Research Article

Heritability and correlation analysis in Bt and non-Bt cotton (*Gossypium hirsutum* L.) genotypes

Arshad Ali Kaleri¹, Abdul Wahid Baloch¹, Munaiza Baloch^{1*}, Niaz Ahmed Wahocho², Tanweer Fatah Abro¹, Qamaruddin Jogi³, Aijaz Ahmed Soomro³, Asad Marri⁴ and Liaquat Ali Bhutto⁵

1. Department of Plant Breeding and Genetics, Sindh Agriculture University Tandojam-Pakistan

2. Department of Horticulture, Sindh Agriculture University Tandojam-Pakistan

3. Department of Agronomy, Sindh Agriculture University Tandojam-Pakistan

4. Institute of Food Sciences and Technology, Sindh Agriculture University Tandojam-Pakistan

5. Oilseeds Section, Agriculture Research Institute, Tandojam-Pakistan

*Corresponding author's email: balochbreeders@yahoo.com

Citation

Arshad Ali Kaleri, Abdul Wahid Baloch, Munaiza Baloch, Niaz Ahmed Wahocho, Tanweer Fatah Abro, Qamaruddin Jogi, Aijaz Ahmed Soomro, Asad Marri and Liaquat Ali Bhutto. Heritability and correlation analysis in Bt and non-Bt cotton (*Gossypium hirsutum* L.) genotypes. Pure and Applied Biology. Vol. 5, Issue 4, pp906-912.

<http://dx.doi.org/10.19045/bspab.2016.50114>

Received: 23/07/2016

Revised: 01/08/2016

Accepted: 15/08/2016

Online First: 25/0082016

Abstract

The present research was carried out to analysis the heritability and correlation in 24 Bt and non-Bt cotton genotypes for yield, yield related and fiber traits, including plant height (cm), first sympodial node number, first effective boll node number, sympodial branches plant⁻¹, bolls plant⁻¹, boll weight (g), seed index (g), micronaire value (µg/inch), staple length (mm), ginning outturn percentage and seed cotton yield plant⁻¹ (g). The results exhibited that genotypes differed significantly at $P \leq 0.01$ for all the traits studied. It indicates that the significant genetic diversity among the genotypes for further evaluation. High heritability estimates in broad sense was found for most of the studied traits except 1st effective boll node number, which displayed moderate heritability estimates. High heritability values for majority of the traits suggested that the variation observed was mainly under genetic control and was less affected by environmental factors, referring the influence of additive gene action for most of the studied traits. Hence, the improvement of these traits can be made through direct phenotypic selection. Among the recorded traits, only four traits i.e. 1st effective boll node number, sympodial branches plant⁻¹, bolls plant⁻¹ and ginning outturn percentage developed a significant and positive associations with seed cotton yield plant⁻¹. Thus, selection for these traits will assist in selecting genotypes with greater seed cotton yield plant⁻¹.

Keywords: Heritability; Correlation; Genetic Advance; Seed cotton yield; Bt-Cotton

Introduction

Cotton (*Gossypium hirsutum* L.) belongs to the family Malvaceae, and is grown almost all over the world from the time

immemorial. Cotton is mainly grown for fiber, which is the economic component and plays a vital role for uplifting the country's economy [1]. In breeding population, the

presence of enough magnitude of variability is more effective and important criteria for selection. Therefore, it is necessary to understand the presence of variability in a population to adopting most appropriate breeding technique for improvement of the various characters in cotton. To maintain the high productivity level of any crop, genetic variability offered in nature or created in the course of crop breeding is of immense significance. During hybridization programs, genetic similarity within a crop species is readily barrier and main cause of genetic vulnerability. To create new genetic complexes, it is very necessary that genetic diversity should be available in cultivated and wild germplasm for higher yield, fiber and tolerance to various biotic and abiotic stresses [2]. Correlation coefficient is one of the key statistical approaches that can assist to plant breeders in selection crop plants for higher yields. Therefore, knowledge of interrelationships between yield and its contributing factors will improve the effectiveness of breeding programs through the use of suitable selection indices [3]. The current study was aimed to estimate heritability and determine correlations among various quantitative and qualitative traits in Bt and non-Bt cotton genotypes.

