



DOI: <https://doi.org/10.71317/kjard.2.7.2026.463>

The Kashmir Journal of Academic Research and Development

Journal homepage: <https://rjsaonline.org/index.php/KJARD>



Performance Assessment of F₃ Cotton Progenies for Morphological, Yield, and Fiber Quality Traits

Nadia Sipio

Department of Plant Breeding & Genetics, Sindh Agriculture University, Tandojam

Abdul Wahid Baloch

Department of Plant Breeding & Genetics, Sindh Agriculture University, Tandojam

Tanveer Fatah Abro

Department of Plant Breeding and Genetics, Sindh Agriculture University Tando Jam

Zaheer Ahmed Deho

Nuclear Institute of Agriculture, NIA, Tandojam

Maahnoor Arain

Department of Plant Breeding & Genetics, Sindh Agriculture University, Tandojam

Madeeha Memon

Department of Plant Breeding & Genetics, Sindh Agriculture University, Tandojam

Shayhaq Sayed

Government of Balochistan Agriculture Cooperatives Department Agriculture Extension Date Farm, Turbat

Shahzaib Kaleri

Department of Plant Breeding & Genetics, Sindh Agriculture University, Tandojam

Email: shahzaibkaleri346@gmail.com

ARTICLE INFO

Received:

June 04, 2026

Revised:

June 21, 2026

Accepted:

July 07, 2026

Available Online:

July 19, 2026

Keywords:

Cotton, F₃ progenies, agronomic traits, fiber quality, seed cotton yield, phenotypic evaluation.

Corresponding Author:

Shahzaib Kaleri

Email:

shahzaibkaleri346@gmail.com

ABSTRACT

Developing high-yielding cotton cultivars with superior fiber quality depends on identifying promising breeding materials through phenotypic evaluation. This study evaluated agronomic, yield, and fiber quality traits in eight F₃ cotton (*Gossypium hirsutum* L.) progenies and their twelve parental genotypes under field conditions at the Nuclear Institute of Agriculture (NIA), Tandojam, Pakistan, during the Kharif 2025 season. The experiment followed a randomized complete block design with three replications. Data recorded for plant height, sympodial branches per plant, bolls per plant, boll weight, seed index, ginning outturn (GOT), staple length, micronaire value, and seed cotton yield per plant. Analysis of variance revealed highly significant differences among genotypes for most of the studied traits, indicating substantial phenotypic variability. Among the parental lines, NIA-95, M-35, and M-23 exhibited superior performance for several yield-related traits. Among the F₃ progenies, NIA-Noori × M-35 produced the highest seed cotton yield (234.09 g plant⁻¹), followed by Sohni × NIAB-878 (230.64 g plant⁻¹) and Sadori × ZAD-1 (229.56 g plant⁻¹). These crosses also demonstrated superior performance for important agronomic and fiber quality traits, including plant height, boll number, boll weight, and ginning outturn. The results indicate that these F₃ populations have considerable breeding potential and may serve as valuable genetic resources for developing improved cotton cultivars with enhanced yield and fiber quality.

