

INTERRELATION OF YIELD AND ITS COMPONENTS IN COTTON (*Gossypium hirsutum* L.) GENOTYPES

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(Received, 27<sup>th</sup> June 2024, Revised 20<sup>th</sup> September 2024, Published 30<sup>th</sup> September 2024)

**Abstract:** Cotton is regarded as a profitable crop that gives people fiber and shelter. Research focuses on how yield, its components, and related attributes work together to enhance cotton. During the Kharif season of 2022, the present study was completed, implementing a randomized complete block design with ten genotypes and three replications. The study took place at the Nuclear Institute of Agriculture (NIA), located in Tandojam. This work aimed to examine the correlation and regression between upland cotton genotypes and heritability estimates for traits associated with yield. The outcomes showed that all of the parameters in the mean square of the ANOVA were significant. In contrast to the remaining genotypes, genotype FH-142 displayed the most favorable performance; it had the tallest plants, more sympodial branches, more bolls per plant, an improved seed index, and the longest staple length. The genotype CRIS-342 came in second, exhibiting good plant height, sympodial branches, a good number of bolls per plant, a ginning outturn, and the highest boll weight among the other genotypes. The findings of the correlation and regression indicated that the number of bolls per plant-1 had a highly significant and positive relationship with monopodial branches plant-1 ( $r = 0.73^*$ ) and ( $b = 2.45$ ) and that the number of bolls per plant had a strong relationship with seed cotton yield plant-1 ( $r = 0.83^*$ ) and ( $b = 3.29$ ). Staple length and seed cotton yield plant-1 had a negative correlation ( $-0.77^*$ ) with regression ( $b = -4.58$ ). The highest heritability estimates in the broad sense are for monopodial branch plants (84.61), ginning outturn% (97.03), bolls plant-1 (93.96), plant height (90.70), staple length (79.31), and seed index (71.42). However, the boll's weight showed a low heritability (23.71). Further breeding programs can utilize genotype FH-142 to increase the number of sympodial branches, increase the number of boll plants, and improve the staple length. Genotype CRIS-342 can be utilized for medium-stature plant height, boll weight, and better ginning outturn. However, genotype NIA-BT-40 can be utilized for short-strategy plants with the highest ginning output.

**Keywords:** Genotypes; Cotton, genetic advance, Yield components.

## Introduction

The cotton plant (1) is a member of the *Gossypium* genus and family of Malvaceae plants. It is also known as "white gold" and is mostly grown for fiber (2). The most widely grown crop and a significant natural fiber supply for the fabric sector is cotton (3). There are roughly fifty species in the genus *Gossypium*. The three most important cultivated species in the genus *Hirsutum* are *barbadense*, *herbaceum*, and *arborescens* (4). It is the world's most important and critical renewable textile fiber, as well as the sixth-largest source of oil (5). It belongs to the *Gossypium* genus, which includes 45 diploid and five tetraploid species. Only four of these species, referred to as old world and new world species, respectively, are tetraploid. (6). For economic reasons, farmers cultivate cotton as an annual crop, despite its perpetual growth cycle. Cotton is mostly composed of cellulose, with minor amounts of waxes, lipids, pectin, and water. Tropical and subtropical regions around the world are home to this plant. Because it is a cash crop, cotton has a significant economic impact on the entire world (7). Cotton

fiber has a wide range of applications in the textile industry, ranging from light voiles and laces to thick-pilled velveteen and heavy sailcloths that are perfect for a multitude of uses (8). Around the world, cotton is a valuable economic resource that is used to create garments and construction materials. One of the crops grown for the textile industry's natural fiber production is this one (9). Reports indicate that *Gossypium hirsutum*, an all-tetraploid with  $2n = 4x-52$ , originated from the ancient genomes of *Gossypium arborescens* and *Gossypium raimondii* (10). Pakistan produces less cotton than other cotton-producing countries; nevertheless, it ranks fourth in terms of bulk production and third in terms of upland cotton consumption (11). According to (12), Pakistan ranks third globally for the export of cotton raw materials but first in the world for the supply of cotton fiber. Pakistan's textile industry is primarily based on cotton. The majority of the cotton produced in our nation is exported as raw materials, yarn, and garments, with the remaining 30 to 40 percent being used locally. Cotton produces 4.8% of the country's agricultural output and 0.8%

