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Genetic variability, heritability and genetic advance studies for seed cotton yield and yield contributing characters in upland cotton

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ABSTRACT

Seed cotton yield in upland cotton (*Gossypium hirsutum* L.) is a complex quantitative trait determined by contribution of several component characters. Screening of available genotypes for yield performance is a pre-requisite for identifying superior material for varietal improvement. The present investigation was undertaken during kharif 2025-26 at the Cotton Research Station, Nanded (Maharashtra), to evaluate seventeen upland cotton genotypes, comprising seventeen elite *hirsutum* entries and three checks (NH 677, NH 545 and NH 615), in a Randomized Block Design with three replications. Observations were recorded on eight yield and yield-contributing characters viz; Days to 50 per cent flowering, days to maturity, plant height, number of sympodia per plant, number of monopodia per plant, number of bolls per plant, boll weight and seed cotton yield per plant. Analysis of variance revealed highly significant ($P \leq 0.01$) differences among genotypes for all the eight characters, confirming the presence of substantial genetic variability in the material evaluated. Seed cotton yield per plant ranged from 49.86 g to 89.96 g with a general mean of 72.27 g; genotype NH 824 (89.96 g) recorded the highest seed cotton yield, followed by the check NH 615 (85.90 g) and genotype NH 821 (84.52 g). High genotypic coefficient of variation (GCV) coupled with high heritability and high genetic advance as per cent of mean was recorded for number of monopodia per plant (GCV 23.80%, $h_{2(bs)}$ 93.23%, GAM 47.33%) and boll weight (GCV 12.06%, $h_{2(bs)}$ 65.09%, GAM 20.04%), indicating predominance of additive gene action for these traits suggesting scope for improvement through direct phenotypic selection, whereas seed cotton yield per plant exhibited moderate GCV (13.65%) with moderate heritability (59.97%) and high genetic advance as per cent of mean (21.77%). On the basis of superior mean performance for seed cotton yield coupled with associated yield components, genotypes NH 824 and NH 821 were identified as the most promising genotypes with potential utility as parents to be used in future hybridization coupled with selection aimed at seed cotton yield improvement in *G. hirsutum* cotton.

Keywords: *Gossypium hirsutum*, Seed cotton yield, Genetic variability, Heritability, Genetic advance, GCV, PCV, Genetic advance % mean

1. Introduction

Cotton, popularly known as the "white gold," is one of the most important commercial fibre crops in the world. Among the cultivated cotton species, *Gossypium hirsutum* (L.), commonly referred to as upland or upland cotton, occupies a predominant position in global cotton production scenario owing to its high yield potential, wide adaptability and superior fibre characteristics. It contributes more than 90 per cent of the world's cotton production (Morales *et al.*, 2022) [1]. India ranks first in the world in area under cotton cultivation, whereas second in total production and consumption. The area under cotton cultivation during 2025-26 was about 114.82 lakh hectares with production of 290.91 lakh bales, with productivity of 428-451 kg per hectare. However, domestic consumption during the same period resulted in a supply gap met partly through imports, underscoring the continuing need to raise productivity through genetic improvement. In recognition of this, the Government of India has approved the five-year Mission for Cotton Productivity (2026-27 to 2030-31) to enhance yield and fibre quality across major cotton-growing states (Telangana Today, 2026). Seed cotton yield is a complex quantitative trait governed by polygenes and strongly influenced by environmental factors, and it is the end product of several interacting yield components such as number of bolls per plant, boll weight, plant height, number of sympodial and monopodial branches, and the duration to flowering and maturity (Fang *et al.*, 2014) [2]. *Gossypium hirsutum* is a tetraploid ($2n = 4x = 52$) species with a broad genetic base; however, intensive breeding and continuous selection for specific traits have narrowed the variability available upland cotton (Zhang *et al.*, 2016) [3]. Systematic evaluation of available genotypes

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for seed cotton yield and its component traits is essential for identifying promising parental material for future breeding programme. Several workers have reported considerable genetic variability for seed cotton yield and its component characters in *hirsutum* cotton (Sahar *et al.*, 2021a; Chapara *et al.*, 2022; Divya *et al.*, 2023) [5, 4, 6], yet there remains a continuous need to evaluate locally adapted genotypes under specific agro-climatic conditions to identify superior lines which can be utilized for cotton improvement programme to develop promising hybrids.

