

GENETIC VARIABILITY AND HERITABILITY STUDIES IN F_3 SEGREGATING INTRA-HIRSUTUM COTTON (*GOSSYPIUM HIRSUTUM* L.) GENOTYPES

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ABSTRACT

Cotton as a significant cash crop is being used by a huge population in the world as fiber and shelter. The present study was aimed to investigate the inheritance studies in F_3 segregating intra-hirsutum cotton (*Gossypium hirsutum* L.) genotypes. The results depicted that the analysis of variance revealed that the genotypes, parents, and hybrids were highly significant at $P > 0.01$ and 0.05 probability level for the traits viz plant height (cm), sympodial branches plant⁻¹, number of bolls plant⁻¹, boll weight (g), ginning out turn- G.O.T (%), lint index, seed cotton yield plant⁻¹(g), micronaire value ($\mu\text{g inch}^{-1}$), staple length (mm). Whereas parents and hybrids showed non-significant for number of bolls plant⁻¹, boll weight (g), seed cotton yield plant⁻¹, ginning outturn percentage, staple length (mm) and micronaire value. Mean performance results depicted that taller plant height was observed in the parent AVP and Russian Red, respectively (98.67) and the minimum height was observed in the genotype BT-86 (96.00). The highest sympodial branches plant⁻¹, number of bolls plant⁻¹ and seed cotton yield plant⁻¹ revealed by the parent CEMB-30 (24.00; 38.33 and 123.67g) followed by BT-85 (20.33;38.33). BT-85 also exhibited more boll weight, seed index (2.86g and 7.75g) and seed cotton yield (124.00). The maximum seed cotton yield in kg per hectare, G.O.T% lint weight and micronaire value was observed in the variety BT-85 (2559.7, 38.30, 4.76 and 4.36) followed by the genotype CEMB-30 (2555.3 and 37.90). Staple length was greater in Shahbaz (28.60) followed by IR-1513 with (28.26). The lowest sympodial branches plant⁻¹, boll weight, G.O.T %, lint weight and staple length were observed by Russian red (14.66; 5.10, 35.30, 2.76 and 27.56). The highest sympodial branches plant⁻¹, number of bolls plant⁻¹, G.O.T % and micronaire value were observed from the cross Okra khaki x CEMB-30 (25.00; 40.33, 43.66 and 3.53) followed by IR1513 x CEMB-30 with maximum sympodial branches plant⁻¹, number of bolls plant⁻¹, seed index, seed cotton yield plant⁻¹, seed cotton yield in kg per hectare, lint weight and micronaire value (22.00, 41.00, 5.73g, 144.00, 3210.7, 4.03 and 3.63). Heritability estimates for

plant height, sympodial branches plant⁻¹, number of bolls plant⁻¹, seed cotton yield plant⁻¹ were greater in the hybrid FH168 x CEMB-30 (85.71%, 88.71%, 86.56% and 84.23%) along with genetic advance as 28.43, 4.43, 10.89. The boll weight revealed highest heritability and genetic advance in BT-86 x AVP (95.88% and 4.39) followed by IR1513 x CEMB-30 (91.005 and GA=3.02), respectively. Hence, among parents BT-86, CEMB-30 and BT-85 may be recommended as best parents and among the hybrids the cross-Okra khaki x CEMB-30 and IR1513 x CEMB-30 can be used for further selection.

Keywords: Cotton, genetic variability, heritability, segregating.

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) falls to the Malvaceae family, with the genus *Gossypium* comprising fifty species (Aslam et al., 2020). Mostly four different types, including two diploids, are planted all over the world. *G. herbaceum* and *G. arboreum*, as well as two tetraploid species, have been discovered and designated as "old world cotton.". New world cottons are *G. hirsutum* and *G. barbadense* (Nadeem et al., 2024). Cotton is recognized as the "king of fibre" because of its name (Huang et al., 2021). Lint fibers and cotton derivatives are two of its many uses. Cotton seed oil and seed cake are also made from cotton seeds, which is a form of feed for animals (Shar et al., 2020). In nature, the cotton plant was growing like a shrub. Cotton is grown in over 60 countries throughout the world in tropical and subtropical climates. (Tauqir et al., 2021). In 2019, it was cultivated in excess of 33 million hectares all over the world. (Riaz et al., 2023). Cotton is mostly cultivated for its fiber and seed oil (Munir et al., 2020). Around the world, there are eighty countries which are cotton producers. Among them top six are China, USA India, Pakistan, Australia and Brazil. (Matloob et al., 2020). Cotton is a significant yield for an agrarian nation like Pakistan. Pakistan produces the fourth-largest amount of cotton in the world and has Asia's third-largest spinning industry (Siyal et al., 2021). The use of various breeding procedures to meet the needs of the textile industry is an approach. (Azanaw et al., 2022). Breeding activities should be carried out to widen the genetic basis of cropped cotton species (Mubarik et al., 2020). There may also be some challenges when breeders choose quantitative features that are heavily influenced by environmental influences (Ali et al., 2023). Genetic variability is the difference between individuals within a population and provides different parameters to the plant breeder like to initiate an efficient breeding programmed,

phenotypic and genotypic coefficient of variation, heritability and genetic advance (Zaki et al., 2022). Hybridization is still an important tool to create genetic variation and allows the most efficient method to select the most superior plants in segregating generations. In *Gossypium hirsutum* L., genetic variability and positive associations were discovered for yield variables (Hussain et al., 2021). To make selection more effective the breeder must depend on the phenotypic, genotypic and environmental variations. The basis of the evolutionary process and the formation of new species is genetic diversity. The term "genetic variability" refers to recognized phenotypic variation in plant populations that is mostly due to genetic differences. The ratio of genotypic variance to phenotypic variance can be characterized as broad sense heritability. In other words, it determines the extent to which qualities are passed down from parents to offspring (Fiaz et al., 2021). The amount and type of available genetic diversity among germplasm provides ample opportunity for use in successful breeding programs aimed at improving a variety of characteristics (Jabbar et al., 2021). Heritability is defined as the degree of resemblance between relatives. It is one of the most important genetic parameter on which different breeding strategies depend. Also, heritability, in combination with genetic advance and genetic variability, is a better tool for selecting appropriate breeding techniques to improve the genetic makeup of cotton plants (Zahid et al., 2022). It is an essential statistical method that is used to effectively select genetic variation from overall phenotypic variation. Heritability is thought to be the best indicator of character transmission from parents to offspring. The extent to which selection is effective is determined by the amount of heredity. (Khan et al., 2020). The selection power of any generation depends on the amount of heritable variation which

could transfer from one generation to the next. High heritable traits are less affected by environmental changes, so simple selection techniques can be effective for improving these traits. Non-allelic interaction played a major role in decreasing heritability estimates (Gibely, 2021). With the advancement of genetics, it is to understand the manner of inherited quantitative traits (Rehman et al., 2020). Genetic variability in breeding material is essential for the identification of better genotypes or populations suitable for genetic improvement (Jamil et al., 2020). Heritability, defined as the ratio of a character's genotypic variance to its phenotypic variance, is a function of the character's heritability, selection pressure, and variance in the base population. Heredity is a measure of selection based on phenotypic manifestation determining the true value of selection (Farooq et al., 2023).