Introduction

Cotton (*Gossypium hirsutum* L.) is one of the world's most important natural fiber crops and plays a vital role in the textile industry and agricultural economy. Owing to its economic importance, cotton is widely cultivated across tropical and subtropical regions, contributing significantly to employment, industrial development, and foreign exchange earnings (Abro et al., 2021 and Bano et al., 2017). In Pakistan, upland cotton occupies the major share of cultivated cotton area because of its high yield potential and superior fiber quality compared with indigenous cotton species (Asim et al., 2024). Increasing seed cotton yield while maintaining desirable fiber quality remains a major objective of cotton breeding programs. However, simultaneously improving yield and quality traits is challenging because these characteristics are quantitatively inherited and influenced by both genetic and environmental factors. Therefore, evaluating segregating populations is essential for identifying superior recombinants that combine favorable agronomic performance with acceptable fiber characteristics (Raza et al., 2023 and Baloch et al., 2017). The F₃ generation is an important stage in plant breeding because segregation continues while homozygosity gradually increases, allowing superior lines to be identified more accurately than in earlier generations (Ahmed and Hussain, 2020). Evaluating F₃ progenies allows breeders to select promising genotypes based on agronomic performance, yield components, and fiber quality before advancing them to later generations (Tariq et al., 2022). Comparative assessment of parental lines and segregating progenies also facilitates the identification of transgressive segregants that outperform both parents. Phenotypic evaluation of morphological, yield, and fiber quality traits remains one of the most reliable approaches for selecting elite breeding materials in cotton improvement programs (Wang, 2024). Traits such as plant height, sympodial branches, boll number, boll weight, seed index, ginning outturn, staple length, micronaire value, and seed cotton yield collectively determine the commercial value of a cotton genotype (Waheed et al., 2021). Therefore, simultaneous assessment of these traits is necessary for effective selection. This investigation evaluated the agronomic, yield, and fiber quality performance of eight F₃ cotton progenies and their parental genotypes under field conditions. The study aimed to identify superior crosses possessing desirable combinations of yield and fiber quality traits that could be utilized in future cotton breeding programs.

Material and Methods

Experimental Site

The experiment was conducted during the Kharif season of 2025 at the Experimental Farm of the Nuclear Institute of Agriculture (NIA), Tandojam, Sindh, Pakistan.

Plant Material

The experimental material consisted of twelve upland cotton (*Gossypium hirsutum* L.) parental genotypes and eight F₃ progenies developed from the following cross combinations:

1. Chandi-95 × NIA-95
2. Sohni × NIAB-878
3. IUB-2013 × Sohni
4. NIA-Ufaq × M-5
5. Sadori × ZAD-1
6. NIA-Noori × M-35
7. NIAB-878 × M-23
8. ZAD-1 × Chandi-95

The parental genotypes included Chandi-95, NIA-95, Sohni, NIAB-878, IUB-2013, NIA-Ufaq, M-5, ZAD-1, Sadori, NIA-Noori, M-35, and M-23.

Experimental Design and Crop Management

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each genotype was planted in two rows with 75 cm row spacing. The recommended dose of nitrogen, phosphorus, and potassium fertilizers was applied at sowing. Standard agronomic practices, including irrigation, weed control, fertilization, and pest management, were uniformly adopted throughout the growing season to ensure optimum crop growth.

Data Collection

Observations were recorded from five randomly selected plants in each replication for the following traits:

- Plant height (cm)
- Sympodial branches per plant
- Number of bolls per plant
- Boll weight (g)
- Seed index (100-seed weight, g)
- Ginning outturn (GOT, %)
- Staple length (mm)
- Micronaire value
- Seed cotton yield per plant (g)

Observations recorded

Plant height

Plant height was measured from the soil surface to the tip of the main stem at maturity. Sympodial branches and mature balls were counted manually. Boll weight was determined using a digital balance. Seed index was calculated from the weight of 100 randomly selected seeds following ginning. Ginning outturn percentage was computed as:

$$\text{GOT (\%)} = (\text{Lint weight} / \text{Seed cotton weight}) \times 100$$

Staple length

Staple length was measured in millimeters, while micronaire value was used to assess fiber fineness. Seed cotton yield was determined by weighing the harvested seed cotton from each selected plant.

Statistical Analysis

The recorded data were subjected to analysis of variance (ANOVA) according to the procedure of Gomez and Gomez (1984). Mean comparisons among genotypes were performed using the Least Significant Difference (LSD) test at the 5% probability level to identify significant differences among parents and F_3 progenies.

Results

The study evaluated the agronomic, yield, and fiber quality performance of twelve parental genotypes and eight F_3 populations of cotton.