Statistical tools such as analysis of variance, estimation of genotypic and phenotypic coefficients of variation, heritability and genetic advance are widely employed to quantify the nature and extent of genetic variability present in a set of genotypes and to determine the scope for improvement through selection. The magnitude of genotypic coefficient of variation together with heritability and genetic advance as per cent of mean indicates whether a character is governed predominantly by additive gene action, rendering it amenable to direct phenotypic selection, or by non-additive gene action. In such scenario hybridization could be useful to exploit heterosis. In view of this the present investigation was undertaken to assess the seed cotton yield performance and the extent of genetic variability for seed cotton yield and yield-contributing traits among a set of *hirsutum* cotton genotypes evaluated at Cotton Research Station, Nanded, Maharashtra.

2. Materials and Methods

2.1 Experimental site, material and design

The present investigation was conducted during *kharif* 2025-26 at Cotton Research Station, Nanded (Maharashtra), India. The experimental material comprised seventeen upland cotton (*Gossypium hirsutum* L.) genotypes (NH 814, NH 816, NH 817, NH 820, NH 821, NH 824, NH 825, NH 826, NH 860, NH 864, NH 866, NH 1136, NH 1187, NH 1201, NH 1212, NH 1222 and NH 1226) along with three checks (NH 677, NH 545 and NH 615) developed at the Cotton Research Station, Nanded. The trial was laid out in a Randomized Block Design (RBD) with three replications. The plot consists of two rows per entry with gross plot size of 1.2×6.0 m² and net plot size of 1.2×5.4 m² with spacing of 60×30 cm. All recommended agronomic package of practices and need-based plant protection measures were followed for healthy crop growth.

2.2 Observations recorded

Observations were recorded on five competitive and randomly selected plants in each replication of every genotype for eight yield and yield-contributing characters. The mean values per plant were worked out. *Days to 50 per cent flowering* was recorded as the number of days from sowing to the date on which at least 50 per cent of plants had flowered. *Plant height (cm)* was measured from the ground level to the growing point of the main stem at final picking. *Days to maturity* was recorded as the number of days from sowing to maturity of 80 per cent of plants in a plot. *Number of sympodia per plant* and *number of monopodia per plant* were recorded by counting the reproductive (fruiting) and vegetative (non-fruiting) branches, respectively, on the main stem at maturity. Number of bolls per plant was recorded by counting the fully matured, open bolls on each observational plant. Boll weight (g) was determined from the average weight of seed cotton of ten bolls per treatment after final picking. Seed cotton yield per plant (g) was recorded as the seed cotton obtained from each of the five randomly selected plants, averaged per treatment.

2.3 Statistical analysis

Replication-wise mean values for all characters were subjected to analysis of variance (ANOVA) as per the standard method of Panse *et al.* (1985) [7] to test the significance of genotypic differences. Genotypic and phenotypic variances were estimated from the respective mean sums of squares following Burton (1952) [8], and the genotypic and phenotypic coefficients of variation (GCV and PCV) were

calculated by the method of Burton (1952) [8] and categorized as low (< 10%), moderate (10-20%) or high ($\geq 20\%$) following Sivasubramanian *et al.* (1973) [9]. Broad-sense heritability (h^2 b.s.) was estimated according to Allard (1960) [10] and classified as low (< 30%), moderate (30-60%) or high ($\geq 60\%$) as suggested by Robinson *et al.* (1949) [11]. Genetic advance (GA) at 5 per cent selection intensity ($K = 2.06$) and genetic advance as per cent of mean (GAM) were computed as per method given by Johnson *et al.* (1955) [12] and classified as low (< 10%), moderate (10-20%) or high ($\geq 20\%$). The standard error of difference between genotypic means and the critical difference (CD) at 5 per cent and 1 per cent levels of significance were also worked out for each character.

3. Results and Discussion

The present investigation was undertaken to evaluate seventeen upland cotton (*Gossypium hirsutum* L.) genotypes, comprising seventeen elite genotypes and three checks (NH 677, NH 545 and NH 615), for their seed cotton yield performance and associated yield-contributing characters. Results of the statistical analyses carried out on the data recorded for the seventeen genotypes for eight yield and yield-contributing traits are presented and discussed below, and are compared with relevant earlier investigations.

