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Agronomic performance for yield and fiber quality of new advanced cotton lines and genetic variability studies

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Abstract: Promising cotton lines included in a varietal trial, set up by block method, in four replicats, were evaluated for productivity and fiber quality. Genetic diversity was also assessed and broad sense heritability and genetic advance were determined. Significant variation between genotypes was found for all the traits under study. The conditions of years have influenced to the greatest extent the seed cotton yield of tested lines. Lines 709, 724, 654 and 678 emerged as the best, combining best productivity, lint percentage and fiber length. High genotypic (GCV) and phenotypic (PCV) coefficients of variations were recorded for seed cotton yield, moderate for boll weight and very low for lint percentage and fiber length. A very high value of genetic advance as percent of mean (GAM) was accounted for seed cotton yield (39.19%), moderate GAM values were recorded for boll weight and low to moderate for lint percentage and fiber length. Seed cotton yield showed high broad sense heritability, coupled with high genetic advance as percent of mean indicating the presence of additive genes and possibility of improving productivity through direct selection. High heritability, coupled with moderate genetic advance was recorded for boll weight, indicating both additive and non-additive genes and recurrent selection using both variances simultaneously could be applied for improving this trait. Lint percentage and fiber length showed high broad sense heritability coupled with low to moderate genetic advance as percent of mean revealing non-additive gene effects. Their improvement could be achieved through heterosis breeding and transgressive variability.

Keywords: cotton; economic traits; variability; heritability; genetic advance

INTRODUCTION

Cotton is an economically important crop for many countries. It is grown manly for fiber in more than 70 countries of the world.

Cotton seeds are a secondary product, but they are an important source of fat and protein for the food and other industries, they are also used for animal feed.

Cotton is a strategic raw material and there is no industry that does not use cotton materials and products to a greater or lesser extent.

Many new cotton varieties have been created in the world, with high productivity and high fiber quality, resistant to pests, diseases, drought, etc. Through selection the architectonics of cotton plant, the productive and quality potential of varieties, and their resistance to biotic and abiotic stress factors have been improved.

At the modern stage, cotton breeding in our country is mainly aimed at improving the productivity and fiber quality. Great attention is paid to the resistance of varieties to biotic and abiotic stress factors. To achieve these goals various selection methods and approaches are used. The classical methods of intra- and interspecific hybridization and experimental mutagenesis are fundamental for creating new genetic diversity and new cotton varieties.

In recent years, at the Field Crops Institute in Chirpan, many new cotton varieties have been created Aida, Anabel, Tiara, Melani (Dimitrova, 2022a; 2022b; 2023), Pirin, Perun (Koleva & Valkova, 2023), Selena (Dimitrova & Nedyalkova, 2024), Kristal, Orfey and Snejina (Koleva et al., 2024). All of these varieties are very early, having higher productivity than the standard varieties, Anabel, Melani and Selena with improved fiber quality. Aida, Tiara, Melani and Selena were obtained through distant hybridization and the rest from intervarietal crossing.

In cotton, the genetic base is very narrow, which limits further improvement of productivity, fiber quality and resistance to stress impacts. Therefore, the creation, evaluation and inclusion of new genetic diversity in the breeding process are of great importance for the creation of new cotton varieties possessing the desired agronomic characteristics. New Bulgarian and foreign cotton varieties and advanced breeding lines are used as starting material in breeding programs.

Many authors are of the opinion that the exploitation of genetic diversity is important to create new desirable genotypes for breeding programs. Successful breeding program can be achieving through genetic diversity and effective selection (Balci et al., 2020).

The study of genetic diversity is associated with the application of various methods of assessment and analysis. Cluster analysis is particularly valuable for the study of genetic diversity and is widely used in breeding programs (Jarwar et al., 2019; Mahmood et al., 2020; Munir et al., 2020; Ullah et al, 2020; Zafar et al. 2021). In our country, this method was used to study the genetic similarity and genetic distance of lines and varieties of cotton obtained through the application of different selection methods (Stoilova & Dechev, 2003a; 2003b; Dimitrova et al., 2004a; 2004b; Stoilova, et al., 2005; Stoilova & Bozhinov, 2006; Stoilova & Valkova, 2010).

In view of the selection strategy, the assessment of certain genetic parameters such as heritability, genetic coefficient of variability, phenotypic coefficient of variability, genetic advance is of great importance. The successful breeding program depends on genetic variability response to selection, heritability and genetic advance (Gibely, 2021).

In cotton, a number of studies have been conducted to evaluate genetic diversity and genetic components such as genetic variability, coefficients of variability, heritability and genetic advance to employ suitable breeding procedures in accordance with breeding objectives (Jarwar et al., 2018; Gnanasekaran et al., 2018; Praveen et al. 2019; Shruti et al., 2019).

Gibely (2021) concluded that the cotton breeders should consider heritability, genetic advance, phenotypic and genotypic variance for quantitative traits as important tools to determining the effectiveness of selection.

Balci et al. (2020) concluded that the relationship of heredity with genetic advance and genetic correlation studies are very important for the improvement of yield and quality of cotton.

Many cotton breeders studied the association between heritability and genetic advance as a percent of mean (GAM) in segregating generation in different cotton crosses and in different accessions (Khokhar et al., 2017; Vrinda & Patil, 2018; Gnanasekaran et al., 2018; Kumar et al., 2019; Ahsan & Mahmmod, 2019).

Heritability estimate along with genetic advance is more useful in predicting the resultant effect of selecting the best individuals. GAM together with heritability estimates gives a relatively better picture of the amount of advance to be expected through selection (Johnson et al. 1955).

The aim of this study was: i) to investigate the potential in terms of productivity and fiber quality of new promising cotton lines, as sources for cotton improvement; ii) to assess the genetic diversity, heritability and genetic advance for the studied traits for effective selection of new cotton varieties with enhanced yield and fiber quality. The information that will be obtained is needed to exploit the lines as sources for cotton improvement and for effective selection to develop new cotton varieties with enhanced yield and fiber quality.