[Citation: Sajid, M.A., Jatoi, W.A., Kaleri, A.A., Manzoor, D., Ullah, N., Afzal, A., Shahzadi, I., Ahmed, M., Ahmed, F., Asghar, S., (2024). Interrelation of yield and its components in cotton (*Gossypium hirsutum* L.) genotypes. *Biol. Clin. Sci. Res. J.*, 2024: 1072. doi: <https://doi.org/10.54112/bcsrj.v2024i1.1072>]

of its total GDP (Economic Survey Report 2018-19). Globally, the textile industry recognizes the cotton crop as its cornerstone and refers to it as "White Gold" (13). In 2019, the world produced cotton on 33.1 million hectares, yielding 136 million bales (14). Pakistan ranks third globally in terms of cotton export quantity, and fourth overall in terms of consumption and production. The main causes of low productivity and poor fiber quality in the country include high temperatures, drought, salinity, and a weak and adulterated seed supply. In addition to its 0.8 GDP share, cotton contributes 4.5% to the value of agriculture. Cotton production is projected to increase by 17.9% between 2021 and 2022. It has increased to 8.3 million bales from the previous year's 7.1 million. In contrast to the previous year's 2,079 thousand hectares, the cropped area decreased to 1,937 thousand hectares (6.8%) in 2021–2022. In comparison to 7.064 million bales produced the previous year, production jumped to 8.329 million bales (17.9%). It produces a yield of 731 kg/hectare, or nearly 26.5% (Economic Survey of Pakistan 2018-19). Pakistan is the world's fifth-largest cotton producer. Cotton and textile products account for around 60% of the country's total exports. It contributes roughly 0.6% of GDP and 2.4% of total agricultural value added. Cotton output has decreased in recent decades as other crops, including rice, sugarcane, maize, potatoes, and others, have taken the place of cotton in terms of cultivation. The cultivated area in 2021-2022 decreased to 1,937 thousand hectares from 2,079 thousand hectares in the previous year (7). The term "heritability" solely describes the extent to which genetics influence a character; understanding a character's heritability enables a breeder to forecast the trait's manifestation in future generations, thereby influencing breeding decisions. Genetic parameter estimation will be a part of every breeding program that tries to enhance a plant's economic character (15). After hybridization, we use heritability to evaluate the response of segregating groups to selection. To account for variation in phenotypic features in populations, heritability measures the amount of genetic variability among individuals that is transmissible from parents to their offspring. Heritability estimates the repeated hereditary probability in breeding and genetics (16). Research into heritability analysis and the genetic potential of various cultivars about their appearance, distinct yield, and morphological attributes is essential for the advancement of prospective paternities for breeding reasons (17). By estimating heritability, breeders can better manage their resources and select desired features while gaining the most genetic benefit possible with the least amount of time and

effort. Additionally, heritability assumes that people who are more closely connected are more likely to look alike than people who are more distantly related (18).

**Methodology**

The experiment at the Nuclear Institute of Agriculture (NIA), Tandojam in the Kharif season of 2022 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.

**Culture Practices**

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

1. NIA-97
2. NIA-98
3. NIA-99
4. NIA-BT-3
5. NIA-BT-40
6. NIA-BT-45
7. Sadori
8. CRIS-342
9. FH-142
10. BT-866

**Statistical analysis**

The data were subjected to analyses of variances (ANOVA) as outlined by Gomez and Gomez (1984) through the Statistics 8.1 computer program for all the traits. The genotype means for each trait were further divided and compared by using the least significant difference (LSD) test at 5% level probability: correlation and regression were compacted as described by Snedecor and Cochran (1980), and heritability was calculated as per the formula given by Falconer (1989).