Analysis of variance

Analysis of variance revealed significant differences among genotypes for all studied traits, with mean squares significant at either $P < 0.05$ or $P < 0.01$. Parents also differed significantly for most traits, while the F_3 populations showed significant variation for all traits except seed index. These results indicate substantial phenotypic variability among the parental genotypes and F_3 populations and provide a basis for further evaluation of genetic parameters. The trait-wise results are presented below Table 1(a) and 1(b).

Table .1(a). Mean squares from analysis of variance for different morphological traits of cotton

Source of variance	D.F	Plant height	Sympodial branches plant ⁻¹	Bolls plant ⁻¹	Boll weight	Seed index (100-seed weight, g)
Replications	2	13.57	6.19	5.02	0.01	0.17
Genotypes	19	529.78**	25.96**	94.85**	0.09*	0.25*
Parents	11	51.12**	2.58*	7.22**	0.08*	0.39*
Hybrids	7	67.07**	2.85*	18.81**	0.03*	0.06ns

Error	38	6.19	1.51	1.93	0.00	0.23
-------	----	------	------	------	------	------

** and * indicate the level of significance at 1% and 5%, respectively. While ns shows non-significance

Table. 1(b). Mean squares from analysis of variance for different fiber and yield traits of cotton

Source of variance	D.F	GOT (%)	Staple length (mm)	Micronaire	Seed cotton yield plant ⁻¹ (g)
Replications	2	10.94	0.03	0.13	16.72
Genotypes	19	15.79**	0.43**	0.04*	2344.9**
Parents	11	3.70**	0.45**	0.04*	450.09**
Hybrids	7	15.44**	0.41**	0.05**	549.76**
Error	38	1.65	0.02	0.01	36.39

** and * indicate the level of significance at 1% and 5%, respectively. While ns shows non-significance.

Mean performance of different characters in parental lines and F₃ progenies of cotton

Plant height (cm)

The highest plant height among the F₃ populations was recorded in NIA-Noori × M-35 (149.07 cm), whereas the lowest was observed in Chandi-95 × NIA-95 (134.93 cm). Among the parental genotypes, Chandi-95 had the greatest plant height (125.40 cm), while Sohni had the lowest (112.40 cm). Heritability estimates for plant height ranged from 5.58% to 92.04%, with genetic advance ranging from 0.84 to 32.24. Details are in Table 3.

Sympodial branches plant⁻¹

The highest number of sympodial branches plant⁻¹ among the F₃ populations was recorded in NIA-Noori × M-35 (34.07), whereas the lowest was observed in Chandi-95 × NIA-95 (31.47) (the corresponding genetic-parameter estimates.2). Among the parental lines, NIA-95 had the highest mean number of sympodial branches plant⁻¹ (28.73), while Sohni had the lowest (25.80). Heritability estimates ranged from 1.74% to 64.10%, with genetic advance ranging from 0.10 to 10.91. The highest heritability ($h^2 = 64.10\%$) was observed in IUB-2013 × Sohni, with a genetic advance of 10.91. Details are in Table 3.

Bolls plant⁻¹

The highest number of bolls plant⁻¹ among the F₃ populations was recorded in NIA-Noori × M-35 (58.80), while the lowest was observed in Chandi-95 × NIA-95 (52.20). Among the parental lines, NIA-95 had the highest number of bolls plant⁻¹ (48.00), whereas NIA-Ufaq had the lowest (42.40) (the corresponding genetic-parameter estimates.2). Heritability estimates ranged from 9.48% to 65.61%, with genetic advance ranging from 1.16 to 17.54. The highest heritability ($h^2 = 65.61\%$) was observed in ZAD-1 × Chandi-95, with a genetic advance of 16.21. Details are in Table 3.

Boll weight (g)

Mean boll weight among the F₃ populations ranged from 3.71 g in Chandi-95 × NIA-95 to 4.04 g in Sadori × ZAD-1 (the corresponding genetic-parameter estimates.2). Among the parental genotypes, M-23 had the highest boll weight (3.99 g), whereas Sadori had the lowest (3.43 g). Details are in Table 3.