Materials and methods

An experiment was conducted at the Experimental Field, Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam (Pakistan). The genetic materials consisted of 24 Bt and non-Bt cotton genotypes, viz. Bt-555, SGA-1, Lalazar, S-1-815, MNH-886, CIM-496, FH-113, CIM-534, Bt-886, FH-901, Bt-905, CRIS-494, IR-3701, IR-1524, CRIS-134, CRIS-342, Bt-142, Bt-703, Tarzan-1,

Neelam-121, AA-804, MG-6, NIAB-78, and CRIS-121. The experiment was arranged in a randomized complete block design with four replications. The space between plant to plant and row to row was kept at 30 and 75 cm, respectively. All recommended agronomic practices were applied at appropriate time. The traits studied were, plant height (cm), bolls plant⁻¹, sympodial branch plant⁻¹, 1st effective boll node number, 1st sympodial node number, boll weight (g), ginning outturn percentage (GOT%), seed index (100-seed weight, g), staple length (mm), micronaire value (µg/inch) and seed cotton yield plant⁻¹ (g). The analysis of variance, mean comparisons and correlation were performed through Statistix v. 8.1 computer software. Heritability analysis was carried out as suggested by Allard [4].

Results and discussion

Analysis of variance

The results revealed that the mean squares (Table 1) of all the genotypes differed highly significantly at $P \leq 0.01$ of probability level for all the studied traits, such as plant height, 1st sympodial node number, 1st effective boll node number, sympodial branches plant⁻¹, bolls plant⁻¹, boll weight, seed index, micronaire value, staple length, ginning outturn percentage and seed cotton yield plant⁻¹, suggesting that studied materials proved its worth for further evaluation, especially for the improvement of yield and fiber traits in upcoming breeding programs. Almost similar results were also reported by several other workers, including Baloch [5], Mugheri [6] and Jatoi [7].

Table 1. Mean squares from analysis of variance for various traits in Bt and non-Bt cotton genotypes

Source of variations	D.F	Characters										
		Plant height	1 st sympodial node number	1 st effective boll node number	Sympodial branches plant ⁻¹	Bolls plant ⁻¹	Boll weight	Seed index	Micronaire value	Stable length	GOT %	Seed cotton yield plant ⁻¹
Replications	3	6.648	0.334	0.013	0.902	7.331	0.049	0.392	0.013	0.503	0.160	78.10
Genotypes	23	447.6**	3.18**	1.60**	122.24**	156.3**	0.29**	1.68**	0.61**	4.64**	78.1**	1925.0**
Error	69	2.793	0.127	0.454	1.813	2.240	0.030	0.155	0.013	0.647	1.046	60.85

Note: ** = indicates significant at 0.01% of the probability level

Mean performance

The data regarding mean performance of genotypes is given in Table-1. The data revealed that genotype CRIS-342 produced the tallest plants of 113.65 cm, while Tarzan-1 recorded the shortest plants measuring 73.85 cm as compared to the rest of the genotypes. In case of first sympodial node number, the genotype MNH-886 showed maximum value (7.95), however, the minimum value (4.60) was recorded in Tarzan-1. With regard to first effective boll node number, the maximum value was recorded in AA-802 (11.25), while Lalazar showed minimum value of 8.85 among rest of the genotypes. For sympodial branches plant⁻¹, S#-1-815 produced the highest number of sympodial branches plant⁻¹ (31.95), whereas CIM-534 produced the lowest number of sympodial branches plant⁻¹ (15.15). With respect to bolls plant⁻¹, the variety S#-1-815 set maximum number of bolls plant⁻¹ (49.90) against other genotypes, while minimum (25.30) number of bolls plant⁻¹ were obtained from Bt-886. MNH-886 weighed bigger bolls of 3.58 g, while the smaller bolls were observed in variety CRIS-134 (2.61 g). Makhdoom [8] suggested that boll mean weight is an important independent yield component and

play a prime role in improving seed cotton yield. The variety IR-3701 gave higher seed index (7.85 g); however, the variety Neelam-121 gave the lower seed index (5.50 g). The maximum micronaire value was observed in Lalazar (4.36 µg/inch) while minimum value was observed in genotype CIM-496 & CIM-534 (3.33 µg/inch). In case of staple length, SGA-1 measured the longer staple length of 29.82 mm, while the shorter staple length (25.46 mm) was recorded in Bt-142. With regard to ginning outturn percentage, the maximum GOT % (44.90) was observed in Bt-886, while the lowest value of GOT % (31.30) was observed in S#1-815. The variety S#-1-815 produced maximum (153.65 g) seed cotton yield plant⁻¹. Rao [9] assessed different hirsutum varieties for yield and other useful traits and observed significant variations for boll weight and showed positive effect on seed cotton yield. Therefore, it was concluded that boll weight is a key yield component and should be considered while breeding for seed cotton yield. Whereas the variety Bt-703 gave the lowest (82.46 g) seed cotton yield plant⁻¹. In general, variety S#-1-815 displayed better performance in terms of sympodial branches plant⁻¹, bolls plant⁻¹ and seed cotton yield plant⁻¹