3.1 Analysis of variance

The mean sum of squares due to replication, treatment (genotypes) and error for the eight yield and yield-contributing characters are presented in Table 1. The analysis of variance revealed highly significant differences ($P \leq 0.01$) among the seventeen genotypes for all the eight characters studied, viz., days to 50 per cent flowering, days to maturity, plant height, number of sympodia per plant, number of monopodia per plant, number of bolls per plant, boll weight and seed cotton yield per plant. This indicated the presence of substantial amount of genetic variability present in seventeen genotypes screened for seed cotton yield and its component traits. This confirms that selection could be effective for improvement of these characters. The mean sum of squares due to replication was comparatively small for all characters, indicating a reasonably uniform experimental environment across the three replications. Similar highly significant genotypic differences for yield and its component traits in upland cotton were earlier reported by Anjani *et al.* (2020) [13] and Chapara *et al.* (2024) [14].

3.2 Mean performance of the genotypes for yield and yield-contributing traits

Mean performance of the seventeen *G. hirsutum* genotypes for the eight yield and yield-contributing characters is furnished in Table 2, along with the general mean, standard error ($SE^{\pm}$), coefficient of variation (CV%) and critical difference (CD) at 5 and 1 per cent levels of significance.

3.2.1 Days to 50 per cent flowering

Mean days to 50 per cent flowering ranged from 66.00 (NH 825) to 76.00 (NH 1136), with a general mean of 72.27 days; NH 1136 was followed by NH 817 and NH 1187 (75.00 days each) for the highest values. The spread between the highest and lowest performing genotypes exceeded the critical difference (CD @ 5% = 4.64), confirming statistically significant genotypic differences for this trait, consistent with the highly significant treatment mean sum of squares in Table 1 and with the findings of Ishaq *et al.* (2025) [15] and Kaleri *et al.* (2025) [16] in upland cotton.

3.2.2 Days to maturity

The maximum mean for days to maturity were recorded by NH 814 (145.67), followed by NH 1212 (144.67) and NH 824 (144.33). Days to maturity ranged from 131.33 to 145.67 days with a general mean of 141.97 days, the spread exceeding the CD @ 5% of 5.56 and indicating appreciable genetic variability for maturity duration. The results are in accordance with the reports of Sendekie *et al.* (2024) [17] and Hugar *et al.* (2024b) [18].

3.2.3 Plant height (cm)

Highest value of plant height was recorded by NH 1187 (206.67 cm), followed by NH 1222 (206.33 cm) and NH 864 (204.80 cm). Whereas, genotype NH 1226 recorded lowest value for plant height (163.33 cm). The general mean was 183.57 cm, with the range (163.33-206.67 cm) exceeding the CD @ 5% value of 9.77 cm, confirming significant genotypic differences. Similar kind of results were reported by Patil *et al.* (2023) [19] and Damtew *et al.* (2022) [20].

3.2.4 Number of sympodia per plant

Mean values for number of sympodia per plant ranged from 25.73 (NH 1212) to 30.74 (NH 1201), with general mean of 28.23. The genotype recorded maximum number of sympodia per plant NH 1201 (30.74) followed by NH 1222 (30.67) and NH 864 (30.47). The difference between the extreme genotypes exceeded the CD @ 5% of 2.87, indicating a statistically significant genotypic difference. The results are in agreement with the reports of Li *et al.* (2022) [21] and Aslan *et al.* (2022) [22].

3.2.5 Number of monopodia per plant

Number of monopodia per plant ranged from 2.80 (NH 1187) to 6.70 (NH 1201), with a general mean of 5.38. The genotype NH 1201 (5.38) recorded maximum monopodia per plant followed by NH 825 (6.67) and NH 820 (6.63). The spread exceeded the CD @ 5% of 0.57, confirming significant genotypic differences. Similar results were reported by Kamran *et al.* (2020) [23] and Manonmani *et al.* (2019) [24].