**Results**

**Analyses of variance**

Ten genotypes were found to be significant based on the mean square of analyses of variance. These genotypes were plant height, number of sympodial branches (plant 1), number of bolls (plant 1), seed index, ginning output, and staple length.

**Table 4.1 Mean square of (ANOVA) for various traits**

Traits	Mean Square		
	Replications D.F=2	Genotypes D.F=9	Error D.F=18
Plant height	61.08	212.15**	15.14
Monopodia branches plant <sup>1</sup>	0.20	0.13*	0.02
Sympodial branches plant <sup>1</sup>	21.025	36.45**	8.91
Bolls plant <sup>1</sup>	4.35	234.23**	10.76
Boll weight	0.006	0.79**	0.56
Seed index	0.07	1.65**	0.02
Seed cotton yield plant <sup>1</sup>	548.80	2404.09**	497.50
Ginning outturn	0.16	36.54**	0.82
Staple length	0.42	0.55**	0.09
Micronaire value	0.05	0.09*	0.08

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Significant at 1% and significant at 5% probability level

**Mean performance**

Table 4.2 displays the mean performance for the nine quantitative traits, respectively.

**Plant height (cm)**

Among the ten genotypes, the FH-142 genotype had the tallest plants (143.30 cm), followed by the CRIS-342 genotype (136.70 cm), while the NIA-99 genotype had the shortest plants, measuring 115.00 cm.

**Monopodial branches plant-1**

The genotypes NIA-97 and NIA-98 exhibited the highest ratio of monopodial branches (1.0), followed by NIA-99, NIA-BT-3, NIA-BT-40, NIA-BT-45, Sadori, FH-142, and BT-866 with a ratio of 0.66. Conversely, the CRIS-342 genotypes displayed the fewest monopodial branches in plant-1 (0.33).

**Sympodial branches plant-1**

The genotype BT-866 had the highest number of sympodial branches (27.00), followed by genotype CRIS-342 with 23.00, despite genotype NIA-99 showing the fewest sympodial branches per plant (14.00).

**Number of bolls plant-1**

The genotype NIA-97 exhibited the highest number of boll plants at 57.50, followed by genotype FH-142 at 42.72, and genotype CRIS-342 had the lowest number of boll plants at 26.13.

**Boll weight (g)**

For the boll weight of traits. It was observed that genotype NIA-BT-45 has the highest boll weight (4.05), followed by (3.88) in genotype NIA-99, whereas the lowest boll weight was found (2.52) in genotype NIA-98.

**The seed index represents 100 seed weights in grams.**

Among the ten genotypes, genotype FH-142 had the lowest seed index (6.50), followed by NIA-BT-45 with a weight of 8.55.

**Seed cotton yield plant-1 (g)**

Genotype NIA-97 (183.33) had the maximum seed cotton yield plant, while genotype CRIS-342 had the lowest (99.00).

**Ginning out turn (%)**

GOT% of all the genotypes were observed, respectively; genotype NIA-BT-40 showed the highest outturn of 44.15, followed by 37.80 in genotype Cris-342, whereas the minimum outturn (30.98) was depicted in BT-866.

**Staple length (mm)**

Genotype NIA-99 recorded the maximum staple measurement of 29.03, followed by NIA-98 with a length of 28.76, while genotype NIA-97 recorded the minimum staple length of 27.66.

**Micronaire value (<0xC2><0xBD> g/inch)**

The genotype BT-866 had the highest micronaire value of 4.23, followed by genotype FH-142 with 4.10; despite genotype NIA-99, NIA-BT-3 showed the lowest (3.73).

