Genetic Variability and Heritability of Yield and Quality Traits in Cotton (*G. hirsutum* L.)

Jamila Dirbas*(1) and Ahmad Aljouma (1)

(1). Cotton Research Administration, General Commission for Scientific Agricultural Research (GCSAR), Damascus, Syria.
(*Corresponding author: Dr. Jamila Dirbas. E-mail: jamila.dirbas@gmail.com)

Received: 01/08/2021 Accepted: 24/08/2021

Abstract

Cotton in Syria is very important cash and industrial crop. Therefor the study endeavors to develop this crop via breeding programs and evaluation of genetic sources. In the present study, fifteen genotypes of cotton namely Fantom, Millinium, Lider, Cherpan432, Coker139, Aleppo 90, Aleppo124, Raqqa5, Aleppo118, Niab kiran, Niab 414, Deir EL-zour22, Coker 310, Samarkent 2, Tashkent 8) were evaluated for detecting genetic variability, heritability and genetic advance of twelve traits. The experiment was conducted at Hama Center of Scientific Agricultural Research, General Commission for Scientific Agricultural Research GCSAR/Syria, during 2019 season according to randomized complete block design RCBD with three replications. Analysis of variance showed high significant differences among the genotypes for all characters. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all traits, indicating environmental influence on these traits. The close agreement was found between phenotypic and genotypic coefficient of variances for no. of monopodia branch/ plant, earliness %, single plant yield, no. of symposia branch/ plant, fiber elongation, ginning out turn, fiber length and fiber strength indicating less environmental influence. High phenotypic and genotypic coefficients of variation estimates were obtained for no. of monopodia branch/ plant, earliness %, single plant yield and hence the best possibilities of improvements could be achieved by selection. High heritability coupled with high genetic advance were observed for single plant yield, fiber elongation and no. of bolls opened/plant, indicating additive gene effects. The quick improvement could well be expected in a short time for these characters by following simple pure line selection. Based on mean performance, the genotypes such as Aleppo118, Aleppo124 and Niab 414 recorded the highest mean values for single plant yield, no. of bolls opened/plant, and fiber elongation. So, they might be utilized as potential donors for breeding programs to improve a particular character in crop improvement.

Key words: Cotton, Genotypic Variation, Heritability, Genetic advance.

Introduction:

Cotton is an important fiber crop in the word because of its multiple uses of lint and seed. *Gossypium hirsutum* follows *Malvacea*e and it is planted in more than 80 countries of the world. In Syria, cotton is very important cash and industrial crop because it forms 4% agricultural area, 35-40% irrigated area, moreover, 18% of people works of its production and textile industry. Therefor we afford to amendment of cotton specifications via looking for a new genetic source which can be exploited in breeding programme. Genetic development is effective only when there is significance variability in the genetic material. As well as knowledge of genetic and environmental variability portion enables to improvement of different economic traits. Information on nature of inheritance and genetic characters is indispensable in selecting desirable breeding techniques in crop improvement (Vineela, 2013; Sun *et al*., 2017). Identification of genetic variability in plant population is of great significance to explain the most appropriate breeding methods for the improvement of different parameters (Chandnani *et al*., 2017; Hinze *et al*., 2017). Selection is good breeding tool depends on presence enough magnitude of variability in the genetic source. Johnson *et al*., (1955) suggested that heritability estimates in conjunction with high genetic advance were usually helpful in predicting its resultant effects for selecting the best individuals. The successful planning to breeding programme bases on understanding of genetic performance and inheritance of characters.

This study was objected to evaluation the phenotypic, genetic variation, heritability and genetic advance of earliness indicators, yield, and yield component and fiber quality in (*Gossypium hirsutum*) genotypes.