Methodology

The experiment at the Nuclear Institute of Agriculture (NIA), Tandojam in the Kharif season of 2020-2021 aimed to evaluate the genetic potential, correlation, regression, and heritability estimates in upland cotton genotypes using a randomized complete block design. The substantial experimental sample consisted of ten genotypes, with each genotype's row-to-row distance being 2.5 feet, while the plant-to-plant distance is 1 to 1.5 feet. The parents and their F₃ crosses are mentioned below:

Culture Practices

The soil underwent meticulous preparation, involving two rounds of ploughing and leveling before seed sowing. During the sowing process, each treatment received the requisite amount of farmyard manure.

Parents

- CEMB-30
- BT-85
- BT-86
- Shahbaz
- Okra Khaki
- IR-1513

- AVP
- Russian Red (RR)
- FH-168

F₃ Hybrids

- BT-86 × AVP
- SHAHBAZ × CEMB-30
- IR-1513 × CEMB-30
- FH-168 × RR
- FH-168 × CEMB-30
- Okra Khaki × CEMB-30
- BT-85 × AVP

Statistical analysis

The obtained data will be subjected to analysis of variance using Steel and Torrie's (1997) approach. The crucial difference between the mean of genotypes of consisted F₃ parents and their seven crossing were determined using L.S.D at P 0.05 for pairwise comparison according to the following formula: using error degree of freedom, L.S.D (5%) = S.E x t value. According to Burton (1953). Broad sense heritability will be calculated. Heritability is divided into three classes, *i.e.*, Low heritability < 0.2, Medium heritability = 0.2–0.5 and High heritability > 0.5.

RESULTS

Cotton (*Gossypium hirsutum* L.) falls to the Malvaceae family, with the genus *Gossypium* comprising fifty species (Aktar et al., 2019). The present study was aimed to determine the genetic variability and heritability in F₃ segregating population in various quantitative and yield traits. Seven F₃ hybrids along with their nine parents were sown at the experimental field of Nuclear Institute of Agriculture (NIA), Tando Jam during kharif season 2020-2021.

Analysis of variance

The mean square of analysis of variance revealed that the genotypes, parents, and hybrids were highly significant at P>0.01 and 0.05 probability level for the traits viz plant height (cm), sympodial branches plant⁻¹, number of bolls plant⁻¹, boll weight (g), ginning out turn- G.O.T (%), Lint index, Seed cotton yield plant⁻¹(g), micronaire value (µg inch⁻¹), staple length (mm) in (Table 1). Whereas parents showed non-significant for

number of bolls plant⁻¹, boll weight (g), seed cotton yield plant⁻¹, ginning outturn percentage, staple length (mm) and micronaire value. Hybrids also showed non-significant results for seed cotton yield plant⁻¹, ginning outturn percentage, staple length and micronaire value. However, parents vs

crosses revealed significant results with plant height (cm), number of bolls plant⁻¹, boll weight (g), seed index (g), seed cotton yield (Kg ha⁻¹), seed cotton yield plant⁻¹, G.O.T%, lint index (g) and staple length (mm), while other parameters were non-significant.

Table 1. Mean square of analysis of variance in various quantitative and qualitative characters in F₃ segregating population of cotton

Characters	Replication D.F. = 2	Genotypes D.F. = 15	Parents (P) D.F. = 8	Hybrids (H) D.F. = 6	P x H D.F. = 1	Error D.F. = 30
Plant height (cm)	36.813	102.421**	215.907**	160.94**	274.426**	13.079
Sympodial branches plant ⁻¹	0.145	31.865**	26.243**	5.968**	0.346ns	0.7903
Number of bolls plant ⁻¹	1.021	9.933*	5.295ns	14.540**	9.902*	4.0208
Boll weight (g)	0.067	0.925**	0.057ns	0.251**	0.617**	0.039
Seed index	0.090	1.277**	1.984**	0.426**	1.133**	0.047
Seed cotton yield (Kg ha ⁻¹)	176.313	296.976**	67128.8*	58916.0*	125747.824**	52.668
Seed cotton yield plant ⁻¹	187.657	300.996**	36.424ns	44.16ns	220.412**	52.344
G.O.T%	2.5408	26.465**	4.471ns	3.064ns	18.954**	1.956
Lint index (g)	0.083	0.659**	1.077**	0.309**	0.727**	0.124
Staple length (mm)	0.436	0.824*	0.237ns	0.125ns	0.462*	0.296
Micronaire value (µg inch ⁻¹)	0.010	0.434**	0.245ns	0.229ns	0.04ns	0.051

** Highly significant at 1 % and * significant at 5 % probability level and ns =non significant

Mean performance

Plant height (cm)

Plant height was ranged among different cotton genotypes from 98.67-96.00, the maximum height of plant was observed from the genotypes AVP and Russian Red each respectively (98.67) and the minimum height was observed in the genotype BT-86 (96.00). Plant height was ranged among different crosses from 109.67-105.33, the maximum height of plant was observed from the cross Shahbaz x CEMB-30 and FH168 x RR each respectively (109.67) and the minimum height was observed in the cross between BT-85x AVP (105.33).

Sympodial branches plant⁻¹

The maximum to minimum values of sympodial branches plant⁻¹ ranges from 24.00-14.66. The mean performance of the sympodial branches per plant is measured from maximum to minimum as follows. The highest were observed from CEMB-

30 (24.00) followed by BT-85 (20.33) while the lowest was observed from the genotype Russian red (14.66). The maximum to minimum values of sympodial branches plant⁻¹ ranges from 25.00-15.33, the highest were observed from the cross-Okra khaki x CEMB-30 (25.00) followed by IR1513 x CEMB-30 (22.00) while the lowest was observed from the cross FH168 x CEMB-30 (15.33).