**Table 4.2a Mean performance for different quantitative traits of cotton genotypes**

Genotypes	Plant height (cm)	Monopodial branches plant <sup>-1</sup>	Sympodial branches plant <sup>-1</sup>	Number of Bolls plant <sup>-1</sup>	Boll weight (g)
NIA-97	124.00 CDE	1.0 A	20.00 ABC	57.50 A	2.53 A
NIA-98	129.678 BCD	1.0 A	20.66 ABC	40.47 B	2.52 A
NIA-99	115.00 E	0.66 A	14.00 C	26.25 C	3.88 A
NIA-BT-3	133.67 ABC	0.66 A	20.66 ABC	37.66 B	3.33 A
NIA-BT-40	119.33 DE	0.66 A	20.66 ABC	39.00 B	3.12 A
NIA-BT-45	127.67 BCD	0.66 A	22.00 ABC	41.0 B	4.05 A
Sadori	125.33 BCDE	0.66 A	17.00 BC	40.50 B	3.33 A
CRIS-342	136.70 AB	0.33 A	23.00 AB	26.13 C	3.79 A
FH-142	143.30 A	0.66 A	18.50 ABC	42.72 B	3.38 A
BT-866	123.00 CDE	0.66 A	27.00 A	36.0 B	3.39 A
LSD (5%)	11.38	1.76	8.73	9.59	2.19

**Table 4.2b Mean performance for various characters of cotton genotypes**

Genotypes	Seed index (g)	Seed cotton yield plant <sup>-1</sup> (g)	Ginning out turn (%)	Staple length (mm)	Micronaire value (µg inch <sup>-1</sup> )
NIA-97	7.90 BC	183.33 A	34.35 CD	27.66 C	4.03 0A
NIA-98	8.16 B	100.67 B	37.29 B	28.76 AB	4.00 A
NIA-99	7.59 C	100.67 B	35.68 BCD	29.03 A	3.73 A
NIA-BT-3	8.820 A	125.67 AB	36.06 BC	28.16 ABC	3.73 A
NIA-BT-40	7.59 C	121.67 AB	44.15 A	28.00 ABC	3.96 A
NIA-BT-45	8.55 A	166.00 A	33.07 DE	27.86 BC	3.83 A
Sadori	7.66 C	135.33 AB	35.97 BC	28.16 ABC	3.73 A
CRIS-342	7.01 D	99.00 B	37.80 B	28.30 ABC	4.03 A
FH-142	6.50 E	143.00 AB	37.61 B	27.86 BC	4.10 A
BT-866	6.80 DE	119.67 AB	30.98 E	27.83 C	4.23 A
LSD (5%)	0.31	65.27	2.66	0.90	0.84

**The number of bolls on plant 1 differs from the number of monopodial branches on plant 1.**

The correlation coefficient (r) between the number of bolls plants (Table 4.3) and monopodial branches was positive

and significant (0.73\*), and their regression analysis (b = 2.45) suggested that an increase in the number of bolls plants would also lead to an increase in monopodial branches. A further coefficient of determination (r<sup>2</sup> = 0.02)

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revealed a 20% variation between the number of bolls plants and monopodial branches per plant.

**Boll weight vs. monopodial branches plant-1**

The correlation coefficient between the boll weight and the monopodial branches of plant-1 was -0.53NS, indicating a non-significant and negative relationship. The regression analysis (b = -0.28) in Table 4.3 demonstrated that an increase in the boll weight would result in a corresponding decrease in the monopodial branches of plant-1. Furthermore, the coefficient determination (r<sup>2</sup> = 0.03) revealed a 30% variation between the boll weight and the monopodial branches of plant 1.

**Plant 1 yields more seed cotton than monopodial branches.**

The correlation coefficient (0.38NS) in Table 4.3 showed a positive and non-significant link between seed cotton yield plant-1 and monopodial branches plant-1. The regression analysis (b = 11.98) showed that if seed cotton yield plant-1 increases at the same time, so does monopodial branches plant-1. The further co-efficient determination (r<sup>2</sup> = 0.03) revealed a 30% variation between the seed cotton yield plant-1 and the monopodial branches plant-1.