Materials and Methods:

The experiment was conducted at Hama Center for Scientific Agricultural Research, Syria, during summer cotton season of 2019. Fifteen genotypes namely Fantom, Millinium, Lider, Cherpan432, Coker139, Aleppo 90, Aleppo124, Raqqa5, Aleppo118, Niab kiran, Niab 414, Deir EL-zour 22, Coker 310, Samarkent 2 and Tashkent 8 were planted in Randomized Complete Block Design RCBD with three replications. 4 rows for each genotype, distance between plants was 30 cm and 75 cm between rows. The agricultural operations were done according to national cotton conference conclusion, 2019 (Syria). From each replication, 5 middle plants were randomly selected for examination sixteen parameters i.e., days to first flower (DFF), days to first boll (DFB), earliness % (E%), nodes to first sympodial branch (NFSB), number of monopodial branch/plant (NMB), plant height (cm) (PH), number of sympodial branches per plant (NSB), number of bolls opened/plant (NBO), boll weight (g) (BW), single plant yield (g) (SPY), Ginning out turn (GOT%), fiber length (inch) (FL), fiber strength (g/tex) (FS), fiber elongation (FE) and fiber fineness (FF). Analysis of variance was carried out using Genestate v12 software. The phenotypic (PV) and genotypic variances (GV) were calculated by utilizing mean sum of square (Lush, 1940). The phenotypic (PCV) and genotypic coefficient (GCV) of variation were estimated using the approach suggested by Burton (1952) and expressed in percentage. Heritability (HBS%) and expected genetic advance as mean (GA%) were calculated according to the formula suggested by Johanson *et al.*, (1955).

Results and Discussion:

The mean performance of studied characters was analyzed and ordered in the Table (1). The results indicated to existence clear range among the 15 genotypes for all traits. As well, the genotypes such as Aleppo118, Aleppo124 and Niab 414 recorded the highest mean values for single plant yield, number of bolls opened/plant and fiber elongation. So, they may be utilized as potential donors for future breeding programs. Also, the highest performer for particular character can be considered as donor such as Aleppo118 (7.17g of boll weight), Deir EL-zour 22 (43.67% of GOT), Fantom (25.86 g/tex of fiber strength) and Coker 310 (1.23 inch of 2.5% span length). So, these genotypes may be utilized for crossing programme to improve that particular character in crop improvement. The analysis of variance showed high significant differences among the 15 genotypes for all studied characters (Table 2). This indicated that there is a broad range for additional enhancement in these genotypes. Similar observations were made by Kumar *et al*., (2019).

The expression of characters is resultant interaction between genetic variability and environment. Genetic variability is only heritable, so it is necessary to estimate it for plan proper breeding programme.

Table 1. Range, mean performance, analysis of variance for studied characters of genotypes.

Parameter	Range	Mean	varieties	Error	Donor
DFF	46-65	54.16	52.04^{**}	7.52	Fantom, Niab 414, Millinium
DFB	90-101	93.53	16.6^{**}	4.3	Fantom, Samarkent 2, Aleppo118, Millinium, Niab kiran, Cherpan432
E %	3.93-98.11	59.52	714.8^{**}	185.1	Samarkent 2, Millinium, Aleppo118, Fantom, Aleppo 90, Raqqa5, Niab 414
NFSB	3.67-7.3	5.51	2.06^{**}	0.41	Millinium, Fantom, Niab 414
NMB	0.67-4	1.96	1.27^{**}	0.37	Niab 414, Aleppo 90, Millinium, Fantom, Samarkent 2, Deir EL-zour 22, Coker139, Cherpan 432, Niab kiran
PH (cm)	61.67-103.3	84.51	214.57^{**}	33.85	Niab 414, Aleppo124, Cherpan 432, Raqqa5, Samarkent 2
NSB	7.667-14	10.45	6.15^{**}	1.06	Aleppo118, Niab 414, Aleppo124, Cherpan 432
NBO	11.33-35	25.85	70.02^{**}	12.23	Aleppo124, Aleppo118, Deir EL-zour 22, Niab kiran, Cherpan 432, Lider, Fantom, Coker 310
BW (g)	4.133-7.17	5.6	1.21^{**}	0.31	Aleppo118, Cherpan 432, Lider, Aleppo 90
SPY (g)	65.4-323	165	7865.9^{**}	947.7	Aleppo118, Aleppo124, Cherpan 432, Fantom, Lider, Coker139, Raqqa5, Niab 414
GOT%	33.92-43.67	38.89	10.77^{**}	1.05	Deir EL-zour 22, Aleppo124, Niab 414, Aleppo 90, Coker 310, Niab kiran, Coker139, Cherpan 432
FL (inch)	1.046-1.23	1.145	3652.1^{**}	547.4	Coker 310, Niab 414, Niab kiran, Samarkent 2, Tashkent 8, Aleppo124
FS (g/tex)	20.48-26.56	24.26	3.29^{*}	1.22	Fantom, Tashkent 8, Millinium, Lider, Aleppo 90
FE	5.4-11.5	7.91	4.78^{**}	0.49	Niab 414, Fantom, Millinium, Aleppo 90, Deir EL-zour 22, Raqqa5, Lider, Niab kiran
FF(Mic)	3.25-5.25	4.38	0.51^{**}	0.10	Aleppo118, Tashkent 8, Fantom, Millinium, Aleppo 90, Niab kiran