Number of bolls plant⁻¹

The maximum to minimum number of bolls plant⁻¹ was ranged from 38.33-34.33. The maximum was observed from genotype CEMB-30 and BT-85 each (38.33) followed by minimum value observed from the genotype AVP (34.33). The maximum to minimum number of bolls plant⁻¹ was ranged from 41.00-38.33. The maximum was observed from the cross between IR1513 x CEMB-30 (41.00) followed by cross Okra-khaki x CEMB-30 (40.33) and the minimum value observed from the cross FH168 x CEMB-30 (38.33).

Boll weight

The highest to lowest values for boll weight measured were from 2.86-2.50 and the highest value was observed in the genotype BT-85 (2.86) followed by the variety AVP (2.63) and the lowest value was observed in the variety IR-1513 (2.50). The highest to lowest values for boll weight measured were from 2.86-2.50. The cross Shahbaz x CEMB-30 (3.73) and the lowest value was observed in the cross FH168 x RR (3.43).

Seed index

The variety with the maximum seed index was Shahbaz (7.75) followed by BT-85 (7.70) and the minimum was from the variety Russian red (5.10). The crosses with the maximum seed index were BT-86 x AVP and IR1513 x CEMB-30 each with the value (6.80) followed by FH168 x RR (5.73) with the minimum value in seed index.

Seed cotton yield plant⁻¹

The genotype BT-85 (124.00) showed maximum mean performance followed by the genotype CEMB-30 (123.67) while the minimum was observed within the genotype AVP (114.33). The seed cotton yield per plant of the cross IR1513 x CEMB-30 (144.00) ranged maximum followed by the cross Shahbaz x CEMB-30 (141.67) while the minimum was observed within the cross BT-86 x AVP (134.00).

Seed cotton yield kg/ha⁻¹

The maximum seed cotton yield in kg per hectare was observed in the variety BT-85 (2559.7) followed by the genotype CEMB-30 (2555.3) whereas the minimum of the value was observed in the variety AVP (2107). The seed cotton yield kg/ha ranged from maximum to minimum as 3210.7-2840.3. (3210.7) followed by the cross Shahbaz x CEMB-30 (2993.7) whereas the minimum of the value was observed in the cross FH168 x CEMB-30 (2840.3).

Ginning outturn percentage%

The G.O.T% values range from maximum to minimum from 38.30-35.30, and the maximum value was observed from the variety BT-85 (38.30) followed by the genotype CEMB-30 (37.90) whereas the lowest value was observed within the

variety Russian red (35.30). The G.O.T% values ranged from maximum to minimum as 44.00-42.00, and the maximum value was observed from the cross Shahbaz x CEMB-30 (44.00) followed by the cross Okra-khaki x CEMB-30 (43.66) whereas the lowest value was observed within the cross FH168 x CEMB-30 (42.00)

Lint weight

Maximum lint weight was observed from the variety BT-85 (4.76) followed by the variety Shahbaz (4.56) while the lowest was from the variety Russian red (2.76). Maximum lint weight was observed from the cross FH168 x CEMB-30 (4.06) followed by the cross IR1513 x CEMB-30 (4.03) while the lowest was from the FH168 x RR (3.13).

Staple length

Staple length of the genotypes was measured and the genotype Shahbaz (28.60) was measured with the maximum staple length followed by IR-1513 with (28.26) and the minimum was recorded in Russian red (27.56). The staple length of the crosses was measured and the crosses BT-86 x AVP and FH168 x RR each showed the same value respectively (29.36) while the minimum value was observed cross Okra-khaki x CEMB-30 (28.70).

Micronaire ($\mu\text{g inch}^{-1}$)

The variety BT-85 (4.36) was observed to have the maximum value followed by the genotype IR-1513 (4.26) and the lowest observed in the variety BT-86 (4.00). The cross IR1513 x CEMB-30 (3.63) was observed to have the maximum value followed by the cross Okra-khaki x CEMB-30 (3.53) and the lowest observed in the cross FH168 x CEMB-30 (3.33).

Table 2. Mean performance of various quantitative and qualitative traits in intra-hirsutum cotton (*Gossypium hirsutum* L.)

Genotypes Parents	Plant height (cm)	Sympodial branches plant ⁻¹	Number of bolls plant ⁻¹	Boll weight (g)	Seed index	Seed cotton yield (kg ha ⁻¹)	Seed cotton yield (g) plant ⁻¹	GOT%	Lint index (g)	Staple index(mm)	Micronaire (µg inch ⁻¹)
Shahbaz	96.331	17.000	37.333	2.5000	7.7520	2376.0	118.33	37.033	4.5667	28.600	4.0333
CEMB-30	96.673	24.000	38.333	2.5000	7.4333	2555.3	123.67	37.900	4.5333	27.767	4.2000
Okra-khaki	94.331	16.333	37.667	2.6000	6.5667	2466.0	121.67	37.033	3.8667	28.133	4.1667
Russain red	98.672	14.667	36.667	2.5667	5.1000	2367.3	120.00	35.300	2.7667	27.567	4.1000
FH-168	96.335	17.667	35.333	2.5000	7.0667	2242.0	117.67	37.600	4.2667	27.900	4.1667
BT-85	96.671	20.333	38.333	2.5667	7.7000	2559.7	124.00	38.300	4.7667	28.200	4.3667
IR-1513	98.335	16.333	37.333	2.5000	6.6333	2462.7	122.67	36.667	4.4000	28.267	4.2667
BT-86	96.000	15.333	36.667	2.8667	6.6000	2289.7	116.33	37.067	3.9000	28.200	4.0000
AVP	98.671	15.667	34.333	2.6333	6.5000	2107.7	114.33	37.467	3.9000	28.067	4.1333
Average	96.986	17.511	36.900	2.666	6.820	2380.7	119.901	37.223	4.112	28.123	4.224
F₃ Hybrids											
BT-85x AVP	105.331	20.333	38.333	3.7667	6.6667	2776.7	134.67	40.733	3.9000	28.267	3.4000
BT-86 x AVP	107.000	20.333	40.000	3.6667	6.8000	2872.3	134.00	42.000	3.8333	29.367	3.4000
Shahbaz x CEMB-30	109.673	19.667	39.333	3.7333	6.6667	2993.7	141.67	44.000	4.0000	28.933	3.4667
IR1513 x CEMB-30	110.000	22.000	41.000	3.6333	6.8000	3210.7	144.6	42.667	4.0333	28.700	3.6333
FH168 x RR	109.671	15.667	40.000	3.4333	5.7333	2961.0	137.33	43.400	3.1333	29.367	3.3667
FH168 x CEMB-30	107.333	15.333	38.333	3.7000	6.5667	2840.3	137.67	42.000	4.0667	28.733	3.3333
Okra-khaki x CEMB-30	106.000	25.000	40.333	3.5667	6.7333	2953.0	136.33	43.667	3.8667	28.700	3.5333
Average	107.900	19.801	39.623	3.633	6.656	2944.0	138.00	42.601	3.842	28.988	3.443
LSD 5%	11.000	2.704	6.099	0.601	0.663	707.22	22.074	4.253	0.828	1.654	0.687