3.2.6 Number of bolls per plant

The highest number of bolls per plant was recorded in NH 826 (28.33), followed by NH 824 (27.53) and NH 615 (27.47). While genotype NH 860 recorded the lowest number of bolls per plant (22.53). The number of bolls per plant ranged from 22.53 to 28.33 with a general mean of 25.61. The spread exceeding the CD @ 5% of 2.52 and confirming appreciable genetic variability. The results are in accordance with results of Shahzad *et al.* (2019) [25] and Bakhsh *et al.* (2019) [26].

3.2.7 Boll weight (g)

Maximum boll weight was recorded by NH 821 (3.50 g), followed by NH 824 (3.27 g) and NH 1136 (3.20 g). Whereas, genotype NH 860 recorded the least boll weight (2.22 g). The general mean for boll weight was 2.82 g, with the range (2.22-3.50 g) exceeding the CD @ 5% of 0.41 g, confirming significant genotypic differences. The results are in agreement with results of Karademir *et al.* (2015) [27] and Karademir *et al.* (2012) [28].

3.2.8 Seed cotton yield per plant (g)

Seed cotton yield per plant is the most important and complex character governed by many genes. It is chief objective to improve seed cotton yield in any cotton improvement programme. Mean values for seed cotton yield ranged from 49.86 g (NH 860) to 89.96 g (NH 824), against a general mean of 72.27 g. Genotype NH 824 recorded the highest mean seed cotton yield, followed by the NH 615 (85.90 g) and NH 821 (84.52 g). The difference between the highest and lowest yielding genotypes exceeded the CD @ 5% of 13.32 g, confirming a statistically significant genotypic difference. The results are in agreement with the reports of Aslan *et al.* (2022) [22] and Karademir *et al.* (2015) [27].

The promising genotypes for seed cotton yield per plant were NH 824, NH 615 (check) and NH 821. These genotypes could be utilized as potential parents or donor lines for seed cotton yield per plant in future hybridization aimed at seed cotton yield improvement in *G. hirsutum* cotton. Considering seed cotton yield and its contributing traits as a whole, NH 824 and NH 821 identified as the most promising entries, exhibiting above-average performance for seed cotton yield per plant coupled with a associated seed cotton yield component traits such as number of bolls per plant and boll weight. These results are in agreement with the reports of Karademir *et al.* (2015) [27],

Bakhsh *et al.* (2019) [26], Aslan *et al.* (2022) [22], Damtew *et al.* (2022) [20] and Sendekie *et al.* (2024) [17] in *G. hirsutum* genotypes. These genotypes could be used for improvement of earliness, plant stature and seed cotton yield attributes.

3.3 Genetic variability, heritability and genetic advance

Estimates of range, mean, genotypic and phenotypic variance, genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (h^2) and genetic advance as per cent of mean (GAM) for the eight yield and yield-contributing characters are presented in Table 3. The phenotypic coefficient of variation was higher in magnitude than the corresponding genotypic coefficient of variation for all eight characters, indicating some influence of environment on trait expression; however, the comparatively narrow gap between GCV and PCV for most characters suggested that a considerable proportion of the observed variability was under genetic control.

3.3.1 Genotypic and phenotypic coefficients of variation

Genotypic and phenotypic coefficients of variation were estimated as per classification given by Sivasubramanian *et al.* (1973) [9]. High GCV ($\geq 20\%$) was recorded for number of monopodia per plant (23.80%). Moderate GCV (10-20%) was observed for seed cotton yield per plant (13.65%) and boll weight (12.06%), while the remaining characters, viz: Days to 50 per cent flowering (2.86%), days to maturity (1.69%), plant height (8.01%), number of sympodia per plant (4.81%) and number of bolls per plant (4.54%), exhibited low GCV. The phenotypic coefficient of variation followed a similar trend but was slightly higher in magnitude for every character. High PCV (24.64%) was recorded only for number of monopodia per plant while moderate PCV for seed cotton yield per plant (17.62%) and boll weight (14.95%). High GCV and PCV for number of monopodia per plant and seed cotton yield per plant indicated substantial genetic variability for these traits, providing considerable scope for improvement through direct selection. The results are in agreement with reports of Sakthi *et al.* (2007) [29] and Devi *et al.* (2020) [30].