MATERIAL AND METHODS

Plant material

The experimental material included 9 new advanced cotton lines, Bulgarian selection, obtained through intra- and interspecific hybridization, and the standard cultivar Chirpan-539. Line 633 was created by crossing of the allotetraploid *Gossypium thurberi* Tod. × *G. raimondii* Ulbr. with *G. hirsutum* L. varieties and backcrossing of the triple hybrid (*G. thurberi* Tod. × *G. raimondii* Ulbr.) × *G. hirsutum* L. with *G. hirsutum* L. Lines 678 and 724 were created by direct hybridization of the *G. hirsutum* L. species with the wild diploid species *G. thurberi* Tod. and saturating backcrosses with the *G. hirsutum* L. The other lines were obtained through intraspecific hybridization within the *G. hirsitim* L. species.

Field trial

The studied lines were included in a varietal trial, set up using a block method, in 4 replications and a harvest plot of 20 m^2. The trial was conducted during the period 2021 - 2023 in the experimental field of the Field Crops Institute in Chirpan. Standard technology for cotton growing in our country under non-irrigated conditions was applied. The traits under study were: seed cotton yield (kg/ha); boll weight (g); fibre length (mm) and lint percentage (%).

Statistical analysis

The experimental data were statistically processed by applying two factor analysis, the ANOVA 123 program was used. Hierarchical cluster analysis was applied to group the genotypes by similarity based on all studied traits. The Euclidean distance between the different groups was used as a measure of difference between them. For clustering the genotypes the Ward's method (1963) was used, which minimizes the variation within the groups. Data standardization was performed in advance.

Phenotypic (σ^2p) and genotypic (σ^2g) variances were obtained from the analysis of variance (ANOVA) (Table 2).

Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed as percentage (Falconer & Mackay, 1996).

$h^2 (\%) = (\sigma^2g/\sigma^2p).100$

Where: σ^2g - genotypic variance and σ^2p - phenotypic variance.

Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were estimated according to Singh & Chaudhary (1985) using the formula:

$PCV\% = \sqrt{\sigma^2p} \,/\, \overline{X} \times 100$; $GCV\% = \sqrt{\sigma^2g} \,/\, \overline{X} \times 100$;

Where: σ^2g - genotypic variance; σ^2p - phenotypic variance and $\overline{X}$ - mean.

Genetic advance (GA) was calculated according to Singh & Chaudhary (1985) by the formula:

$GA = k \times \sigma p \times h^2$

Where: k = 2,063 (constant for 5% selection intensity); σp - square root of phenotypic variance; h^2 - broad sense heritability.

Genetic advance in percentage of mean was calculated as:

$GAM = (GA/\overline{X}) \times 100$

Where: GA- genetic advance; $\overline{X}$ - mean.

RESULTS AND DISCUSSION

Agro climatic characteristics

The studied period included years with different temperature and rainfall conditions (Table 1). Cotton sowing in our country takes place in the second half of April. The temperature conditions in 2021 and 2023 were very unfavorable for sowing the temperature sum in both years for the month of April was way below normal. In 2021, in the month of April, rainfall was well above normal, while in 2022 was below normal. The distribution of rainfall during the cotton growing season in individual years is also of great importance for the seed cotton yield and fiber quality.

Rainfall in May is important for the timely germination of cotton, in June for growth and development, for higher setting of fruiting branches and the formation of flower buds. In May, when germination occurs, the temperature sum in 2023 was well below normal, and in 2021 and 2022, rainfall was insufficient, 21.9 mm and 27.4 mm below normal, respectively. Conditions for cotton growth and development in June 2021 were unfavorable, with temperature and rainfall be-

Table 1. Agro climatic characteristics of the region of the Field Crops Institute in Chirpan for the period IV-IX of 2021-2023, compared to average values of the base period 1991-2020

Years	***Months***						Σ IV-IX	Σ VI-VIII	Σ V-IX
	IV	V	VI	VII	VIII	IX			
Sum of temperatures Σ t °C									
1991– 2020	**369**	**532**	**641**	**741**	**745**	**575**	**3603**	**2127**	**3234**
2021	309	524	616	793	789	546	3577	2198	3268
±	-60	-8	-25	+52	+44	-29	-26	+71	+34
2022	367	537	659	774	782	565	3684	2215	3317
±	-2	5	18	+33	+37	-10	+81	88	+83
2023	333	475	628	818	811	617	3682	2257	3349
±	-36	-57	-13	+77	+66	+42	+79	130	+115
Rainfall - mm									
1991 - 2020	**43.9**	**56.8**	**53.9**	**55.2**	**35.0**	**51.1**	**295.9**	**144.1**	**252.0**
2021	84.0	34.9	42.8	49.0	34.4	5.0	250.1	126.2	166.1
±	+40.1	-21.9	-11.1	-6.2	-0.6	-46.1	-45.8	-17.9	-85.9
2022	36	29.4	80.5	7.7	68.8	34.9	257.3	157	221.3
±	-7.9	-27.4	26.6	-47.5	+33.8	-16.2	-38.6	12.9	-30.7
2023	68.2	54.8	69.5	25.4	26.5	30.1	274.5	121.4	206.3
±	24.3	-2	15.6	-29.8	-8.5	-21	-21.4	-22.7	-45.7

Table 2. Analysis of variance of studied characters of 10 cotton lines tested in three years 2021-2023

Sources of variation	Degree of freedom	Sum of squares,%	Mean squares	Sum of squares,%	Mean squares
		Seed cotton yield, kg/ha		Boll weight, g	
Genotypes - G	9	5.00	103206***	6.20	0.21**
Years - Y	2	70.76	6569513***	57.15	8.78***
Interaction G ×Y	18	16.57	170982***	16.98	0.29***
Error	87	7.67	15737	18.44	0.06
		Lint percentage, %		Fiber length, mm	
Genotypes - G	9	17.15	4.33***	16.95	2.25***
Years - Y	2	47.77	54.34***	19.03	11.39***
Interaction G ×Y	18	15.38	1.944***	19.66	1.31***
Error	87	19.17	0.50	44.24	0.61