Heritability estimates

The genetic variability studies in F₃ segregants observed that enough variation was present in the population for all the characters studied. The heritability and genetic advance for different trait has been explained as below:

Plant height (cm)

Table 3 showed genotypic, environmental, phenotypic and heritability variation for the character plant height. The results depicted that the

genotypic and environmental ranged from 69.70-90.50 and 23.24-79.83, respectively. Heritability and genetic advance ranged from low to high. Maximum heritability was observed by the cross FH168 x CEMB-30 (85.71%) along with genetic advance as 28.43. Moderate heritability and genetic gain were exhibited in the cross Shahbaz x CEMB-30 (61.59% and 19.15). Whereas low heritability was observed in the cross FH168 x RR (9.12% and GA=2.22).

Table 3. Phenotypic variance ($\delta^2 p$), environmental variance ($\delta^2 e$), genetic variance ($\delta^2 g$), heritability (h^2 %) and genetic advance (GA) of F₃ populations for plant height (cm)

F ₃ populations	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	h^2 %	G.A.
BT-85 x AVP	21.04	50.20	71.24	29.54	6.48
BT-86 x AVP	45.26	79.24	90.50	36.35	10.55
IR1513 x CEMB-30	24.35	79.63	81.43	23.42	6.21
FH168 x RR	8.01	79.83	87.84	9.12	2.22
Shahbaz x CEMB-30	88.07	54.92	72.47	61.59	19.15
FH168 x CEMB-30	59.74	23.24	69.70	85.71	28.43
Okra-khaki x CEMB-30	23.53	50.45	73.98	48.26	19.56

Sympodial branches plant⁻¹

The results of environmental and genotypic variance of sympodial branches plant⁻¹ ranged from 0.56- 27.50 and 3.95-34.10. Heritability and genetic advances seem to have low, moderate and high heritability for this trait. The highest

heritability exhibited in the cross FH168 x CEMB-30 was 85.71% with a genetic gain of 4.43. However, moderate heritability and genetic advance were observed in the cross IR1513 x CEMB-30 (69.55% and 6.52) followed by BT-85 x AVP (67.20% and 6.48), respectively.

Table 4. Phenotypic variance ($\delta^2 p$), environmental variance ($\delta^2 e$), genetic variance ($\delta^2 g$), heritability (h^2 %) and genetic advance (GA) of F₃ populations for sympodial branches plant⁻¹

F ₃ populations	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	h^2 %	G.A.
BT-85 x AVP	5.17	2.52	7.69	67.20	4.85
BT-86 x AVP	2.13	3.40	5.53	38.53	2.35
IR1513 x CEMB-30	9.03	3.95	12.98	69.55	6.52
FH168 x RR	1.22	3.27	4.50	27.19	1.50
Shahbaz x CEMB-30	1.11	3.84	4.95	22.50	1.30
FH168 x CEMB-30	3.39	0.56	3.95	85.71	4.43
Okra-khaki x CEMB-30	6.60	27.50	34.10	19.34	2.94

Number of bolls plant⁻¹

This trait declared that genotypic and environmental variance ranged from 23.88-72.47 and 0.92-45.76. The highest heritability was found in the cross FH168 x RR (96.25% and 12.36) followed by FH168 x CEMB-30 (85.71% and

10.89). Moderate heritability was depicted in BT-86 x AVP as 76.85% and 15.49. Lowest heritability was found in Bt-85 X AVP and IR1513 x CEMB-30 (30.03 and 30.17%), respectively.

Table 5. Phenotypic variance ($\delta^2 p$), environmental variance ($\delta^2 e$), genetic variance ($\delta^2 g$), heritability (h^2 %) and genetic advance (GA) of F_3 populations for number of bolls plant⁻¹

F₃ populations	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	h^2 %	G.A.
BT-85 x AVP	9.59	22.34	31.92	30.03	4.41
BT-86 x AVP	46.20	13.92	60.12	76.85	15.49
IR1513 x CEMB-30	19.77	45.76	65.52	30.17	6.35
FH168 x RR	23.49	0.92	24.41	96.25	12.36
Shahbaz x CEMB-30	17.55	54.92	72.47	24.22	5.36
FH168 x CEMB-30	20.47	3.41	23.88	85.71	10.89
Okra-khaki x CEMB-30	17.42	30.65	48.07	36.24	6.53

Boll weight (g)

The boll weight of environmental and genotypic results ranged from 0.01-0.15 and 0.05-3.1. The highest heritability and genetic advance were observed in BT-86 x AVP (95.88% and 4.39)

followed by IR1513 x CEMB-30 (91.00% and GA=3.02), respectively. The lowest heritability was found in the cross BT-85 x AVP (42.39 and GA=0.51).

Table 6. Phenotypic variance ($\delta^2 p$), environmental variance ($\delta^2 e$), genetic variance ($\delta^2 g$), heritability (h^2 %) and genetic advance (GA) of F_3 populations for boll weight (g)

F₃ populations	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	h^2 %	G.A.
BT-85 x AVP	0.09	0.12	0.21	42.39	0.51
BT-86 x AVP	2.97	0.13	3.1	95.88	4.39
IR1513 x CEMB-30	1.49	0.15	1.63	91.00	3.02
FH168 x RR	0.03	0.01	0.04	84.13	0.44
Shahbaz x CEMB-30	0.65	0.13	0.78	82.95	1.91
FH168 x CEMB-30	0.05	0.01	0.05	85.71	0.52
Okra-khaki x CEMB-30	0.07	0.08	0.15	46.49	0.46

Seed index (g)

The character seed index showed that the environmental and genotypic variance ranged from 0.02-0.24 and 0.11-2.86. The highest heritability predicted in the cross FH168 x RR (95.37% and

GA=4.20) followed by Okra-khaki x CEMB-30 (92.01% and GA=2.28), respectively. The lowest heritability and genetic advance were found in the cross Shahbaz x CEMB-30 (0.28).