Seed index (100-seed weight, g)

The highest 100-seed weight among the F₃ populations was recorded in Sohni × NIAB-878 (9.13 g), while the lowest was observed in ZAD-1 × Chandi-95 (7.94 g). Among the parental lines, M-35 had the highest seed index (8.85 g), whereas Sadori had the lowest (7.73 g). Details are in Table 3.

Ginning outturn percentage (%)

The highest ginning outturn (GOT) among the F₃ populations was recorded in NIA-Noori × M-35 (41.80%), whereas the lowest was observed in NIA-Ufaq × M-5 (34.92%). Among the parental lines, M-23 had the highest GOT (43.63%), while NIAB-878 and IUB-2013 had the lowest (40.62%). Details are in Table 3.

Staple length (mm)

The longest staple length among the F_3 populations was recorded in IUB-2013 $\times$ Sohni (29.53 mm), whereas the shortest was observed in Sohni $\times$ NIAB-878 (29.07 mm). Among the parental genotypes, ZAD-1 had the longest staple length (30.07 mm), while NIA-95 had the shortest (28.67 mm). Details are in Table 3.

Micronaire value

The highest micronaire value among the F_3 populations was recorded in ZAD-1 $\times$ Chandi-95 (4.09), whereas the lowest was observed in NIA-Ufaq $\times$ M-5 (3.69). Among the parental genotypes, NIA-Ufaq had the highest micronaire value (4.01), while M-23 had the lowest (3.67). Details are in Table 3.

Seed cotton yield plant⁻¹ (g)

The highest seed cotton yield plant⁻¹ among the F_3 populations was recorded in NIA-Noori $\times$ M-35 (234.09 g), followed by Sohni $\times$ NIAB-878 (230.64 g) and Sadori $\times$ ZAD-1 (229.56 g). The lowest yield was observed in Chandi-95 $\times$ NIA-95 (193.93 g). Among the parental genotypes, NIA-95 had the highest seed cotton yield (189.77 g), whereas NIA-Ufaq had the lowest (149.55 g). Details are in Table 3.

Table 2: Mean performance of different characters in parental lines and F_3 progenies of cotton

Parents	Plant height (cm)	Sympodial Branches plant ⁻¹	Bolls plant ⁻¹	Boll weight (g)	Seed index (100-seed weight, g)	GOT (%)	Staple length (mm)	Micro naire	Seed cotton yield plant ⁻¹ (g)
Chandi-95	125.40	27.33	47.07	3.73	8.69	42.38	29.33	3.93	175.32
NIA-95	123.53	28.73	48.00	3.95	8.84	41.01	28.67	4.0	189.77
Sohni	112.40	25.80	44.07	3.80	8.29	41.61	29.33	3.9	167.35
NIAB-878	114.20	25.93	45.13	3.67	7.96	40.62	29.40	3.94	165.58
IUB-2013	113.07	27.00	45.00	3.80	8.45	40.62	29.27	3.97	171.09
NIA-Ufaq	119.47	28.07	42.40	3.53	7.86	41.55	29.40	4.01	149.55
M-5	117.93	27.73	44.13	3.73	8.07	43.52	29.33	3.68	164.71
ZAD-1	121.60	27.27	46.07	3.81	8.58	43.10	30.07	3.89	175.71
Sadori	117.60	27.87	44.60	3.43	7.73	40.97	29.33	3.87	152.71
NIA-Noori	115.47	26.53	44.13	3.71	7.98	40.99	29.60	3.97	161.24
M-35	120.27	27.40	46.73	3.93	8.85	42.49	29.00	3.94	183.91
M-23	120.80	28.53	45.73	3.99	8.46	43.63	28.80	3.67	182.48
LSD (5%)	2.78	2.23	2.26	0.08	0.21	1.81	0.78	0.20	10.59
F_3 progenies									
Chandi-95 $\times$ NIA-95	134.93	31.47	52.20	3.71	8.57	41.08	29.47	4.07	193.93
Sohni $\times$ NIAB-878	148.20	34.00	58.27	3.96	9.13	36.55	29.07	3.92	230.64
IUB-2013 $\times$ Sohni	146.07	33.80	57.60	3.89	8.69	39.37	29.53	3.99	224.27
NIA-Ufaq $\times$ M-5	142.20	32.47	53.87	3.90	8.49	34.92	29.27	3.69	209.93
Sadori $\times$ ZAD-1	144.33	32.27	56.80	4.04	8.08	38.54	29.20	3.95	229.56
NIA-Noori $\times$ M-35	149.07	34.07	58.80	3.98	8.55	41.80	29.27	3.99	234.09
NIAB-878 $\times$ M-23	144.40	33.07	55.60	4.03	8.31	39.21	29.33	4.00	223.92
ZAD-1 $\times$ Chandi-95	139.00	32.13	53.00	4.00	7.94	37.6	29.27	4.09	211.91
LSD (5%)	6.17	2.01	2.72	0.11	0.31	2.84	0.91	0.18	10.35