η^2% - Correlation relationship / Sum of squares %; MS - Mean squares
*** - Significance at 1% probability level; *** - at 0.1%*

low normal. Rainfall in 2023 was also insufficient. The months of July and August, during the three years of the study, were characterized by high, stressful temperatures for cotton, temperature sum during these months were well above the norm. Of greatest importance for fruit formation (which begins in June and continues through July and August) and for the retention of fruit elements (buds, flowers and bolls) are the rainfall in July and early August. In 2022, rainfall in July was only 7.7 mm, compared to a normal of 55.2 mm, and in August it was 33.8 mm above normal. In 2021, rainfall in both months was close to normal. In 2023, rainfall in July was 29.8 mm below normal, and in August it was slightly below normal.

In terms of temperature security during the cotton growing season, during the months of May-September, the years were characterized as follows: 2021 was average (P%=45.16); 2022 was moderately warm (P%=37.5); 2023 was warm (P%=15.15).

In terms of rainfall supply during the months of May-August, 2021 was moderately dry (P%=74.12); 2022 and 2023 were average (P %=46.87; 51.51).

P – Coefficient of security, respectively temperature and rainfall. The period 1991-2020 (30 years) was taken as the climatic norm (Alexandrov et al., 2010).

Analysis of variance of studied characters

Table 2 presents an analysis of variance for the studied traits. The influence of all sources of variation of which the phenotypic manifestation of the traits depended has been significant. The significant genotypic influence shows that the lines differed in the studied traits.

The conditions of years had the greatest importance for the variation of seed cotton yield, boll weight and lint percentage. The years of study determined 70.6% of the total variation of seed cotton yield and over half for boll weight and lint percentage.

Genotypes had very weak influence on the variation of seed cotton yield and boll weight. Regarding fiber length, the three sources of variation had relatively equal influence on the total variation of this trait.

The influence of genotypes on fiber length and lint percentage was relatively equal for both traits, which could be explained by their strong interdependence. The significant genotype-environment interaction showed that the lines for the studied traits responded differently to different environmental conditions.

Performance of lines for productivity and fiber quality

Despite the adverse climatic conditions during the cotton growing season in the three years of study the average yields of studied lines were within the range of 1290 – 1628 kg/ha (Table 3). The highest yields were obtained in 2022 the lack of rainfall in July was compensated by the rainfall in August, which was 33.8% above the norm. Compared to the other two years the temperature sums in the two summer months of this year were lower and had a less stressful impact.

In 2021 and 2023 seed cotton yields were relatively similar, despite the different rainfall levels in July and August. Rainfall in 2021 for both months was around normal, while in 2023, for July it was below the norm. In 2021, there was a large shortage of rainfall in May, which delayed germination. Characteristic of both years was that the temperature sums in July and August were well above normal and had a stressful effect on flowering and fruit formation.

The studied lines had different productive potential. In 2021 four lines exceeded the standard in seed cotton yield by 15.0% to 24.7% with the most productive were No. 724 and No. 678. In 2022, all lines achieved a higher yield than the standard and exceeded it by 8.0% to 29.1%, the most productive were No. 724 and No. 692. In the third year, only two lines No. 709 and No. 721 had a significant higher yield than the standard by 13.7% and 31.6%.

On average for the three years, five lines – 654, 678, 692, 709 and 724 had significant higher seed cotton yield than the standard cultivar, surpassing it by 7.7% to 18.4%, with the last two – No. 709 and No. 724 were the most productive. Line

Table 3. Seed cotton yield of lines included in varietal trial in 2021-2023 (Average for 3 years)

Line No.	2021		2022		2023		Average for 3 years	
	kg/ha	%	kg/ha	%	kg/ha	%	kg/ha	%
Chirpan-539	1249	100.0	179.5	100.0	138.1	100.0	147.5	100.0
581	1401	112.2	1938	108.0	1366	98.9	1569	106.4
633	1469	117.6^{*}	1975	110.0^{*}	1245	90.2	1563	106.0
654	1436	115.0^{*}	1975	110.0^{*}	1413	102.3	1608	109.0^{*}
678	1486	119.0^{*}	2063	114.9^{***}	1220	88.3^{0}	1589	107.7^{*}
692	1290	103.3	2185	121.7^{***}	1316	95.3	1597	108.3^{*}
709	1314	105.2	2048	114.1^{**}	1570	113.7^{*}	1644	111.5^{**}
718	896	71.7^{000}	2058	114.7^{**}	1242	89.9	1398	94.8
721	847	67.8^{000}	2052	114.3^{**}	1817	131.6^{***}	1572	106.6
724	1558	124.7^{**}	2317	129.1^{***}	1366	98.9	1747	118.4^{***}
General mean	1295	103.7	2041	113.7	1394	100.9	1576	106.8
GD 5.0%	18.7	14.7	15.5	8.6	15.9	11.5	10.2	6.9
GD 1.0%	24.9	19.6	20.5	11.4	21.2	15.3	13.5	9.2
GD 0.1%	32.3	25.4	26.6	14.8	27.6	20.0	17.4	11.8

724 was in first place in seed cotton yield in the first two years, line 709 significantly surpassed the standard in the second and third years. All these lines are of interest for breeding programs aimed at improving productivity.