Table 7. Phenotypic variance ($\delta^2 p$), environmental variance ($\delta^2 e$), genetic variance ($\delta^2 g$), heritability (h^2 %) and genetic advance (GA) of F_3 populations for seed index (g)

F₃ populations	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	h^2 %	G.A.
BT-85 x AVP	0.05	0.09	0.14	50.16	0.40
BT-86 x AVP	0.03	0.08	0.11	29.67	0.26
IR1513 x CEMB-30	0.17	0.24	0.41	42.14	0.70
FH168 x RR	2.73	0.13	2.86	95.37	4.20
Shahbaz x CEMB-30	0.10	0.75	0.85	11.73	0.28
FH168 x CEMB-30	0.11	0.02	0.13	85.71	0.79
Okra-khaki x CEMB-30	0.84	0.07	0.91	92.01	2.28

Seed cotton yield plant⁻¹

The seed cotton yield plant⁻¹ revealed that environmental and genotypic variance observed ranged from 6.09-98.44 and 42.62-112.49. The

maximum heritability and genetic advance were found in the cross FH168 x CEMB-30 (85.71% and 14.55). Moderate heritability was observed in the cross Okra-khaki x CEMB-30 (43.06 and

GA=11.90). Whereas lowest heritability revealed in the hybrid Shahbaz x CEMB-30 (13.59 and GA=3.48).

Table 8. Phenotypic variance ($\delta^2 p$), environmental variance ($\delta^2 e$), genetic variance ($\delta^2 g$), heritability (h^2 %) and genetic advance (GA) of F_3 populations for seed cotton yield plant⁻¹

F₃ populations	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	h^2 %	G.A.
BT-85 x AVP	20.18	66.02	86.20	23.41	5.65
BT-86 x AVP	21.13	50.50	71.63	29.49	6.49
IR1513 x CEMB-30	14.05	98.44	112.49	31.76	6.93
FH168 x RR	13.56	30.60	44.16	30.71	5.31
Shahbaz x CEMB-30	13.1	83.72	96.89	13.59	3.48
FH168 x CEMB-30	36.53	6.09	42.62	85.71	14.55
Okra-khaki x CEMB-30	48.62	64.30	112.92	43.06	11.90

Ginning outturn percentage %

The genotypic and environmental variances ranged from 1.21-11.25 and 0.68-2.22. The highest heritability and genetic advance were observed in the cross Okra-khaki x CEMB-30 (76.44,% and

3.38). Maximum moderate heritability depicted in the cross BT-86 x AVP and FH168 x RR (48.53 and 48.23%), respectively. The lowest heritability was found in the cross IR1513 x CEMB-30 (20.72 and GA=1.81), respectively.

Table 09. Phenotypic variance ($\delta^2 p$), environmental variance ($\delta^2 e$), genetic variance ($\delta^2 g$), heritability (h^2 %) and genetic advance (GA) of F_3 populations for G.O.T%

F₃ populations	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	h^2 %	G.A.
BT-85 x AVP	0.62	1.02	1.64	37.95	1.26
BT-86 x AVP	2.10	2.22	4.32	48.53	2.62
IR1513 x CEMB-30	2.33	8.92	11.25	20.72	1.81
FH168 x RR	1.59	1.71	3.30	48.23	2.28
Shahbaz x CEMB-30	0.31	0.90	1.21	25.69	0.74
FH168 x CEMB-30	0.53	0.69	1.21	43.41	1.24
Okra-khaki x CEMB-30	2.21	0.68	2.89	76.44	3.38

Lint index%

The genotypic and environmental variances for lint index % ranged from 2.3-56.84 and 1.71-42.06. The highest heritability was found in the cross FH168 x CEMB-30 (85.71% and GA=13.27).

Moderate heritability was observed in the hybrid FH168 x RR (53.08 and GA=4.07). Lowest heritability revealed in the cross Shahbaz x CEMB-30 (3.53 and GA=0.61).

Table 10. Phenotypic variance ($\delta^2 p$), environmental variance ($\delta^2 e$), genetic variance ($\delta^2 g$), heritability (h^2 %) and genetic advance (GA) of F_3 populations for lint index%

F₃ populations	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	h^2 %	G.A.
BT-85 x AVP	1.00	9.65	10.65	9.39	0.80
BT-86 x AVP	0.59	1.71	2.3	25.52	1.01
IR1513 x CEMB-30	16.66	40.18	56.84	29.31	5.75
FH168 x RR	4.62	4.09	8.71	53.08	4.07
Shahbaz x CEMB-30	1.54	42.06	43.60	3.53	0.61
FH168 x CEMB-30	30.41	5.07	35.48	85.71	13.27
Okra-khaki x CEMB-30	19.03	20.22	39.25	48.49	7.90

Staple length (mm)

The genotypic and environmental variances ranged from 0.20-1.41 and 0.05-0.59. The highest heritability and genetic advance depicted in the cross Okra-khaki x CEMB-30 (92.01% and 2.28) followed by the cross FH168 x CEMB-30 (85.71

and GA=1.28). The moderate heritability and genetic advance revealed in the cross BT-85 x AVP and IR1513 x CEMB-30 (60.20 and 58.16%), respectively. The lowest heritability was found in the cross BT-86 x AVP (13.06% and GA=0.15).

Table 11. Phenotypic variance ($\delta^2 p$), environmental variance ($\delta^2 e$), genetic variance ($\delta^2 g$), heritability (h^2 %) and genetic advance (GA) of F_3 populations for staple length (mm)

F_3 populations	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	h^2 %	G.A.
BT-85 x AVP	0.30	0.20	0.50	60.20	1.11
BT-86 x AVP	0.03	0.17	0.20	13.16	0.15
IR1513 x CEMB-30	0.82	0.59	1.41	58.16	1.80
FH168 x RR	0.08	0.11	0.39	71.93	1.16
Shahbaz x CEMB-30	0.33	0.65	0.98	33.76	0.87
FH168 x CEMB-30	0.28	0.05	0.33	85.71	1.28
Okra-khaki x CEMB-30	0.84	0.07	0.91	92.01	2.28

Microniare ($\mu g \text{ inch}^{-1}$)

The microniare value environmental and genotypic variances ranged from 0.12-11.80 and 0.01-8.90, respectively. The maximum heritability was found in the cross FH168 x RR (96.00 and GA=1.44). Moderate heritability was observed in the crosses

Shahbaz x CEMB-30, BT-85 x AVP and FH168 x CEMB-30 (74.04, 69.86 and 67.53%), respectively. The lowest heritability and genetic advance were found in the cross IR1513 x CEMB-30 as 17.46 and 0.21, respectively.