**Micronaire value vs. sympodial branches plant-1**

Table 4.3 suggests a positive and highly significant correlation (0.66\*) between the micronaire value and the sympodial branches of plant-1, implying that an increase in the micronaire value will also lead to an increase in the sympodial branches. The correlation between the micronaire value and sympodial branches plant-1 resulted in a coefficient of determination (r<sup>2</sup> = 0.02), which represents the percentage of the total variance in sympodial branches plant-1. The regression coefficient (b) shows that a unit increase in the micronaire value decreases (0.01) the number of sympodial branches in plant-1.

The correlation coefficient (r = -0.63\*) showed a strongly negative relationship between the length of the staple and the number of bolls per plant. Regression analysis (b = -0.03) showed that if the length of the staple goes up, so does the number of bolls per plant. Furthermore, Table 4.3 displays the coefficient of determination (r<sup>2</sup> = 0.28), which demonstrates the variation between staple length and the number of bolls per plant.

The correlation coefficient of seed cotton yield plant-1 (0.83\*\*) showed a significant and positive association with the number of bolls per plant-1. Their regression analysis (b = 3.29, Table 4.3) suggested that an increase in seed cotton yield plant-1 would also lead to an increase in the number of bolls per plant-1. The further determination of the co-

efficient (r<sup>2</sup> = 0.96) revealed a variation between the seed cotton yield per plant-1 and the number of bolls per plant-1.

**GOT% vs. boll weight**

The GOT% (-0.37NS) correlation coefficient with washbowl weight was negative and non-significant. Their regression analysis (b = 10.32) suggested that if GOT% increases, the boll weight will also decrease at the same time, as shown in Table 4.3. A higher coefficient of determination (r<sup>2</sup> = 0.93) revealed a 93% variation between the GOT% and boll weight.

**Seed cotton yield plant-1 vs. GOT%**

The relationship between seed cotton yield plant-1 and GOT% (r = -0.30 NS) in Table 4.3 was not significant and negative. Their regression analysis (b = -3.51) showed that if seed cotton yield plant-1 goes up, GOT% goes down at the same time. Furthermore, the coefficient of determination (0.92) demonstrated a 92% variation between seed cotton yield plant-1 and GOT%.

**Micronaire value vs. staple length**

The correlation coefficient of the micronaire value (r = -0.42NS) indicates a non-significant and negative association with staple length. Their regression analysis (b = -0.13) in Table 4.3 suggests that an increase in the micronaire value coincides with an increase in the staple length. Furthermore, the coefficient of determination (r<sup>2</sup> = 0.999) reveals a 99% variation between the micronaire value and staple length.

**The seed cotton yield at plant-1 is compared with the staple length.**

The correlation coefficient (r) between seed cotton yield plant-1 and staple length was negative and significant (-0.77\*), and their regression analysis (b = -4.58) indicated in Table 4.3 that an increase in seed cotton yield plant-1 coincides with an increase in staple length. The further coefficient of determination (r<sup>2</sup> = 0.93) revealed a 93% variation between the seed cotton yield plant-1 and the staple length.

**Seed index vs. micronaire value**

The correlation coefficient (r) indicates a negative and highly significant correlation (-0.66\*) between the seed index and the micronaire value, suggesting that an increase in the seed index will also lead to an increase in the micronaire value. The correlation with the seed index caused the coefficient of determination (r<sup>2</sup> = 0.98) to be 98 percent of the total variance in micronaire value (Table 4.3). The regression coefficient (b) shows that a unit increase in the seed index decreases the micronaire value by (-1.92).