Table 4. Economic qualities of lines included in varietal trials in 2021-2023 (Average for 3 years)

Lines No.	Boll weight g	Lint percentage %	Fiber length mm
Chirpan-539	5.0	39.4	24.6
581	5.2^{*}	38.0^{000}	25.2^{***}
633	5.2^{*}	39.8	25.1^{**}
654	5.1	39.3	25.3^{***}
678	5.4^{***}	39.9	25.3^{***}
692	5.3^{**}	39.4	24.5
709	5.0	38.8^{0}	25.6^{***}
718	5.0	38.9^{0}	25.3^{***}
721	5.2^{*}	38.4^{000}	25.9^{***}
724	5.0	39.1	25.6^{***}
General mean	***5.1***	***39.1***	***25.2***
GD 5.0%	0.2	0.6	0.3
GD 1.0%	0.3	0.8	0.4
GD 0.1%	0.4	1.0	0.6

The boll weight varied from 5.0 g to 5.4 g (Table 4). There were 5 lines with significant larger bolls than the standard cultivar, with the largest bolls were No. 678 and No. 692. These two lines had 0.4 g and 0.3 g larger boll weight than the standard.

The lint percentage varied from 38.0% to 39.9%. The standard cultivar had high lint percentage of 39.4%. Five lines were equal to it in lint percentage, four were significant to be inferior. The lines with high lint percentage were No. 633 – 39.8% and No. 678 – 39.9%.

All lines, except one - No. 692, had a significant longer fiber length than the standard cultivar and exceeded it by 0.5 mm to 1.3 mm.

Line 721 formed the largest fiber length - 25.9 mm, followed by lines 709 and 724 - 25.6 mm, with 24.6 mm for the standard cultivar.

Grouping of lines by similarity using cluster analysis

In order to better evaluate the lines and select the most valuable genotypes based on the studied traits cluster analysis was applied. The studied 9 lines and the standard cultivar were clustered based on the studied 4 traits.

The cluster analysis performed shows that the lines belong to two main clusters, each with two subgroups (Figure 1). The first main cluster includes lines 709, 724, 581 and 721, which in terms of seed cotton yield and boll weight significant and non-significant were superior to the standard and had significant and non-significant lower lint percentage. The lines in this cluster, with the exception of No. 581, had the longest fiber length. Lines 709 and 724 performed best in terms of productivity of all lines. Although these two lines showed similarity, No. 724 had higher productivity and higher lint percentage than No. 709. The other two lines, No. 591 and No. 721 are separated from them, which had non-significant higher yield than the standard and lower lint percentage. These two lines were similar in productivity, boll weight and lint percentage, but differed in fiber length. Line 721 had the longest fiber among the lines.

The second main cluster includes the remaining five lines and the standard cultivar. The standard cultivar and line 718 formed one subgroup the remaining four lines formed the other subgroup. The two subgroups differed most strongly in productivity.

Line 718 was equal in productivity to the standard, but had lower lint percentage and longer fiber. Line 678 was separated from this subgroup, which was significantly more productive and has fallen into the second subgroup. In the second subgroup, lines 633 and 654 show similarity, with the first having slightly higher lint percentage and the second having slightly longer fiber. Line 692 was separated from them, which had a shorter fiber. This line and the standard cultivar had the shortest fiber in the experiment.

Based on the analysis of results for economic qualities and the applied cluster analysis, the following lines emerged as the best in a comprehensive assessment: No. 709 and No. 724 with the best performance in productivity, which they combined with a longer fiber length than the standard and high lint percentage in the second line; No. 692 and No. 678 with significant higher productivity than the standard, larger bolls and high lint percentage coupled with a longer fiber than the standard in line 678. These lines could be used for the selection of better performing genotypes for further improvement of productivity and fiber quality.

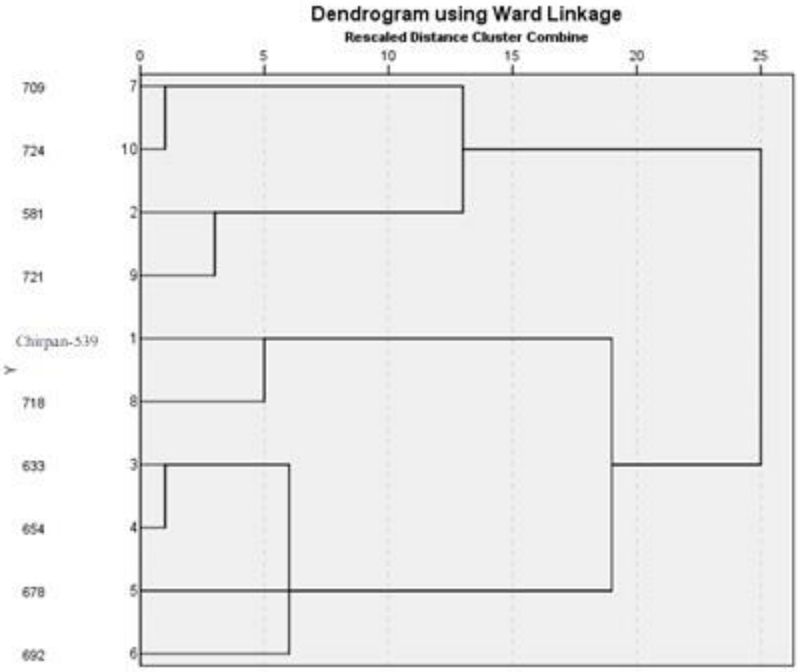

Figure 1. Dendrogram of 9 cotton genotypes by 4 traits, average for 2021-2023

In order to improve the economic traits, lines 709 and 724 from the first main cluster could be included in crosses with lines 654 and 678 from the second main cluster. These four lines could be included in crosses with some earlier foreign varieties having high lint percentage and longer fiber to create greater genetic diversity.

Four candidate varieties have been released from these lines: No. 678 approved as Selena variety in 2024; No. 724 approved as Siyana variety in 2025 and No. 692 and 721 included for testing in the IASAS system in 2025.

Genetic variability studies

Regarding the effective use of genotypes in breeding programs information on genetic diversity, heritability and selection advance expected from selection is very valuable (Eswary et al. 2017).

Table 5 presents the results for the genotypic variance (σ^2g), phenotypic variance (σ^2p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2), the effect of selection – genetic advance (GA) and the effect of selection expressed as a percentage of the trait mean value – genetic advance in % (GAM).