Table 13. Phenotypic variance ($\delta^2 p$), environmental variance ($\delta^2 e$), genetic variance ($\delta^2 g$), heritability (h^2 %) and genetic advance (GA) of F_3 populations for microniare ($\mu g \text{ inch}^{-1}$)

F_3 populations	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	h^2 %	G.A.
BT-85 x AVP	0.17	0.07	0.24	69.86	0.90
BT-86 x AVP	0.04	0.08	0.12	31.94	0.01
IR1513 x CEMB-30	0.04	0.17	0.21	17.46	0.21
FH168 x RR	0.32	0.01	0.33	96.00	1.44
Shahbaz x CEMB-30	0.12	0.04	0.16	74.04	0.77
FH168 x CEMB-30	0.22	0.11	0.32	67.53	1.00
Okra-khaki x CEMB-30	2.90	8.90	11.80	24.60	2.20

DISCUSSION

Cotton is recognized as the "king of fibre" because of its name (Dhunde et al., 2022). Lint fibers and cotton derivatives are two of its many uses. Cotton seed oil and seed cake are also made from cotton seeds, which is a form of feed for animals (Saha et al., 2020). The present study was aimed to investigate the inheritance of segregating F_3 generation in various cotton genotypes (nine parents and seven hybrids). The mean square of analysis of variance revealed that the genotypes, parents, and hybrids were highly significant at

$P > 0.01$ and 0.05 probability level for various traits. Whereas parents showed non-significant for number of bolls plant⁻¹, boll weight (g), seed cotton yield plant⁻¹, ginning outturn percentage, staple length (mm) and microniare value. Hybrids also showed non-significant results for seed cotton yield plant⁻¹, ginning outturn percentage, staple length and microniare value. However, parents vs crosses revealed significant results with plant height (cm), number of bolls plant⁻¹, boll weight (g), seed index (g), seed cotton yield (Kg ha⁻¹), seed cotton yield plant⁻¹, G.O.T%, lint index (g) and

staple length (mm), while other parameters were non-significant. Velmourougane et al. (2021) also revealed that analysis of variances in F_3 families have been shown highly significant differences between genotypes and the variance within F_3 had lower than among families for all the studied traits over the two crosses. Mean performance results depicted that taller plant height was observed in the parent AVP and Russian Red, respectively (98.67) and the minimum height was observed in the genotype BT-86 (96.00). The maximum seed cotton yield in kg per hectare, G.O.T% lint weight and micronaire value was observed in the variety BT-85 (2559.7, 38.30, 4.76 and 4.36) followed by the genotype CEMB-30 (2555.3 and 37.90). Staple length was greater in Shahbaz (28.60) followed by IR-1513 with (28.26). The lowest sympodial branches plant⁻¹, boll weight, G.O.T %, lint weight and staple length were observed by Russian red (14.66; 5.10, 35.30, 2.76 and 27.56). The highest sympodial branches plant⁻¹, number of bolls plant⁻¹, G.O.T % and micronaire value were observed from the cross Okra khaki x CEMB-30 (25.00; 40.33, 43.66 and 3.53) followed by IR1513 x CEMB-30 with maximum sympodial branches plant⁻¹, number of bolls plant⁻¹, seed index, seed cotton yield plant⁻¹, seed cotton yield in kg per hectare, lint weight and micronaire value (22.00, 41.00, 5.73g, 144.00, 3210.7, 4.03 and 3.63). Shahbaz x CEMB-30 (3.73) exhibited greater boll weight and G.O.T% (3.73 and 44.0). Among crosses, the highest boll weight and seed index was depicted in the cross BT-85 x AVP (3.77 and 6.80). Minimum plant height and more staple length was found in the crosses BT-86 x AVP and FH168 x RR (109.67 and 105.33; 29.36) while the minimum value was observed cross Okra-khaki x CEMB-30 (28.70). Khokhar et al., 2017 also performed an experiment in upland cotton to investigate genetic diversity, coefficients of variation, heritability and genetic advance among 20 F_1 hybrid and 9 parents. For all traits except fibre fineness, analysis of variance has revealed significant differences at the 1% level of significance. The average performance of F_1 populations was higher than that of their parents. r of sympodial branches and seed cotton yield. Heritability estimates were variable in various characters varying from low, moderate and high heritability. The highest heritability exhibited

in the hybrid FH168 x CEMB-30 (85.71% ,88.71%, 86.56% and 84.23%) along with genetic advance as 28.43, 4.43, 10.89. The boll weight revealed highest heritability and genetic advance in BT-86 x AVP (95.88% and 4.39) followed by IR1513 x CEMB-30 (91.005 and GA=3.02), respectively. The seed index showed highest heritability and genetic advance was observed in the cross FH168 x RR (95.37% and 4.20) followed by Okra-khaki x CEMB-30 (92.01% and GA=2.28), respectively. G.O.T % The highest heritability and genetic advance were observed in the cross Okra-khaki x CEMB-30 (76.44 % and 3.38). Moderate heritability was observed in the hybrid FH168 x RR (53.08 and GA=4.07). Lowest heritability revealed in the cross Shahbaz x CEMB-30 (3.53 and GA=0.61). The highest heritability and genetic advance depicted in the cross Okra-khaki x CEMB-30 (92.01% and 2.28) followed by the cross FH168 x CEMB-30 (85.71 and GA=1.28). The maximum heritability was found in the cross FH168 x RR (96.00 and GA=1.44). Moderate heritability was observed in the crosses Shahbaz x CEMB-30, BT-85 x AVP and FH168 x CEMB-30 (74.04, 69.86 and 67.53%), respectively. Parre et al., (2021) studied genetic variability among F_3 lines. PCV has been observed high for seed cotton yield per plant as followed by the number of monopodial and stem diameter traits. High genotypic coefficient of variation (GCV) has been observed in the number of monopodia per plant followed by seed cotton yield per plant and stem diameter.