$^{*, **}$ **significant to 5% and 1%, respectively**

In Table (2), the highest phenotypic variance PV and genetic variance GV were recorded by single plant yield (3253.8, 2306.1), while the lowest values for phenotypic and genotypic variance presented by fiber fineness (0.2, 0.1). The PCV and GCV were calculated for all the characters under study. The

PCV ranged from 3.1 (days to first boll) to 41.9% (number of monopodia branch/ plant). Number of monopodia branch/plant, single plant yield and earliness % showed high PCV and GCV indicating the presence of significant genetic variability in this character. Selection pressure can be applied on this character to separate promising genotypes. This results accordance to reported results by Amanu *et al.*, (2020). While number of nodes to first sympodial branch and number of sympodial branch/plant recorded moderate PCV and GCV. Days to first flower, days to first boll, ginning out turn (GOT, %), fiber length and fiber strength displayed low PCV and GCV. High PCV coupled with moderate GCV was recorded in number of bolls opened/plant, but moderate PCV coupled with low GCV presented by plant height, boll weight and fiber fineness. The close agreement between PCV and GCV for most of the traits indicating that the obtained variation could largely due to genetic, and there was only less influence of environmental effects, so may be exercise selection based on the phenotypic performance.

Table 2. Components of variance for studied characters of genotypes.

Parameter	**PV**	**GV**	**PCV (%)**	**GCV (%)**	**HBS%**	**GA%**
DFF	22.4	14.8	8.7	7.1	66.4	11.9
DFB	8.4	4.1	3.1	2.2	48.9	3.1
E %	361.7	176.6	32.0	22.3	48.8	32.1
NFSB	1.0	0.6	17.7	13.5	57.7	21.1
NMB	0.7	0.3	41.9	28.0	44.6	38.5
PH (cm)	94.1	60.2	11.5	9.2	64.0	15.1
NSB	2.8	1.7	15.9	12.5	61.6	20.2
NBO	31.5	19.3	21.7	17.0	61.2	27.4
BW (g)	0.6	0.3	13.9	9.8	49.7	14.2
SPY (g)	3253.8	2306.1	34.6	29.1	70.9	50.5
GOT%	4.3	3.2	5.3	4.6	75.6	8.3
FL (inch)	1582.3	1034.9	3.5	2.8	65.4	4.7
FS (g/tex)	1.9	0.7	5.7	3.4	36.0	4.2
FE	1.9	1.4	17.5	15.1	74.3	26.8
FF(Mic)	0.2	0.1	11.1	8.4	57.4	13.1

Heritability refers to magnitude of genetic variation in heritance trait, and considered as measurement of selection efficiency. The high heritability was registered in the traits *viz* Ginning Out Turn (GOT, %), Fiber elongation, single plant yield, days to first flower, plant height, fiber length, number of sympodial branch/ plant and number of bolls opened/plant. Dirbas, (2018) observed high heritability for several traits.

Moderate heritability was recorded in the traits *viz* no of node to first sympodial branch, fiber fineness, boll weight, days to first boll, earliness % and number of monopodial branch/ plants, whereas low heritability was shown in fiber strength.

However, based on heritability alone is not enough for exercise selection because it does not give an idea about expected genetic gain in the next generation, but it has to be considered in conjunction with genetic advance. Hence it is necessary to estimation of genetic advance.

Genetic advance as mean (GA %) ranged between 50.5 (single plant yield) and 3.1 (days to first boll). High GA was noticed in characters such as single plant yield, number of monopodial branch/plant, earliness %, number of bolls opened/plant, fiber elongation and number of node to first sympodial branch, whereas moderate GA was noticed in plant height, boll weight, fiber fineness and days to first flower. Low GA was noticed in ginning out turn, fiber length, fiber strength and days to first boll.