Genotypic and phenotypic variance were highest for seed cotton yield and lowest for boll weight.

Genotypic coefficients of variation (GCV) *and phenotypic coefficients of variation* (PCV)

Genotypic coefficient of variation and phenotypic coefficient of variation gives the idea about the extent of variability presents in genetic populations (Meena et al., 2022). The genotypic coefficient of variation was from 5.33% for fiber yield to 20.38% for seed cotton yield. The phenotypic coefficient of variation was from 5.62% for fiber yield to 21.88% for seed cotton yield. The genotypic and phenotypic coefficients of variation were categorized as low (0-10%), moderate (10-20%) and high (over 20%) (Shivasubramanian and Menon, 1973).

In the present study the genotypic coefficient of variation and the phenotypic coefficient of variation were high for seed cotton yield (20.38% and 21.88%, respectively) and indicate high variability amongst all the genotypes studied and the possibility of improving this trait through effective selection.

Similar results were reported by Aarthi et al. (2018), Pandiyan et al. (2019), Praveen et al. (2019), Siva Reddy et al. (2019), Naik et al. (2019), Sahar et al. (2021) and Meena et al. (2022), that high GVC and PCV were registered for seed cotton yield. Moderate GCV and PCV values for raw cotton yield were reported by Eswary et al. (2017).

The genotypic coefficient of variation and phenotypic coefficient of variation for boll weight were moderate (9.01% and 10.30%) and indicate moderate variability for this trait, which according to Meena et al. (2022), can be exploited through selection for efficient breeding program. The results are in support with the findings of Eswary et al. (2017), Aarthi et al. (2018), Pandiyan et al. (2019), Shruti et al. (2019), Meena et al., 2022. High GCV and PCV for boll weight were reported by Khokhar et al. (2017), Sahar et al. (2021).

Table 5. Estimates of variance and genetic parameters for studied traits in 9 advanced cotton lines

Traits	σ^2g	σ^2p	h^2, %	GCV, %	PCV, %	GA	GAM
Seed cotton yield	1032.06	1189.43	86.80	20.38	21.88	61.76	39.19
Boll weight	0.21	0.28	76.46	9.01	10.30	0.83	16.24
Lint percentage	4.33	4.84	89. 64	5.33	5.62	4.07	10.40
Fiber length	2.25	2.86	78.74	5.96	6.72	2.75	10.90

σ^2g – genotypic variance, σ^2p – phenotypic variance, h^2, % – broad-sense heritability, GCV, % – genotypic coefficient of variation, PCV, % – phenotypic coefficient of variation, GA – genetic advance, GAM – GA as % of mean

GCV and PCV values for lint percentage (5.33% and 5.62%) and fiber length (5.96% and 6.72%) were low indicating low variability among the tested lines. For these traits increasing diversity could be achieved through hybridization or by applying other selection techniques. These results are in agreement with the findings of Eswary et al. (2017), Aarthi et al. (2018), Pandiyan et al. (2019), Shruti et al. (2019), Siva Reddy et al. (2019), Naik et al. (2019), Meena et al. (2022).

Naik et al. (2019) and Sahar et al. (2021) reported that the Phenotypic Coefficient of Variation (PCV) was slightly higher than Genotypic Coefficient of Variation (GCV) for all the characters, indicating the influence of the environment.

It is known that the smaller the difference between the phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV), the less the influence of environmental conditions on the phenotypic expression of the trait.

In this study this difference is the smallest for lint percentage followed by fiber length, boll weight, and seed cotton yield. The first two traits lint percentage and fiber length are genetically determined and were less affected by the environmental conditions, while seed cotton yield and boll weight were strongly dependent on the year conditions (Table 2).

Heritability in broad sense – h^2

Heritability is useful in predicting the role of transmission genetic factors in phenotypes expression and in the end the selection of best genotypes from the segregating populations (Meena et al, 2022).

Heritability in broad-sense was classified into three groups - Low 0-30%, Moderate 30-60%, and High over 60.0% (Johnson et al., 1955).

In the current study, the values of broad sense heritability (h^2) ranged from 76.45% to 89.64%. The highest heritability was reported for lint percentage (89.64%) and seed cotton yield (86.80 %), followed by fiber length (78.74%) and boll weight (76.45%). Heritability estimations are of great importance for plant breeders. The traits with higher heritability (> 80%) make the selection procedure easier (Sahar et al., 2021). High heritability estimates for seed cotton yield and boll weight were recorded by Eswari et al. (2017), Aarthi et al. (2018), Deshmukh et al. (2019), Manonmani et al. (2019), Pandiyan et al. (2019), Praveen et al. (2019), Shruti at el. (2019), Siva Reddy et al. (2019), Naik et al. (2019) and Meena et al. (2022). Very high heritability estimates for boll weight were also recorded by Khokhar et al. (2017) and for seed cotton yield per plant - by Nawaz et al. (2019). High estimates of heritability for ginning percentage and 2.5 % span length reported Eswaryet al. (2017) and Sunayana and Somveer (2017), whereas Jarwar et al. (2018), Meena et al. (2022) recorded low heritability for ginning percent and concluded that selection would be ineffective for this trait. Moderate heritability was observed for 2.5% span length by Monisha et al. (2018) and Meena et al. (2022).

Genetic advance (GA)

Genetic advance was also categorized as low 0-10%, moderate 10- 20% and high above 20% (Johnson et al., 1955).

In this study, the genetic advance (GA) was highest for seed cotton yield (61.76%) and lowest for boll weight (0.83%). Low values of this indicator were accounted for lint percentage (4.08%) and fiber length (2.75%).

High genetic advance for seed cotton yield was recorded by Vineela et al. (2013), Dhivya et al. (2014), Kumar et al. (2019).

Genetic advance expressed as per cent of mean – GAM

Genetic advance as per cent of mean (GAM) was also categorized as low (0–10%), moderate (10–20%), and high (above 20%) (Johnson et al., 1955).