CONCLUSIONS AND RECOMONDATIONS

Conclusions

The present study was aimed to investigate the inheritance of segregating F_3 generation in various cotton genotypes (nine parents and seven hybrids). The mean square of analysis of variance revealed that the genotypes, parents, and hybrids were highly significant at $P>0.01$ and 0.05 probability level for various important fiber and yield traits. Whereas parents showed non-significant for number of bolls plant⁻¹, boll weight (g), seed cotton yield plant⁻¹, ginning outturn percentage, staple length (mm) and micronaire value. Hybrids also showed non-significant results for seed cotton yield plant⁻¹, ginning outturn percentage, staple

length and micronaire value. However, parents vs crosses revealed significant results with plant height (cm), number of bolls plant⁻¹, boll weight (g), seed index (g), seed cotton yield (Kg ha⁻¹), seed cotton yield plant⁻¹, G.O.T%, lint index (g) and staple length (mm), while other parameters were non-significant. Gibely, 2021 also revealed that analysis of variances in F₃ families have been shown highly significant differences between genotypes and the variance within F₃ had lower than among families for all the studied traits over the two crosses. Mean performance results depicted that taller plant height was observed in the parent AVP and Russian Red, respectively (98.67) and the minimum height was observed in the genotype BT-86 (96.00). The highest seed cotton yield plant⁻¹ was revealed by the parent CEMB-30 (24.00; 38.33 and 123.67g) followed by BT-85 (20.33;38.33). BT-85 also exhibited more boll weight, seed index (2.86g and 7.75g) and seed cotton yield (124.00). The maximum seed cotton yield in kg per hectare, G.O.T% lint weight and micronaire value was observed in the variety BT-85 (2559.7, 38.30, 4.76 and 4.36) followed by the genotype CEMB-30 (2555.3 and 37.90) . Staple length was greater in Shahbaz (28.60) followed by IR-1513 with (28.26). The cross-Okra khaki x CEMB-30 (25.00; 40.33, 43.66 and 3.53) followed by IR1513 x CEMB-30 with maximum sympodial branches plant⁻¹, number of bolls plant⁻¹, seed index, seed cotton yield plant⁻¹, seed cotton yield in kg per hectare, lint weight and micronaire value (22.00, 41.00,5.73g , 144.00, 3210.7, 4.03 and 3.63). Shahbaz x CEMB-30 (3.73) exhibited greater boll weight and G.O.T% (3.73 and 44.0). Among crosses, the highest boll weight and seed index was depicted in the cross BT-85 x AVP (3.77 and 6.80). The minimum plant height and more staple length was found in the crosses BT-86 x AVP and FH168 x RR (109.67 and 105.33; 29.36) while the minimum value was observed cross Okra-khaki x CEMB-30 (28.70). Heritability estimates were variable in various characters varying from low, moderate and high heritability. For plant height, sympodial branches plant⁻¹, number of bolls plant⁻¹ , seed cotton yield plant⁻¹ the highest heritability exhibited in the hybrid FH168 x CEMB-30 (85.71% ,88.71%, 86.56% and 84.23%) along with genetic advance as 28.43,

4.43. 10.89. The boll weight revealed highest heritability and genetic advance in BT-86 x AVP (95.88% and 4.39) followed by IR1513 x CEMB-30 (91.005 and GA=3.02), respectively. Seed index showed highest heritability in the cross FH168 x RR (95.37% and 4.20) followed by Okra-khaki x CEMB-30 (92.01% and GA=2.28), respectively. G.O.T % . The cross Okra-khaki x CEMB-30 (h76.44 % and 3.38). The highest heritability and genetic advance were found in the cross FH168 x CEMB-30 (85.71% and GA=13.27). Moderate heritability was observed in the hybrid FH168 x RR (53.08 and GA=4.07). Lowest heritability revealed in the cross Shahbaz x CEMB-30 (3.53 and GA=0.61). The highest heritability and genetic advance depicted in the cross Okra-khaki x CEMB-30 (92.01% and 2.28) followed by the cross FH168 x CEMB-30 (85.71 and GA=1.28). The maximum heritability was found in the cross FH168 x RR (96.00 and GA=1.44). Moderate heritability was observed in the crosses Shahbaz x CEMB-30, BT-85 x AVP and FH168 x CEMB-30 (74.04, 69.86 and 67.53%), respectively.

Recommendations

1. BT-86, CEMB-30 and BT-85 possessed highest sympodial branches plant⁻¹, number of bolls plant⁻¹ and seed cotton yield plant⁻¹ and may be recommended as best parents.
2. Among the hybrids, Okra khaki x CEMB-30 and IR1513 x CEMB-30
3. Shahbaz x CEMB-30 (3.73) exhibited greater boll weight and G.O.T%

REFERENCES

- Ahmed, A., Rahman, S., Islam, M., Chowdhury, F., & Badhan, I. A. (2023). Challenges and Opportunities in Implementing Machine Learning For Healthcare Supply Chain Optimization: A Data-Driven Examination. *International journal of business and management sciences*, 3(07), 6-31.
- Ali, Z., Maryam, H., Saddique, M. A. B., & Ikram, R. M. (2023). Exploiting genetic diversity in enhancing phenotypic plasticity to develop climate-resilient cotton. *Genetic Resources and Crop Evolution*, 70(5), 1305-1320.