**Table 4.3 Correlation and regression analyses for different quantitative traits of cotton**

Traits	Correlation (r)	Coefficient Determinant (r <sup>2</sup> )	of Regression (b)
Number of bolls per plant <sup>1</sup> VS Monopodial branches plant <sup>-1</sup>	0.73*	0.02	2.45
Boll weight VS Monopodial branches plant <sup>-1</sup>	-0.53 <sup>NS</sup>	0.03	-0.28
Seed cotton yield plant <sup>1</sup> VS Monopodial branches plant <sup>-1</sup>	0.38 <sup>NS</sup>	0.03	11.98
Micronaire value VS Sympodial branches plant <sup>-1</sup>	0.66*	0.02	0.01
Staple length VS Number of boll per plant <sup>1</sup>	-0.63*	0.28	-0.03
Seed cotton yield plant <sup>1</sup> VS Number of boll plant <sup>-1</sup>	0.83**	0.96	3.29
GOT VS Boll weight	-0.37 <sup>NS</sup>	0.93	10.32
Seed cotton yield plant <sup>1</sup> VS GOT	-0.30 <sup>NS</sup>	0.92	-3.51
Micronaire value VS Staple length	-0.42 <sup>NS</sup>	0.99	-0.13
Seed cotton yield plant <sup>1</sup> VS Staple length	-0.77*	0.93	-4.58
Seed index VS Micronaire value	-0.66*	0.98	-1.92

[Citation: Sajid, M.A., Jatoi, W.A., Kaleri, A.A., Manzoor, D., Ullah, N., Afzal, A., Shahzadi, I., Ahmed, M., Ahmed, F., Asghar, S., (2024). Interrelation of yield and its components in cotton (*Gossypium hirsutum* L.) genotypes. *Biol. Clin. Sci. Res. J.*, 2024: 1072. doi: <https://doi.org/10.54112/bcsrj.v2024i1.1072>]



\*\* Significant 1%

\* Significant 5% probability level and

NS for non-significant

#### Estimation of heritability

Table 4.4 displays the estimated heritability for each quantitative variable in upland cotton (*Gossypium hirsutum* L.). Each trait had a range of heritabilities. For example, GOT had a high heritability of 97.03 percent, a genetic variance of 35.72 percent, an environmental variance of 0.27 percent, and a phenotypic variance of 36.81 percent. Conversely, the number of bolls per plant exhibits a heritability of 93.96%, with a genetic variance of 223.47, an environmental variance of 3.58, and a phenotypic variance

of 237.81. Additionally, the plant's height demonstrates a heritability of 90.70, a genetic variance of 197.01, an environmental variance of 5.04, and a phenotypic variance of 217.196. The monopodial branch plant demonstrated a high heritability of 84.61%, accompanied by genetic variance of 0.11, 0.00, and 0.13 and phenotypic variances of 0.13. Meanwhile, the staple length showed a heritability of 79.31, with genetic variances of 0.46, 0.03, and 0.58, as well as phenotypic variances of 0.58. Typical variance (0.58). It was found that the trait Micronaire value exhibited the lowest heritability (9.09), genetic variance (0.01), environmental variance (0.02), and phenotypic variance (0.11).

**Table 4.4 Estimation of heritability in a broad sense for various traits of upland cotton genotypes**

Traits	Genetic Variance ( $\sigma^2_g$ )	Environmental Variance ( $\sigma^2_e$ )	Phenotypic Variance ( $\sigma^2_p$ )	Heritability ( $h^2$ b.s %)
Plant height	197.01	5.046	217.196	90.70
Monopodial branches plant <sup>-1</sup>	0.11	0.00	0.13	84.61
Sympodial branches plant <sup>-1</sup>	27.54	2.97	39.42	69.86
No. of bolls per plant <sup>-1</sup>	223.47	3.58	237.81	93.96
Boll weight	0.23	0.18	0.97	23.71
Seed cotton yield plant <sup>-1</sup>	1906.59	165.83	2569.92	74.18
GOT (%)	35.72	0.27	36.81	97.03
Staple length	0.46	0.03	0.58	79.31
Micronaire value	0.01	0.02	0.11	9.09
Seed index	0.05	0.001	0.07	71.42

#### Discussion

Cotton, a valuable economic commodity globally, serves as a material for clothing and shelter, and it's a key crop for natural fiber production (19). Understanding the associations between key traits simplifies the selection of cotton cultivars with high-yield and high-quality fiber (20). Heritability holds significant importance as it reveals the extent to which genes in a population impact a phenotypic trait. This study examined correlation analysis and heritability estimates for fiber and yield variables of several cotton genotypes in the current study. Cotton genotypes were examined.