Table 2. Mean performance of BTt and non-Bt cotton genotypes for various traits

Genotypes	Plant height (cm)	1 st sympodial node number	1 st effective boll node number	Sympodial branches plant ⁻¹	Bolls plant ⁻¹	Boll weight (g)	Seed index (100 seed wt, g)	Micronaire value (µg/inch)	Staple length (mm)	GOT %	Seed cotton yield plant ¹ (g)
CRIS-134	87.65	5.60	10.40	15.30	35.00	2.61	6.95	3.36	27.68	36.40	91.08
AA-802	75.15	5.15	11.25	16.50	29.65	3.27	7.4	3.46	28.13	38.55	98.35
NIAB-78	96.50	4.75	11.05	16.15	35.75	2.98	7.42	3.44	28.31	34.45	105.63
CIM-496	106.75	5.30	9.75	26.90	43.55	3.11	7.45	3.33	27.48	31.80	134.22
IR-3701	88.80	5.60	9.40	17.75	29.30	3.14	7.85	4.25	28.66	43.70	88.11
IR-1524	82.75	5.40	10.60	26.00	38.40	3.37	7.80	3.38	28.42	34.00	129.64
CIM-534	90.55	5.70	9.95	15.15	33.80	2.75	7.40	3.33	29.40	33.30	93.25
FH-113	101.75	4.90	9.40	31.65	43.55	3.15	7.15	3.42	29.10	44.15	137.5
MG-6	91.65	5.10	9.90	23.55	35.95	3.06	6.90	3.40	27.19	32.75	110.69
Bt-555	96.15	4.65	9.95	19.55	29.85	3.51	6.90	3.42	28.02	35.75	98.72
Bt-886	86.55	4.75	9.85	26.25	25.30	2.71	6.93	4.19	29.12	44.90	68.37
SGA-1	77.55	5.00	9.45	15.70	30.50	3.14	6.40	3.36	29.82	34.06	95.56
FH-901	85.70	5.20	9.20	17.95	29.15	3.04	6.15	4.27	26.81	43.40	89.38
Bt-703	111.45	5.55	9.40	21.20	28.70	2.87	5.80	4.26	27.72	41.85	82.46
LALAZAR	89.95	5.50	8.85	28.00	30.60	3.15	6.30	4.36	26.75	32.35	96.38
Bt-905	83.80	4.80	10.05	17.30	26.85	3.11	6.25	3.39	28.16	39.30	83.99
TARZAN-1	73.85	4.60	10.05	25.20	29.25	3.22	6.15	3.46	26.72	36.00	94.06
S#1-815	95.50	4.90	10.35	31.95	49.90	3.08	6.15	3.39	27.47	31.30	153.65
CRIS-342	113.65	5.10	9.55	27.30	31.40	3.08	6.45	3.44	28.15	33.10	96.98
CRIS-494	89.95	6.95	9.65	18.80	25.65	3.55	7.10	3.51	26.83	38.85	90.86
Neelam121	84.40	6.25	10.40	24.55	38.10	3.52	5.50	3.57	26.88	35.60	133.86
CIM-598	102.55	7.70	9.45	31.35	28.65	3.54	7.55	3.55	27.26	34.55	101.56
MNH-886	91.85	7.95	10.90	23.80	40.10	3.58	7.20	3.46	29.06	44.25	143.2
Bt-142	80.40	5.70	8.95	24.30	32.05	3.45	6.60	4.33	25.46	39.00	110.51
LSD (0.5%)	2.357	0.504	0.951	1.899	2.111	0.246	0.556	0.166	1.135	1.443	11.00

Heritability estimates

Heritability estimates are helpful in deciding the characters to be considered while making selection. High heritability estimates (h^2 b.s.) were observed for plant height ($h^2=97.55\%$), 1st sympodial node number ($h^2=85.70\%$), sympodial branches plant⁻¹ ($h^2=94.32$), bolls plant⁻¹ ($h^2=94.50\%$), seed index ($h^2=71.18\%$), boll weight ($h^2=69.07$), micronaire value ($h^2=92.07$), staple length ($h^2=60.66$), ginning outturn percentage ($h^2=94.85$) and seed cotton yield plant⁻¹ ($h^2=88.45\%$), whereas moderate heritability

was observed for 1st effective boll node number ($h^2=45.35$). High heritability for these traits indicate that the variation observed was mainly under genetic control and was less influenced by environment, indicating the influence of additive gene action for these traits. Hence, the improvement of these traits can be made through direct phenotypic selection. In agreement to our results, several researchers like Jatoi [6] and Mugheri [7] also observed high heritability for variety of traits in cotton.