The highest GAM value was accounted for seed cotton yield (39.19%). Moderately high GAM value was recorded for boll weight (16.20%) and low to moderately high were GAM values for lint percentage (10.43%) and fiber length (10.91%).

Similar results for ginning percentage were observed by Sunayana & Somveer (2017). Moderate estimate of genetic advance as per cent of mean for this trait was reported by Gauswami et al. (2021).

Heritability (h^2) coupled with genetic advance as per cent of mean (GAM)

Heritability when coupled with genetics advance and genetic variability could be powerful tool for plant researcher to select proper breeding program (Chandio et al., 2003; Baloch, 2004).

Heritability along with genetic advance favours the fixation of genetic factors for any particular trait (Meena et al., 2022).

Heritability can be due to additive and non-additive gene effects. If heritability is mainly due to non-additive gene effect, the expected genetic advance would be low, and if there is additive gene effect, high genetic advance may be expected (Panse, 1957).

In this study, high heritability coupled with high genetic advance as per cent of mean was found for seed cotton yield, indicating the presence of additive genes and improvement in this trait can be achieved through direct selection.

Meena et al. (2022) reported high heritability coupled with high genetic advance as per cent of mean for seed cotton yield per plant indicating the role of additive genes and less environmental influence. Similar results were also reported by Eswary et al. (2017), Aarthi et al. (2018), Monisha et al. (2018), Pandiyan et al. (2019), Praveen et al. (2019), Naik et al. (2019), Gauswami et al. (2021), Sahar et al. (2021).

Productivity is a complex trait and genetic progress can be achieved by genetically improving the structural elements of yield (Balci et al., 2020; Meena et al., 2022). In this study, high heritability coupled with moderate genetic advance as per cent of mean was accounted for boll weight, revealing that the heritability was due to additive and non-additive gene effects. Genetic improvement of this trait could be effective for improving productivity.

For the selection improvement of boll weight it is necessary to apply a system that uses both variances additive and non-additive simultaneously. It is believed that such a system could be recurrent selection, associated with alternating selection and crossing over of desired segregates in the cross.

Monisha et al. (2018), Naik et al. (2019) Meena et al. (2022) reported similar results, high heritability coupled with moderate genetic advance as percentage of mean was found for boll weight, revealing the role of additive and non-additive gene action. High heritability coupled with high genetic advance as percent of mean for boll weight, indicating the preponderance of additive gene action was found by Eswary et al. (2017) and Gauswami et al. (2021).

In the present investigation, high heritability combined with low to moderate genetic progress as percent of mean was accounted for lint percentage and fiber length, indicating the presence of non-additive gene action and desired results may not be obtained by simple selection.

High heritability coupled with low genetic advance as per cent of mean for ginning outturn and 2.5% span length was reported by Naik et al. (2019). High heritability associated with moderate genetic advance expressed as per cent of mean for ginning percentage was observed by Gauswami et al. (2021).

The presence of non-additive gene action indicates that the high heritability of the two traits – lint percentage and fiber length was mainly due to the influence of environment, rather than the genotype and means limited improvement, simple selection will not be effective.

According to Meena et al. (2022), in the presence of non-additive gene action improvement in traits is possible through heterosis breeding, transgressive variation rather than simple selection. Naik et al. (2019) concluded that the characters which are governed by non-additive gene action need to be exploited by heterosis breeding or population improvement through various forms of recurrent selection

CONCLUSION

The factors determining the phenotypic expression of studied traits had significant, but different influence on their formation. The conditions of years had the greatest influence on seed cotton yield, boll weight and lint percentage of tested lines.

In a complex assessment the lines 709, 724, 654 and 678 were the best, combining best productivity, yield and fiber length and could be used for further improvement of yield and fiber quality in cotton.

According to applied cluster analysis lines 709 and 724 were relatively genetically most distant from lines 654 and 678 and could be included in one selection program to achieve greater genetic progress.

The low phenotypic and genotypic coefficients of variation for lint percentage and fiber length indicate low variability among the tested lines and for these traits an increase in diversity can be achieved through hybridization or other selection techniques.

Very high value of the genetic advance as per cent of mean (GAM) was found for seed cotton yield, moderate GAM values were found for boll weight, lint percentage and fiber length.

High heritability coupled with high genetic advance as percent of mean was found for seed cotton yield indicating the presence of additive genes and effectiveness of simple selection for this trait.

High heritability coupled with moderate genetic advance was recorded for boll weight, indicating both additive and non-additive genes, and recurrent selection using both variances simultaneously could be applied to improve this trait. Lint percentage and fiber length showed high broad sense heritability coupled with low to moderate genetic advance as percent of mean revealing non-additive gene effects, and their improvement could be achieved by using heterosis breeding and transgressive variability.

REFERENCE

Aarthi, V., Amla Balu, P., & Premalatha, N. (2018). Genetic variability studies in germplasm of upland cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*, *9*(4),1600-1605.

Ahsan, M. Z., & Mahmmod, H. T. (2019). Genetic variability and heritability in F2 population of Gossypium hirsutum for seed cotton yield and its components. *International Journal of Cotton Research and Technology*, *1*(1), 29-31. https://doi.org/10.33865/IJCRT.001.01.0245

Alexandrov, V., Simeonov, P., Kazandzhiev, V., Korchev, G. & Yotova, A. (2010). Climate change. Research Institute of Mechanization and Hydrotechnics, Bulgarian Academy of Sciences (edited by Prof. Veselin Alexandrov Dr.Sc.) (Bg).

Balcı, Ş., Çınar, V. M., & Ünay, A. (2020). A Study on genetic advance and heritability for quantitative traits in cotton (*Gossypium hirsutum* L.). *Adnan Menderes Üniversitesi Ziraat Fakültesi Dergisi*, *17*(1), 81-84.

Baloch, M. J. (2004). Genetic variability and heritability estimates of some polygenic traits in upland cotton. *Pakistan Journal of Scientific and Industrial Research*, 42, 451-454.