3.3.2 Heritability (broad sense)

Heritability was estimated as per classification of Robinson *et al.* (1949) [11]. High heritability ($\geq 60\%$) was recorded for number of monopodia per plant (93.23%), plant height (86.09%) and boll weight (65.09%). While moderate heritability (30-60%) was observed for seed cotton yield per plant (59.97%), number of sympodia per plant (37.86%), number of bolls per plant (36.72%), days to 50 per cent flowering (35.14%) and days to maturity (33.73%). The high heritability for number of monopodia per plant indicated that this character was least influenced by environment and direct selection could be effective for improvement of it. These results are consistent with the reports of Sakthi *et al.* (2007) [29] and Meena *et al.* (2001) [31].

3.3.3 Genetic advance as per cent of mean

Genetic advance as per cent of mean was estimated as per classification of Johnson *et al.* (1955) [12]. High genetic advance as per cent of mean ($\geq 20\%$) was recorded for number of monopodia per plant (47.33%), seed cotton yield per plant (21.77%) and boll weight (20.04%). While the remaining characters showed low to moderate GAM. Plant height recorded a moderate value of 15.31 per cent. Characters coupled high heritability and high GAM are viz: Number of monopodia per plant and boll weight, indicated that heritability in these traits was largely attributable to additive gene action, so that selection based on phenotypic expression would be effective for their improvement. Seed cotton yield per plant, despite only moderate heritability, combined this with a high genetic advance as per cent of mean (21.77%), suggesting that a meaningful part of its heritable variation is additive in nature and amenable to selection gains, notwithstanding some environmental influence on its expression. In contrast, plant height exhibited high heritability (86.09%) but only moderate GAM (15.31%), suggesting the possible involvement of non-additive gene action (dominance and epistasis) in its expression, in which case recurrent selection would be effective (Selection after in

terminating of individuals). These findings are in accordance with the findings of Desalegn *et al.* (2009) [32], Sakthi *et al.* (2007) [29] and Meena *et al.* (2001) [31] for yield and its component traits in *G. hirsutum*.

Taken together, the results of the present investigation demonstrated the presence of appreciable genetic variability for seed cotton yield and its contributing characters among the seventeen *hirsutum* cotton genotypes evaluated. Substantial amount of genetic variability was noticed for number of monopodia per plant, boll weight and seed cotton yield per plant. These characters combining reasonably high heritability with high genetic advance, and therefore amenable to improvement through direct selection. Genotypes NH 824, NH 821 and the check NH 615, which expressed high seed cotton yield with a desirable magnitude of yield components, emerged as promising genetic material for use as parents/donors in hybridization programmes directed at seed cotton yield improvement in upland cotton.

4. Conclusion

The present investigation demonstrated highly significant genotypic differences among seventeen upland cotton genotypes for all eight yield and yield-contributing traits studied. Which revealed presence of substantial amount of genetic variability that is largely under genetic control. Whereas, environmental influence is negligible. Seed

cotton yield per plant ranged from 49.86 g to 89.96 g, and genotypes NH 824, NH 821 and the check NH 615 were identified as the most promising entries, combining superior yield with favourable expression of number of bolls per plant and boll weight. Number of monopodia per plant, boll weight and seed cotton yield per plant, which combined moderate-to-high heritability with high genetic advance as per cent of mean, appeared to be governed predominantly by additive gene action and are therefore amenable to improvement through direct phenotypic selection, whereas plant height, which showed high heritability but only moderate genetic advance, would benefit from hybridization-based breeding approaches. These findings provide valuable genetic information to cotton breeders to select genetically diverse superior parental genotypes to be utilized in cotton improvement programmes in upland cotton. Furthermore these genotypes must be tested at multi-locations in multi-season trials to confirm the stable performance prior to their use in breeding or release.

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traits in seventeen upland cotton genotypes

Table 1. Analysis of variance (mean sum of squares) for yield and yield-contributing

Sr. No.	Trait	Replication (df = 2)	Treatment (df = 19)	Error (df = 38)
1	Days to 50% flowering	20.76	20.66**	7.87
2	Days to maturity	2.32	28.59**	11.32
3	Plant height (cm)	90.05	683.62**	34.94
4	Number of sympodia/plant	0.81	8.54**	3.02
5	Number of monopodia/plant	0.06	5.04**	0.12
6	Number of bolls/plant	0.37	6.37**	2.33
7	Boll weight (g)	0.08	0.40**	0.06
8	Seed cotton yield/plant (g)	86.55	356.85**	64.95

*, ** Significant at 5% level 1% level of probability.