Discussion

The present study evaluated the agronomic, yield, and fiber quality performance of twelve parental cotton genotypes and their eight F_3 progenies under field conditions. Analysis of variance revealed highly significant differences among genotypes for most studied traits, indicating substantial phenotypic variation that can be effectively utilized in cotton breeding programs.

Significant variability among parental lines and segregating populations reflects diverse genetic backgrounds and provides opportunities to select superior recombinants. Similar findings have been reported by Kumar et al. (2020), Lande and Shanon (2091), and Li et al. (2021), who also observed significant variation among cotton genotypes for important agronomic, yield, and fiber quality traits. The F₃ progenies exhibited considerable variation for plant height, sympodial branches, boll number, boll weight, seed index, ginning outturn, staple length, micronaire value, and seed cotton yield. Such variability is expected in segregating generations because recombination and segregation generate new gene combinations that can enhance the expression of economically important traits (Li and Chen, 2025; Rajpar et al., 2018 and Junejo et al., 2019). The wide phenotypic variation indicates that effective selection can be practiced in subsequent generations to identify stable, high-performing breeding lines (Mirza et al., 2024).

Among the evaluated crosses, NIA-Noori × M-35 consistently outperformed the remaining progenies for several important traits, including plant height, sympodial branches per plant, number of bolls per plant, ginning outturn, and seed cotton yield (Khan et al., 2021 and Kakar et al., 2021). The superior performance of this cross suggests that both parents contributed favorable alleles governing yield and its associated components. Likewise, Sohni × NIAB-878 and Sadori × ZAD-1 also recorded excellent performance for several agronomic and yield-related traits, indicating their suitability for further advancement in cotton breeding programs. These superior crosses performed better than many parental genotypes, suggesting transgressive segregation resulting from favorable recombination of genes inherited from both parents (Baloch et al., 2018; Joha et al., 2025). The parental genotypes also differed considerably in their performance. NIA-95 recorded the highest seed cotton yield among the parents, while M-35 and M-23 performed well for seed index, boll weight, and ginning outturn. These parents may therefore serve as valuable donor genotypes in future hybridization programs aimed at improving productivity and fiber quality. The superiority of these parents further supports their utilization in developing elite breeding populations (Ishaq et al., 2021). Cotton yield improvement depends largely on the combined performance of several component traits rather than a single character. In the present study, higher seed cotton yield was generally associated with increased numbers of sympodial branches and bolls per plant together with desirable boll weight. These findings suggest that simultaneous selection for these yield-contributing traits may effectively enhance overall productivity in future breeding programs. Similar relationships among yield components have been reported in previous cotton improvement studies (Gupta et al., 2022). Although fiber quality traits showed less variation than yield components, significant differences were still evident for ginning outturn, staple length, and micronaire value.