Table 3. Heritability estimates for various traits in Bt and non-Bt cotton

Characters	Genotypic variance (δ^2g)	Phenotypic variance (δ^2p)	Heritability % (Broad sense)
Plant height	111.218	114.01	97.55
1st sympodial node #	0.764	0.891	85.70
1 st effective boll node #	0.288	0.635	45.35
Sympodial branches plant ⁻¹	30.107	31.92	94.32
Bolls plant ⁻¹	38.529	40.769	94.50
Boll weight	0.067	0.097	69.07
Seed index	0.383	0.538	71.18
Micronaire value	0.151	0.164	92.07
Staple length	0.998	1.645	60.66
GOT%	19.277	20.323	94.85
Seed cotton yield plant ⁻¹	466.28	527.13	88.4

Correlation coefficients

Cotton seed yield is the resultant product of component character which is not under the direct control of any single gene. Thus, an improvement of component characters leads to a consequent improvement in the yield. Therefore, the understanding of the mechanism of association that is, cause and effect relationship provides the foundation for formulating suitable selection criteria for breeding program on the basis of yield components for achieving rational improvement of yield and its components [10]. The estimates of correlation coefficients were worked out among 11 yield and fiber quality related characters with seed cotton yield plant⁻¹ (Table 4). Of the total traits, three traits, namely 1st effective boll node number ($r=0.240^*$), sympodial branches plant⁻¹ ($r=0.498^{**}$) and bolls plant⁻¹ ($r=0.895^{**}$) had significant positive association with seed cotton yield plant⁻¹. Hence, selection for these traits will help in selecting genotypes with higher seed cotton yield plant⁻¹. Similar results of positive association between yield and fiber quality traits were reported by Ashokkumar

and Ravikesavan [11]. The inter correlation among the important component traits is also imperative in order to decide which trait to be given due weightage in exercising selection. The inter correlation among the quantitative and qualitative traits viz, plant height with sympodial branches plant⁻¹ ($r=0.373^{**}$) and bolls plant⁻¹ ($r=0.252^*$); 1st sympodial node number with micronaire value ($r=0.282^{**}$); 1st effective boll node number with bolls plant⁻¹ ($r=0.237^*$) and staple length ($r=0.203^*$); sympodial branches plant⁻¹ with bolls plant⁻¹ ($r=0.440^{**}$) and ginning outturn percentage with micronaire value ($r=0.717^{**}$) were positive and significant, indicating the possibility of simultaneous improvement of these traits. Similar results were reported by Kalpande et al. [12]. However, among the yield contributing traits, it is interesting to note that bolls plant⁻¹ developed significant negative inter correlation with ginning outturn percentage ($r=-0.295^{**}$) and micronaire value ($r=-0.241^*$), suggesting that great care should be taken while selection is being carried out for bolls plant⁻¹.

Table 4. Correlation coefficients between yield and fiber traits in Bt and non-Bt cotton genotypes

Characters	Plant height	1 st sympodial node number	1 st effective boll node number	Sympodia l branches plant ⁻¹	Bolls plant ⁻¹	Boll weight	GOT %	Seed index	Micronaire value	Staple length
1 st sympodial node number	0.121 ^{NS}									
1 st effective boll node number	-0.164 ^{NS}	0.040 ^{NS}								
Sympodial branches plant ⁻¹	0.373 ^{**}	0.126 ^{NS}	-0.179 ^{NS}							
Bolls plant ⁻¹	0.252 [*]	0.002 ^{NS}	0.237 [*]	0.440 ^{**}						
Boll weight	-0.006 ^{NS}	0.190 ^{NS}	-0.037 ^{NS}	-0.012 ^{NS}	0.101 ^{NS}					
GOT %	-0.107 ^{NS}	0.138 ^{NS}	-0.097 ^{NS}	-0.140 ^{NS}	0.295 ^{**}	0.096 ^{NS}				
Seed index	0.067 ^{NS}	0.147 ^{NS}	0.139 ^{NS}	-0.982 ^{NS}	0.089 ^{NS}	0.056 ^{NS}	-0.008 ^{NS}			
Micronaire value	-0.014 ^{NS}	0.282 ^{**}	-0.169 ^{NS}	-0.046 ^{NS}	-0.241 [*]	-0.055 ^{NS}	0.717 ^{**}	-0.106 ^{NS}		
Staple length	0.019 ^{NS}	-0.010 ^{NS}	0.203 [*]	-0.158 ^{NS}	0.151 ^{NS}	-0.096 ^{NS}	0.137 ^{NS}	-0.010 ^{NS}	-0.051 ^{NS}	
Seed cotton yield plant ⁻¹	0.154 ^{NS}	0.176 ^{NS}	0.240 [*]	0.498 ^{**}	0.895 ^{**}	-0.055 ^{NS}	0.244 [*]	0.083 ^{NS}	-0.164 ^{NS}	0.086 ^{NS}