As result, high heritability associated to high GA was recorded for single plant yield, fiber elongation and number of bolls opened/plant, this clearly indicated to control of additive genes in the expression of these traits. This suggested that improvement could well be expected in a short time for these characters by following simple pure line selection. Similar results were reported by Dhivya *et al*., (2014). High heritability coupled with low to moderate genetic advance as percent of mean was observed for fiber length, ginning out turn, days to first flower and plant height, and this clearly indicated the characters are mainly under the control of non-additive genes. This suggested that the improvement cannot be expected by resorting to simple selection procedures for these characters. These characters could well be exploited by resorting to hybrid breeding. Low heritability coupled with low genetic advance was observed in fiber strength which showed that although there was some improvement in the characters, they are still to a greater extent influenced by the environment and controlled by a non-additive gene, hence they need further confirmation and evaluation for their fixation and that could be possible through recurrent selection in the succeeding generations.

Conclusion:

From the results of the present study, among the study material some of the genotypes were identified as potential donors for the improvement of different characters. The direct selection could be done for most of the yield contributing traits which exhibited high genetic variability and high range of variation. A high PCV over GCV for the characters studied indicated that environment influences the expression of these characters under study. High heritability combined with genetic advance was recorded for single plant yield, fiber elongation and number of bolls opened/plant indicated that simple pure line selection could be followed to improve these characters in the future crop improvement programmes.

Based on mean performance, the genotypes such as Aleppo118, Aleppo124 and Niab 414 recorded highest mean values for single plant yield, number of bolls opened/plant, number of bolls opened/plant and fiber elongation. So, they might be utilized as potential donors for breeding programs to improve a particular character in crop improvement.

References:

Amanu, A.W.; H. Mohammed; and B. Amsalu (2020). Genetic variability and heritability studies of seed cotton yield and fiber quality in F5 segregating generation of upland cotton (*Gossypium hirustum* L.) in Ethiopia. African Journal of Plant Breeding. 7(3): 001-011.

Burton, G.W. (1952). Quantitative inheritance in grasses. Proceedings of the Sixth International Congress, pp. 277-283.

Chandnani, R.; Z. Zhang, J.D. Patel; J. Adhikari; S. Khanal; D. He; N. Brown; P.W. Chee; and A.H. Paterson (2017). Comparative genetic variation of fiber quality traits in reciprocal advanced backcross populations. Euphytica.11: 213-241.

Dhivya, R.; P. Amalabalu; R. Pushpa; and D. Kavithamani (2014). Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.). African Journal of Plant Science. 8(1):1-5.

Dirbas, J.; (2018). Combining ability and heritability of some productivity characters in some hybrids of cotton (*Gossypium hirsutum* L.). Syrian Journal of Scientific Agricultural Research. 5(3): 113-124.

Johnson, H.W.; H.F. Robinson; and R.E. Comstock (1955). Estimation pf genetic and environmental in Soybeans. Agronomy Journal, 47 (7): 314-318.

Lush, J.L, (1940). Intra-Sire correlation and regression of offspring on dams as a method of estimating heritability of characters. In Proc. Am. Soc. Anim. Prod., 33:293-301.

Kumar, P.K.; S. Raju; R. Ebenezer Babu Rajan; A. Muraleedharan; and B. Darling Suji (2019). Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). Plant Archives. 19(1): 934-937.

Sun, Z.; X. Wang; Z. Liu; Q. Gu; Y. Zhang; Z. Li; H. Ke; J. Yang; J. Wu; L. Wu; G. Zhang; C. Zhang and Z. Ma (2017). Genome-wide association study discovered genetic variation and candidate genes of fiber quality traits in *Gossypium hirsutum* L. Plant Biotechnol. J., 15(8): 982-996.

Vineela, N.; J.S.V. Samba Murthy; P.V. Ramakumar; and K.S. Ratna (2013). Variability studies for physic morphological and yield components traits in American cotton (*Gossypium hirsutum* L.). J. Agric. Vet. Sci., 4(3): 7-10.