The crosses IUB-2013 × Sohni, NIA-Noori × M-35, and ZAD-1 × Chandi-95 exhibited desirable fiber characteristics while maintaining satisfactory yield performance. This demonstrates that simultaneous improvement of yield and fiber quality is achievable through careful selection of appropriate parental combinations (Haq et al., 2017). Combining superior yield with acceptable fiber quality is particularly important for meeting the demands of both cotton growers and the textile industry. Overall, the observed phenotypic variation among the F₃ populations demonstrates the effectiveness of hybridization in generating superior recombinants. The outstanding performance of NIA-Noori × M-35, Sohni × NIAB-878, and Sadori × ZAD-1 across several agronomic and yield traits indicates that these populations possess excellent breeding potential. These promising progenies should be advanced to later generations and evaluated across multiple environments to confirm performance stability before incorporation into cultivar development programs (Abro et al., 2021; Ahmed and Hussain, 2020). The results of the present study provide valuable information for cotton breeders in selecting superior breeding materials for developing high-yielding cultivars with improved agronomic performance and acceptable fiber quality.

Conclusion

The significant variation observed among the parental genotypes and F₃ progenies demonstrates the potential of these breeding materials for cotton improvement. Among the evaluated crosses, NIA-Noori × M-35, followed by Sohni × NIAB-878 and Sadori × ZAD-1, showed superior agronomic, yield, and fiber quality performance, making them promising candidates for developing high-yielding cotton cultivars.

References

- Abro, S. A., Soomro, A. H., Memon, S., & Khokhar, M. F. (2021). Genetic variability and heritability studies for yield and fiber quality traits in upland cotton (*Gossypium hirsutum* L.). *Pakistan Journal of Agricultural Research*, 34(2), 250-260.
- Ahmed, S., & Hussain, M. (2020). Early flowering and reproductive traits in upland cotton: Heritability and genetic advance. *Plant Breeding and Genetics Journal*, 8(3), 101-112.
- Baloch, S. K., Bhutto, M. A., Anjum, R., Nizamani, G. S., Bughio, A. Y., Khan, I. A., & Kaleri, R. R. (2018). 4. Evaluation of genetic variability in the regenerated population of sugarcane. *Pure and Applied Biology (PAB)*, 7(1), 26-32.