Chandio, M. A., Kalwar, M. S., & Baloch, G. M. (2003). Gene action for some quantitative characters in upland cotton (*G. hirsutum*). *Pakistan Journal of Scientific and Industrial Research*, *54*(1-2), 31-35.

Deshmukh, M. R., Deosarkar, D. B., Chinchane, V. N., & Deshmukh, S. B. (2019). Studies of genetic parameters for yield yield contributing and fibre quality characters in desi cotton (Gossypium arboreum L.). *Journal of Cotton Research and Development*, *33*(1), 44-49.

Dhivya, R, Amalabalu, P., Pushpa, R. & Kavithamani, D. (2014). Variability, Heritability and Genetic Advance in Upland Cotton (*Gossypium hirsutum* L.). *African Journal of Plant Science*, *8*(1), 1-5.

Dimitrova, V. (2022a). A new cotton variety Aida. *Bulgarian Journal of Crop Science*, *59*(1), 43-50 (Bg).

Dimitrova, V. (2022b). Anabel – a new cotton variety. *Bulgarian Journal of Crop Science*, *59*(4), 56-63.

Dimitrova, V. (2023). Agronomic performance and fiber quality of the new cotton varieties Tiara and Melani. *Bulgarian Journal of Agricultural Science*, *29*(4).

Dimitrova, V., & Nedyalkova, S. (2024). Selena a new cotton variety. *Bulgarian Journal of Crop Science*, 6 (1), 31-41. ISSN 0568-465X (print) 2534-9848 (online)

Dimitrova, V., Stoilova, A., & Genov, G. (2004a). Evaluation of cotton samples by cluster analysis. Scientific Conference with International participation, June 3-4 Stara Zagora, 2004. In: *Agricultural Sciences - Plant Breeding, Volume I, Part I. Genetics and Selection, Weeds, Diseases and Pests.* Ed. „Union of Scientists" St. Zagora, 86-90 (Bg).

Dimitrova, V., Stoilova, A., & Genov, G. (2004b). Study of the genetic diversity by the fiber length and lint percentage in Bulgarian and foreign cotton samples by cluster analysis. In: *Scientific works. Scientific conference dedicated to 60 years of the Union of Scientists in Bulgaria and 20 years of the Kardzhali branch,* October, 2004, Kardzhali, 262-266 (Bg).

Eswari, K. B., Kumar, S., Gopinath, S., & Rao M. V. B. (2017). Genetic variability, heritability and genetic advance studies in cotton. *International Journal of Development Research,* 7(1), 10902-10904.

Falconer, D. S., & Mackay, T. F. C. (1996). Introduction to Quantitative Genetics, Benjamin Cummings, London, UK., 4th Edn. ISBN 0-582-24302-5 Longmans Green, Harlow, Essex, UK.

Gauswami, J. J., Valu, M. G., & Odedara, G. N. (2021). Genetic Variability, Coefficient of Variance, Heritability and Genetic Advance in American Cotton (*Gossypium hirsutum L.*), *Ind. J. Pure App. Biosci*., *9*(3), 180-186.

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. http://jsas.journals.ekb.eg/

Gnanasekaran, M., Thiyagu, K., & Gunasekaran M. (2018). Genetic variability heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.). *Electronic J. of Plant Breeding, 9*(1), 377-382.

Jarwar, A. H. X., Wang, L., Wang, Q. M., & Fan, S. (2018). Genetic advancement, variability and heritability in upland cotton (*Gossypium hirsutum* L.). *Journal of Environmental and Agricultural Sciences,*16, 24-31.

Jarwar, A. H., Wang, X., Iqbal M., Sarfraz, Z., Wang, L., Qifeng M. A., & Shuli, F. (2019). Genetic divergence on the basis of principal component, correlation and cluster analysis of yield and quality traits in cotton cultivars. *Pakistan Journal of Botany*, 51(3), 1143-1148. DOI: 10.30848/PJB2019-3(38)

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal,* 47, 314-318.

Khokhar, E. S., Shakeel, A., Maqbool, M. A., Anwar, M. W., Tanveer, Z., & Irfan, M. F. (2017). Genetic study of cotton (*Gossypium hirsutum* L.) genotypes for different agronomic yield and quality traits. *Pakistan J. of Agric. Res., 30*(4), 363-372.

Koleva, M., Valkova, N., & Nedyalkova, S. (2024). New Bulgarian high yielding cotton varieties - Kristal, Orfey and Snejina. *Scientific Papers. Series A. Agronomy*, LXVII, 1, 483-492.

Koleva, M., & Valkova, N. (2023). Characteristics of the new cotton varieties Pirin and Perun. *Bulgarian Journal of Crop Science*, *60*(1), 69-77.

Kumar, C. P. S., Prasad, V., Joshi, J. L., Rajan, R. E. B. & Thirugnanakumar, S. (2019). Studies on Genetic Variability, Heritability and Genetic Advance in Cotton (*Gossypium hirsutum* L.). *Plant Archives 19*(1), 618-620.

Kumar, C. P. S., Raju, S., Rajan, R. E. B., Muraleedharan, A. & Suji, D.B. (2019). Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). *Plant Archives, 19*(1), 934-937.

Mahmood, B. J., Ahmed, L. Q., Kamal, K., Hamedi, A. & Ahmad, A. (2020). Cluster analysis among nine cotton genotypes. *Iraqi Journal of Agricultural Science*, *51*(2), 592–599. https://doi.org/10.36103/ijas.v51i2.986

Manonmani, K., Mahalingam, L., Malarvizhi, D., Sritharan, N., & Premalatha, N. (2019). Genetic variability, correlation and path analysis for seed cotton yield improvement in upland cotton (*Gossypium hirsutum* L.). *Journal of Pharmacognosy and Phytochemistry*, *8*(4), 1358- 1361.

