOTYPES	YEAR-WISE MEAN PERFORMANCE FOR GOT%		
	2012	2013	2014
TH-17/09	36.500	37.600	36.500
TH-19/09	35.000	37.500	34.000
TH-55/09	34.010	37.400	33.300
TH-88/11	36.000	38.200	34.100
TH-96/09	36.020	37.900	34.500
TH-105/09	35.000	37.800	35.200
SINDH-1	35.000	36.200	36.200
CRIS-134	34.050	34.500	35.000
Average	254.842	256.678	254.756
LSD 5%	Year=4.0083	Genotypes=6.5455	Year x Genotypes=11.337

**,*= Significant at P<0.01 and P<0.05probability level, ns. = Non-significant

Table 4. Mean performance of Interaction between years and genotypes among various quantitative and qualitative characters for staple length

GENOTYPES	YEAR-WISE MEAN PERFORMANCE FOR STAPLE LENGTH		
	2012	2013	2014
TH-17/09	29.000	29.300	29.000
TH-19/09	28.000	28.500	28.200
TH-55/09	27.900	29.000	29.200
TH-88/11	28.000	28.300	28.400
TH-96/09	28.600	28.200	28.200
TH-105/09	28.400	27.300	28.600
SINDH-1	27.000	28.000	28.200
CRIS-134	28.000	27.500	27.500
Average	248.544444	248.789	249.033
LSD 5%	Year=3.7577	Genotypes=6.1362	Year x Genotypes=10.628

**,*= Significant at P<0.01 and P<0.05probability level, ns. = Non-significant

Table 5. Mean performance of Interaction between years and genotypes among various quantitative and qualitative characters for yield.

GENOTYPES	YEAR-WISE MEAN PERFORMANCE FOR YIELD KG HECTARE^{-1}		
	2012	2013	2014
TH-17/09	4500.0	5358.0	4825.0
TH-19/09	4000.0	4424.0	4320.0
TH-55/09	4038.0	4320.0	4250.0
TH-88/11	3905.0	4203.0	4031.0
TH-96/09	3814.0	4170.0	4400.0
TH-105/09	3680.0	4037.0	4321.0
SINDH-1	4150.0	4567.0	4457.0
CRIS-134	4000.0	4024.0	4501.0
Average	3788.77778	4124	4124.33
LSD 5%	Year=350.35	Genotypes=572.12	Year x Genotypes=990.95

**,*= Significant at P<0.01 and P<0.05probability level, ns. = Non-significant

Correlation analysis among qualitative and quantitative traits

Characters	Plant population	Got%	Staple length	Yield kg/ha^{-1}
Plant population	1.0000**	1		
Got%	-0.0094^{NS}	1.0000**	1	
Staple length	-0.0064^{NS}	0.1232^{NS}	1.0000**	1
Yield kg/ha^{-1}	-0.1435^{NS}	0.1443^{NS}	0.1253^{NS}	1.0000**

**,*= Significant at P<0.01 and P<0.05probability level, ns. = Non-significant