- Araf Nishan, et al., A continuous cuffless blood pressure measurement from optimal PPG characteristic features using machine learning algorithms, *Heliyon* 10 (2024) e27779, <https://doi.org/10.1016/j.heliyon.2024.e27779>, 6.
- Aslam, S., Khan, S. H., Ahmed, A., & Dandekar, A. M. (2020). The tale of cotton plant: From wild type to domestication, leading to its improvement by genetic transformation. *American Journal of Molecular Biology*, 10(2), 91-127.
- Azanaw, A., Birlie, B., Teshome, B., & Jemberie, M. (2022). Textile effluent treatment methods and eco-friendly resolution of textile wastewater. *Case Studies in Chemical and Environmental Engineering*, 6, 100230.
- Badhan, I. A., Hasnain, M. N., & Rahman, M. H. (2022). Enhancing Operational Efficiency: A Comprehensive Analysis of Machine Learning Integration in Industrial Automation. *Journal of Business Insight and Innovation*, 1(2), 61-77.
- Badhan, I. A., Neeroj, M. H., & Chowdhury, I. (2024). THE EFFECT OF AI-DRIVEN INVENTORY MANAGEMENT SYSTEMS ON HEALTHCARE OUTCOMES AND SUPPLY CHAIN PERFORMANCE: A DATA-DRIVEN ANALYSIS. *Frontline Marketing, Management and Economics Journal*, 4(11), 15-52.
- Dhunde, A. D., Naik, V. G., Malve, D. B., Kadam, J. R., Dhekale, J. S., Torane, S. R., & Sundaramoorthy, C. (2022). An Evaluation of Organic and Conventional Cotton Production in Maharashtra, India. *International Journal of Environment and Climate Change*, 12(12), 1780-1785.
- Farooq, A., Shakeel, A., Saeed, A., Farooq, J., Rizwan, M., Chattha, W. S., ... & Ramzan, Y. (2023). Genetic variability predicting breeding potential of upland cotton (*Gossypium hirsutum* L.) for high temperature tolerance. *Journal of Cotton Research*, 6(1), 7.
- Fiaz, S., Wang, X., Younas, A., Alharthi, B., Riaz, A., & Ali, H. (2021). Apomixis and strategies to induce apomixis to preserve hybrid vigor for multiple generations. *GM crops & food*, 12(1), 57-70.
- Gibely, R. H. (2021). Variability, genetic components and selection response in segregating generations among some cotton crosses. *Journal of Sustainable Agricultural Sciences*, 47(1), 1-12.
- Huang, G., Huang, J. Q., Chen, X. Y., & Zhu, Y. X. (2021). Recent advances and future perspectives in cotton research. *Annual review of plant biology*, 72(1), 437-462.
- Hussain, A., Arshad, K., Abdullah, J., Aslam, A., Azam, A., Bilal, M., ... & Abdullah, M. (2021). A Comprehensive Review on Breeding Technologies and Selection Methods of Self-pollinated and Cross-Pollinated Crops. *Asian Journal of Biotechnology and Genetic Engineering*, 4(3), 35-47.
- Jabbar, T., Khalid, S., Atif, R. M., Rehman, H. M., & Rana, I. A. (2021). Wild Relatives and Modern Plant Breeding Technologies. *Wild Germplasm for Genetic Improvement in Crop Plants*, 343-371.
- Jamil, A., Khan, S. J., & Ullah, K. (2020). Genetic diversity for cell membrane thermostability, yield and quality attributes in cotton (*Gossypium hirsutum* L.). *Genetic Resources and Crop Evolution*, 67(6), 1405-1414.
- Khan, A. H., Hassan, M., & Khan, M. N. (2020). Conventional plant breeding program for disease resistance. *Plant disease management strategies for sustainable agriculture through traditional and modern approaches*, 27-51.
- Matloob, A., Aslam, F., Rehman, H. U., Khaliq, A., Ahmad, S., Yasmeen, A., & Hussain, N. (2020). Cotton-based cropping systems and their impacts on production. *Cotton Production and Uses: Agronomy, Crop Protection, and Postharvest Technologies*, 283-310.

- Mubarik, M. S., Ma, C., Majeed, S., Du, X., & Azhar, M. T. (2020). Revamping of cotton breeding programs for efficient use of genetic resources under changing climate. *Agronomy*, *10*(8), 1190.
- Munir, H., Rasul, F., Ahmad, A., Sajid, M., Ayub, S., Arif, M., & Khan, M. A. (2020). Diverse uses of cotton: From products to byproducts. *Cotton Production and Uses: Agronomy, Crop Protection, and Postharvest Technologies*, 629-641.
- Nadeem, S., Riaz Ahmed, S., Luqman, T., Tan, D. K., Maryum, Z., Akhtar, K. P., ... & Liu, Y. (2024). A comprehensive review on *Gossypium hirsutum* resistance against cotton leaf curl virus. *Frontiers in Genetics*, *15*, 1306469.
- Rehman, A., Mustafa, N., Du, X., & Azhar, M. T. (2020). Heritability and correlation analysis of morphological and yield traits in genetically modified cotton. *Journal of cotton research*, *3*, 1-9.
- Riaz, T., Iqbal, M. W., Mahmood, S., Yasmin, I., Leghari, A. A., Rehman, A., ... & Bilal, M. (2023). Cottonseed oil: A review of extraction techniques, physicochemical, functional, and nutritional properties. *Critical Reviews in Food Science and Nutrition*, *63*(9), 1219-1237. ISSN (E): 3006-7030 (P): 3006-7022
- S.T.U. Raju, S.A. Dipto, M.I. Hossain, M.A.S. Chowdhury, F. Haque, A.T. Nashrah, A. Nishan, M.M.H. Khan, M. Hashem, DNN-BP: a novel framework for cuffless blood pressure measurement from optimal PPG features using deep learning model, *Med. Biol. Eng. Comput.* (2024) 1–22.
- Saha, S., Bellaloui, N., Jenkins, J. N., McCarty, J. C., & Stelly, D. M. (2020). Effect of chromosome substitutions from *Gossypium barbadense* L., *G. tomentosum* Nutt. Ex Seem and *G. mustelinum* Watt into *G. hirsutum* L. on cottonseed protein and oil content. *Euphytica*, *216*(7), 118.
- Shar, Z. H., Pirkash, O., Shar, H. H., Sherazi, S. T. H., & Mahesar, S. A. (2020). Aflatoxins in cotton seeds and cotton seed cake from Pakistan. *Food Additives & Contaminants: Part B*, *13*(1), 72-76.
- Siyal, A. L., Mahesar, T. G., Sufyan, F., Siyal, F. K., Jatt, T., Mangi, F. H., ... & Hossain, A. (2021). Climate change: Impacts on the production of cotton in Pakistan. *European Journal of Agriculture and Food Sciences*, *3*(3), 97-100.
- Tauqir, N. A., Bilal, R. M., Faraz, A., Khan, A. H., Ashfaq, F., Abbassi, B. H. A., & Yameen, K. (2021). Palm Oil Cake Can Substitute Cottonseed Cake in the Feed of Milking Nili Buffaloes. *Pak-Euro Journal of Medical and Life Sciences*, *4*(3), 153-160.
- Velmourougane, K., Blaise, D., Savitha, S., & Waghmare, V. N. (2021). Valorization of cotton wastes for agricultural and industrial applications: present status and future prospects. *Valorization of Agri-Food Wastes and By-Products*, 665-692.
- Zahid, G., Iftikhar, S., Farooq, M. U., & Soomro, S. A. (2022). Advances in DNA based Molecular Markers for the Improvement of Fruit Cultivars in Pakistan-A Review. *Sarhad Journal of Agriculture*, *38*(3).
- Zaki, H. E., & Radwan, K. S. (2022). Estimates of genotypic and phenotypic variance, heritability, and genetic advance of horticultural traits in developed crosses of cowpea (*Vigna unguiculata* [L.] Walp). *Frontiers in Plant Science*, *13*, 987985.