The analysis of variance revealed variations in genotypes at the P0.01 and P0.05 probability levels, specifically in terms of plant height. Plants with monopodial (non-fruiting) branches and those with sympodial (fruiting) branches showed variation in genotypes. The number of bolls per plant-1, the seed index (100 seed weights in g), the percentage of bolt weight (g), and the staple length (mm) are all significant. The ANOVA results revealed significant variances among all the identified characters, and the analysis of variance also confirmed the significance of all the observed traits. (21) found the same significant results for all the characters. The same significant results for all the characters (21).

Figure 4.2 displays the average results for cotton genotype performance, highlighting both the best and worst performance across all genotypes in terms of various attributes such as plant height, based on ten genotypes observed. The genotype FH-142 exhibited the tallest plants at 143.30 cm, trailed by the CRIS-342 genotype at 136.70 cm, whereas the NIA-99 genotype exhibited the shortest plants at 15.00 cm. For the monopodial branches, genotypes NIA-97 and NIA-98 showed the highest ratio of

monopodial branches (1.0), followed by genotypes NIA-99, NIA-BT-3, NIA-BT-40, NIA-BT-45, Sadori, FH-142, and BT-866 (0.66). The genotype CRIS-342 displayed the fewest monopodial branches in plant-1, with a count of 0.33. BT-866 had the highest number of sympodial branches (27.00), followed by genotype CRIS-342 with 3.00, despite genotype NIA-99 showing the fewest sympodial branches per plant (14.00). The genotype NIA-97 exhibited the highest number of boll plants, at 57.50, followed by the genotype FH-142 at 42.72, while the genotype NIA-99 had the lowest number of boll plants, at 26.25. The research by Li et al. (2020) yielded similar results. The genotype NIA-BT-45 has the highest boll weight (4.05), followed by NIA-99 (3.88), while genotype NIA-98 (2.52) has the lowest boll weight. The character seed index for NIA-BT-3 was 8.82, followed by 8.16 in NIA-98, and genotype FH-142 had the lowest seed index at 6.50. In terms of GOT, genotype NIA-BT-40 demonstrated the highest outturn with 44.15, followed by genotype CRIS-342 with 37.80, and genotype BT-866 with a minimum outturn of 30.98. Breeders have prioritized ginning outturn due to its correlation with yield-related traits (22). The genotype NIA-99 recorded a maximum staple length of 29.03, followed by NIA-98 with a length of 28.76, while genotype NIA-97 recorded a minimum staple length of 27.66. (28.76) length, although the minimum staple length was recorded (27.66) in genotype NIA-97. Whereas the micronaire value remains, genotype BT-866 had the highest micronaire value of 4.23, followed by genotype FH-142 with 4.10; despite genotype NIA-99, NIA-BT-3 showed the lowest (3.73).