- Baloch, Q. B., Hussain, A., Wahocho, N. A., Baloch, N. A., Wahocho, S. A., Kaleri, A. A., Kaleri, R. R., & Gola, A. Q. (2017). Response of various nitrogen levels on the growth and yield performance of tomato (*Lycopersicon esculentum* Mill.). *Journal of Basic & Applied Sciences*, 13, 583-588.
- Bano, S., Kaleri, A. A., Keerio, R., Memon, S., Kaleri, R. R., Akram, R., Laghari, A. L., Chandio, I. A., and Nazeer, S. (2017). Analysis of Correlation and regression among M2 wheat mutant population for yield and its associated traits. *Journal of Basic & Applied Sciences*, 13, 522-526.
- Gupta, R., Sharma, P., & Singh, A. (2022). Genetic variability and heritability of yield-related traits in fiber crops. *Crop Science Journal*, 62(4), 1457-1469.
- Gomez, K. A., & Gomez, A. A. (1984). *Statistical procedures for agricultural research* (2nd ed.). John Wiley & Sons.
- Haq, M. A. (2017). Determinants of seed cotton yield in Pakistan: An agronomic perspective. *Pakistan Journal of Agricultural Research*, 30(1), 12-20.
- Ishaq, M., Hassan, A., Munir, S., Shahzad, A., Anjam, M., Bhutta, M., & Qureshi, M. K. (2021). Effect of heritability, genetic advance and correlation on yield contributing traits in upland cotton. *Journal of Agricultural Sciences*, 27(3), 353-359.
- Jatoi, W. A., Baloch, M. J., & Shah, M. H. (2022). Global cultivation trends of upland cotton (*Gossypium hirsutum* L.). *Agricultural Reviews*, 43(2), 89-98.
- Joha, M. R. K., Turin, M. T. S., Jahan, N., Rahman, M. N., & Syfullah, K. (2025). Interspecific hybridization between *Gossypium hirsutum* (American cotton) and *Gossypium barbadense* (Egyptian cotton) for quality improvement. *Asian Journal of Research in Crop Science*, 10(1), 51-61.
- Junejo, G. S., Tamayo, N. V., Jarwar, A. D., Jogi, Q., Hullio, M. H., Junejo, G. Q., and Kaleri, R. R. (2019). Ratooning ability & performance of hybrid Variety mestizo7 (NSIC Rc136H), for yield characters under different NPK levels at irrigated low land conditions of rice. *Proceedings of the Pakistan Academy of Sciences: B. Life and Environmental Sciences* 56 (2):38-42.
- Kakar, M. A., Baloch, A. W., Sootaher, J. K., Gandahi, N., Chang, M. S., Khail, G. F. K., ... & Kasi, U. A. (2021). Assessment of genetic divergence and character association in upland cotton (*Gossypium hirsutum* L.) genotypes. *International Journal of Biology and Biotechnology*, 18(2), 321-327.
- Khan, A., Iqbal, S., & Tariq, H. (2021). Genetic variability and selection potential in F2 populations of upland cotton. *Journal of Cotton Research*, 34(2), 112-126.
- Kumar, C. P. S., Raju, S., Rajan, R. E. B., Muraleedharan, A., & Suji, D. B. (2019). Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). *Plant Archives*, 19(1), 934-937.
- Lande, R., & Shannon, S. (2019). Genetic correlations and multivariate selection in plants. *Evolutionary Applications*, 12(6), 1234-1248.
- Li, H., Wang, J., & Zhao, L. (2025). QTL mapping for fiber quality traits in segregating populations of cotton across multiple generations. *Theoretical and Applied Genetics*, 138(4), 975-990.
- Li, Q., & Chen, S. (2021). Marker-assisted selection for fiber traits in cotton. *Molecular Breeding*, 41(5), 34.
- Mirza, S., Tariq, M., & Haider, Z. (2024). Sustainable practices and pest management in cotton cultivation. *Journal of Crop Protection*, 15(1), 55-70.
- Rajper, A. A., Baloch, S. K., Baloch, K., Ahmed, S., Kaleri, A. A., Leghari, A. L., & Kaleri, R. R. (2018). 14. Analysis path coefficient of yield earliness traits in wheat (*Triticum aestivum* L.). *Pure and Applied Biology (PAB)*, 7(1), 112-120.
- Singh, V., Kumar, R., & Gupta, P. (2024). Genomic approaches in cotton breeding for low-expression traits. *Frontiers in Plant Science*, 15, 101-116.
- Tariq, A., Farooq, M., & Hussain, S. (2022). Cluster analysis of segregating populations in Egyptian cotton for yield and fiber quality traits. *Genetics and Molecular Research*, 21(1), 1-15.
- Waheed, Ali, Khan, Muhammad S., & Rahman, Sajid. (2021). Genomic selection strategies for accelerating genetic gain in cotton breeding. *Theoretical and Applied Genetics*, 134(6), 1901-1915.

Wang, Y. (2024). Genetic mechanisms underlying fiber quality traits in cotton: A comprehensive review of additive, dominant, and epistatic effects. *Journal of Cotton Genetics*, 19(2), 55-70.



2026 by the authors; Journal of The *Kashmir Journal of Academic Research and Development*. This is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC-BY) license (<http://creativecommons.org/licenses/by/4.0/>).