Table 2. Mean performance of seventeen upland cotton genotypes for yield and yield-contributing traits

Sr.No.	Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Sympodia/ plant	Monopodia/ plant	Bolls/ plant	Boll weight (g)	Seed cotton yield/plant (g)
1	NH 814	73	146	170.00	26.70	5.2	25.8	2.83	73.22
2	NH 816	73	144	172.00	28.60	6.6	26.27	2.79	73.04
3	NH 817	75	142	164.00	29.90	5.2	24.47	3.19	78.35
4	NH 820	74	141	184.33	29.77	6.63	25.00	2.72	68.15
5	NH 821	73	142	174.00	27.60	5.3	24.07	3.5	84.52
6	NH 824	74	144	187.40	28.8	6.3	27.53	3.27	89.96
7	NH 825	66	144	188.47	26.73	6.67	24.40	2.92	70.98
8	NH 826	71	142	202.87	27.87	6.27	28.33	2.94	83.030
9	NH 860	73	143	191.80	26.47	4.3	22.53	2.22	49.86
10	NH 864	72	141	204.80	30.47	3.3	26.00	2.6	67.38
11	NH 866	74	144	179.93	25.87	5.3	25.40	2.34	59.26
12	NH 1136	76	142	186.40	28.73	3.3	25.80	3.2	82.39
13	NH 1187	75	141	206.67	26.5	2.8	25.33	2.56	64.60
14	NH 1201	74	142	187.00	30.74	6.7	24.10	3.13	75.63
15	NH 1212	73	145	200.80	25.73	3.4	25.00	2.55	63.95
16	NH 1222	72	143	206.33	30.67	5.8	24.13	2.3	55.73
17	NH 1226	71	142	163.33	27.87	6.43	27.00	2.25	60.92
18	NH 677 (check)	70	131	168.00	26.33	6.57	26.20	3.01	79.13

(continued on next page)

Sr.No.	Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Sympodia/ plant	Monopodia/ plant	Bolls/ plant	Boll weight (g)	Seed cotton yield/plant (g)
19	NH 545 (check)	69	137	167.67	29.87	6.2	27.33	2.9	79.46
20	NH 615 (check)	67	142	165.67	29.47	5.4	27.47	3.12	85.90
	General Mean	72	142	183.57	28.23	5.38	25.61	2.82	72.27
	SE [±]	1.62	1.94	3.41	0.95	0.2	0.88	0.14	4.65
	CV (%)	3.88	2.37	3.22	6.16	6.41	5.96	8.83	11.15
	CD @ 5%	4.64	5.56	9.77	2.87	0.57	2.52	0.41	13.32
	CD @ 1%	6.21	7.45	13.09	3.85	0.76	3.38	0.55	17.84

Table 3. Genetic variability, heritability and genetic advance for yield and yield-contributing traits in seventeen upland cotton genotypes

Character	Range	Mean	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	h ² (bs) (%)	GA	GA as % mean
Days to 50% flowering	66.00–76.00	72	4.26	12.14	2.86	4.82	35.14	2.52	3.49
Days to maturity	131.33–145.67	142	5.76	17.08	1.69	2.91	33.73	2.87	2.02
Plant height (cm)	163.33–206.67	183.57	216.23	251.17	8.01	8.63	86.09	28.11	15.31
Number of sympodia/plant	25.73–30.74	28.23	1.84	4.86	4.81	7.81	37.86	1.72	6.09
Number of monopodia/plant	2.80–6.70	5.38	1.64	1.76	23.8	24.64	93.23	2.55	47.33
Number of bolls/plant	22.53–28.33	25.61	1.35	3.68	4.54	7.49	36.72	1.45	5.66
Boll weight (g)	2.22–3.50	2.82	0.12	0.18	12.06	14.95	65.09	0.56	20.04
Test weight (g)	61.67–81.67	71.3	25.77	48.04	7.12	9.72	53.64	7.66	10.74
Seed cotton yield(g)	55.73–89.96	72.27	97.30	162.25	13.65	17.62	59.97	15.74	21.77

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