Correlation and regression are critical in plant breeding because they serve as indirect selection measures for yield-related traits. The association results for various quantitative characters of upland cotton are presented in Table 4.3. The

association study revealed a highly significant and positive correlation between the number of bolls per plant and monopodial (non-fruited) branches per plant, with a regression coefficient of  $b = 2.45$ . Conversely, the weight of the boll showed a significantly non-significant negative correlation with monopodial (non-fruited) branches per plant, with a regression coefficient of  $b = -0.28$ . Plant-1's seed cotton yield demonstrated a non-significant positive association with monopodial branches, with a regression value of 11.98. In their study, (8) also observed both positive and negative associations with the character of monopodial branches plant-1. The study found that the monopodial branches plant-1 exhibited a highly significant relationship with the number of bolls, the micronaire value showed a positive but significant correlation with the sympodial branches plant-1, and the regression was both positive ( $b = 0.01$ ) and negative ( $b = -0.03$ ) with the staple length and the number of bolls per plant-1. Additionally, the seed cotton yield plant-1 showed a significant relationship with the number of bolls per plant-1 ( $b = 3.29$ ). (23) also observed similar results for the character seed cotton yield plant-1. The trait micronaire value showed a non-significant and negative correlation with staple length, as revealed by the regression ( $b = -0.13$ ), and the seed cotton yield plant-1 showed a negative correlation with staple length, which was also highly significant, as indicated by the regression ( $b = -4.58$ ). According to (24), the seed index expressed highly significant results with a micronaire value; however, it also showed a negative connection with the regression ( $b = -1.92$ ). GOT showed a negative, non-significant relationship with staple length.

Heritability analyses are useful in deciding which qualities to take into account when putting together a choice. Table 4.4 displays the estimates of heritability, genotypic variance, and phenotypic variation derived from corresponding variables for various traits. For the character plant height, it is demonstrated strong heritability (90.70) with genetic variance (197.01), environmental variance (5.046), and phenotypic variance (217.196). (16) (2017) found additive gene action, and experimental heritability estimations showed that heredity influenced plant height characteristics more than the environment. Genetic variance (27.54) along with phenotypic variance (39.42) was recorded for the sympodial branches of plant 1. It exhibited moderate heritability (69.86). Plant-1's monopodial branches exhibited a genetic variance of 0.11, a phenotypic variance of 0.13, and a strong heritability of 84.61. However, boll plant-1 also demonstrated high heritability (93.96), genetic variance (223.47), and phenotypic variance (237.81). (25) also displayed these heritability estimates, showing a fluctuation from moderate to high in assortment for all appearances. The study recorded a genetic variance of 0.23 for the character boll weight, a phenotypic variance of 0.97, and a low heritability of 23.71. (26) also observed low heritability and a low response to selection, confirming the same findings. Staple length showed high heritability (79.31), with genetic variance (0.46) and phenotypic variance (0.58). On the other hand, GOT exhibited great heritability (97.03), with genetic variance (35.72) and phenotypic variance (36.81). (27) also showed the same heritability percentage. The character seed index, with a genetic variance of 0.05 and a phenotypic variance of 0.07, also showed high heritability (71.42). The genetic variance (0.01) and phenotypic variance (0.11) have low heritability

for the micronaire value (9.09). Other researchers, like (28), also observed high heritability for various traits.

## Conclusion

Analyses of variance revealed significant variation and existence among experimental genotypes. Among the ten investigated genotypes, FH-142 showed maximum performance as compared to the rest of the genotypes. It displayed the tallest plants, more sympodial branches, more boll plant count, improved seed index, and longest staple length among the investigated genotypes. Genotype CRIS-342 outperformed FH-142 in terms of plant height, sympodial branch count, number of bolls per plant ginning outturn%, and boll weight, displaying the highest value among all investigated attributes. In the correlation studies, the variables of plant tallness, sympodial branch plant, boll count plant, and seed index demonstrated a positive and significant correlation with the majority of yield-related traits observed in the study. Heritability estimation revealed that all the characters exhibited strong heritability except monopodial branches, which expressed moderate heritability. It was concluded that these selected genotypes can be used in breeding programs for further improvement.

## Declarations

### Data Availability statement

All data generated or analyzed during the study are included in the manuscript.

### Ethics approval and consent to participate.

Approved by the department concerned.

### Consent for publication

Approved

### Funding

Not applicable

## Conflict of interest

The authors declared an absence of conflict of interest.

## Authors Contribution

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