** & * = indicates significant at 0.01 & 0.05%, respectively; NS indicates non-significant

Conclusions

It was concluded that high heritability values was observed for majority of the traits. This suggests that the variations observed was mainly under genetic control and was less affected by environmental factors, referring the influence of additive gene action for most of the studied traits. Of the important note, 1st effective boll node number, sympodial branches plant⁻¹, bolls plant⁻¹ and ginning outturn percentage established a significant and positive associations with seed cotton yield plant⁻¹. Thus, selection for these traits will help in selecting genotypes with superior seed cotton yield plant⁻¹.

Authors' contributions

Conceived and designed the experiments: AA Kaleri, AW Baloch & TF Abro, Performed the experiments: AA Kaleri, Analyzed the data: NA Wahocho & A Marri, Contributed reagents/ materials/ analysis tools: AW Baloch & L Bhutto. Wrote the paper: M Baloch, AW Baloch, AA Soomro, Q Jogi & AA Kaleri.

References

1. Wendel JF & Crown RC (2003). Polyploidy and the evolutionary history of cotton. *Adv Agron* 78: 140–186.
2. Sanghera GS, Kashyap SC, Rana V & Parray GA (2014). Agro-morphological and genetic diversity among elite wheat genotypes grown under Kashmir conditions. *Int J Current Res* 6(8): 7735-7740.
3. Mohammadi, SA, Prasanna BM & Singh NN (2003). Sequential path model for determining interrelationships among grain yield and related characters in maize. *Crop Sci* 43:1690-1697.
4. Allard RW (1960). Principles of Plant Breeding. Johan Wiley and Sons Inc, USA.
5. Baloch AW, Sahito JA, Ali M, Baloch GA, Abro S, Channa SA, Baloch AM, Baloch GH & Baloch GM (2014). Association analysis of yield and fiber traits in advance Pakistani cotton cultivars (*Gossypium hirsutum* L). *Adv Appl Agri Sci* 2(12): 73-80.
6. Jatoti SH (2015). Genetic analysis of yield and fiber traits in selected Bt cotton

- germplasm. MSc thesis submitted through department of Plant Breeding and Genetics to Sindh Agriculture Univ. Tando Jam.
7. Mugheri MA (2015). Genetic variability analysis of some agronomical traits in Bt cotton genotypes (*Gossypium hirsutum* L.). M.Sc thesis submitted through department of Plant Breeding and Genetics to Sindh Agriculture Univ. Tando Jam.
 8. Makhdoom K, Khan NU, Batool S, Bibi Z, Farhatullah, Khan S, Mohammad F, Hussain D, Raziuddin, Sajjad M & Khan N (2010). Genetic aptitude and correlation studies in *Gossypium hirsutum* L. *Pak J Bot* 42(3): 2011-2017.
 9. Rao IA (2006). Future of Bt-cotton in Asia. Pakissan 23, May 2007, online website available at <http://www.pakistan.com/english/advisory/biotechnology/future.ofBtcotton.in.asia.shtml>.
 10. Wang L, Liu F, Talat F, Khan MKR, Li S, Wang C, Zhang X, Wang Y, Hua J & Wang K (2012). Multivariate analysis for yield and some agronomic traits in F_{2:3} population of cotton hybrid under three different locations. *African J Agri Res* 7(35): 4919-4926.
 11. Ashokkumar J & Ravikesavan R (2010). Genetic studies of correlation and path coefficient analysis for seed, oil, yield and fiber quality traits in cotton (*G. hirsutum* L.). *Aust J Basic Appl Sci* 4(11): 5496-5499.
 12. Kalpande HV, Bhale SD, Kale UV, Deshmukh JD, Gite VK & Kakde SS (2008). Genetic variability and correlation studies in F₃ generation of cotton (*Gossypium hirsutum* L.) *Int J Plant Sci* (3): 94-97.