Meena, R. K., Parmar, L. D., Meena, R. K., Patel, P. R., Tanwar, J., & Joshi, D. P. (2022). Genetic variability studies of yield and its component traits in upland cotton (*Gossypium hirsutum* L.). *The Pharma Innovation Journal, 11*(5), 380-384.

Monisha, K., Premalatha, N., Sakthivel, N., & Kumar, M. (2018). Genetic variability and correlation studies in upland cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding, 9*(3), 1053-1059.

Munir, S., Qureshi, M. K., Shahzad, A. N., Nawaz, I., Anjam, S., Rasul, S., & Zulfiqar, M. A. (2020). Genetic dissection of interspecific and intraspecific hybrids of cotton for morpho-yield and fiber traits using multivariate analysis. *Pakistan Journal of Agricultural Research, 33*(1), 9-16.

Naik, K. S., Satish, Y., Dayal Prasad Babu, J., & Srinivasa Rao, V. (2019). Genetic Variability, Heritability and Genetic Advance Studies for Yield and Fibre Quality Traits in Cotton (Gossypium Hirsutum L. *The Andhra Agric. J*, *66*(2), 305-308.

Nawaz, B., Sattar, S., & Tanwir, A. M. (2019). Genetic analysis of yield components and fiber quality parameters in upland cotton. *Int. Multi. Discip. Res. J.,* 9, 13-19.

Pandiyan, J., Ramalingam, A., Arumugam, P. M., & Saravanan, S. (2019). Genetic parameters of economic and fibre characters in upland cotton (Gossypium hirsutum L.). *International Journal of Current Microbiology and Applied Sciences*, *8*(6), 2084-2090.

Panse, V. G. (1957). Genetics of quantitative traits in relation to plant breeding. *Indian Journal of Genetics and Plan Breeding, 17*(3), 318-328.

Praveen, S. K. C., Raju, S., Ebenezer, B. R. R., Ajish, M., & Darling, B. S. (2019). Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). *Plant Archives*, *19*(1), 934-937.

Sahar, A., Zafar, M. M., Razzaq, A., Manan, A., & Haroon, M. (2021). Genetic variability for yield and fiber related traits in genetically modified cotton. *Journal of Cotton Research*, *4*(19), 1-10.

Shivasubramanian, S., & Menon, N. (1973). Heterosis and inbreeding depression in rice. *Madras Agricultural Journal*, 60, 1139-1144.

Shruti, Sowmya, H. C., Nidagundi, J. M., Lokesha, R., Arunkumar, B., & Shankar Murthy, M. (2019).

Genetic variability studies for yield, yield attributing and fibre quality traits in cotton (*Gossypium hirsutum* L.). *International Journal of Current Microbiology and Applied Sciences, 8*(10), 2677-2687.

Singh, R. K., & Chaudhary, B. D. (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New-Delhi, Ludhiana, India. Revd Ed., pp. 39-78.

Siva Reddy, K. V., Balakrishna, B., & Chenga Reddy, V. (2019). Genetic Variability Studies for Quantitative and Qualitative Traits in Upland Cotton (*Gossypium hirsutum* L.). *International Journal of Pure and Applied Bioscience*, *7*(3), 350-353.

Stoilova, A. & Valkova, N. (2010). Assessment of new Bulgarian and foreign cotton varieties by applying of cluster analysis. *Journal of International Scientific Publication: Materials, Methods & Technologies*, *4*(1), 49-64 (Bg).

Stoilova, A. & Bozhinov, M. (2006). Evaluation of foreign cotton varieties by cluster analysis. *Field Crops Studies*, Vol. III –3, 391-395 (Bg).

Stoilova, A. & Dechev, D. (2003a). Grouping of cotton lines by phenotypic stability by cluster analysis. *Plant Sciences*, 40, 33-37 (Bg).

Stoilova, A. & Dechev, D. (2003b). Selection evaluation of new cotton lines by cluster analysis. *Proceedings „Selection and Seed Production in Agricultural Crops*“, Sofia, 41-46 (Bg).

Stoilova, A., Valkova, N., & Genov, G. (2005). Genetic distance of foreign cotton varieties by some economic traits. *Field Crops Studies*, Vol. II, № 2, 221-226 (Bg).

Sunayana, S. R. S., & Somveer, N. (2017). Studies on association, path analysis and genetic parameters for seed cotton yield and its contributing characters in desi cotton (*Gossypium arboreum* L.). *Int. J. Curr. Microbiol. App. Science*s, *6*(11), 104-111.

Ullah, Q., Ahmad, M. Z., Ullah, K., Sayal, O., Jamil, A., Mohibullah, M., & Ahmad, B. (2020). Investigation of Cotton Germplasm for Genetic Divergence Regarding Yield Related Trait Using Principal Component Analysis. *Research Square*.

DOI: https://doi.org/10.21203/rs.3.rs-94514/v1

Vineela, N., Samba-Murthy, J. S. V., Ramakumar, P. V., & Ratna Kumari, S. (2013). Variability Studies for Physio Morphological and Yield Components Traits in American Cotton (*Gossypium hirsutum* L). *Journal of Agriculture and Veterinary Science*s, *4*(3), 7-10.

Vrinda, J., & Patil, B. R. (2018). Genetic variability and heritability study in F2 population for yield, yield attributes and Fiber quality traits in cotton (*Gossypium hirsutum* L.). *J. of Pharmacognosy and Phytochemistry*, *7*(4), 2816-2818.

Ward, J. H. (1963). Hierarchical grouping to optimize an objective function. *Journal of American Statistical Association,* 58, 234-244.

Zafar, M. M., Manan, A., Razzaq, A., Zulfqar, M., Saeed, A., Kashif, M., Khan, A. I., Sarfraz, Z., Mo H., Iqbal, M. S., Shakeel, A., & Ren, M. (2021). Exploiting Agronomic and Biochemical Traits to Develop Heat Resilient Cotton Cultivars under Climate Change Scenarios. *Agronomy*, *11*(9), 1885.

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