

Genetic Variability, Association and Path-Analysis in Upland Cotton (*G. arboreum* L.) Genotypes

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Abstract The experiment was conducted during *rabi* of 2012-13 in rainfed situation to study the variability, correlation and path analysis for the yield and yield attributing traits in 144 *G. arboreum* genotypes. Genotypes were shown high range of variability for all the six characters indicates existence of significant variability among the genotypes and scope for selection. Relative values of GCV were lower than PCV for all the six traits indicates influence of environment in observed variability. Most of the traits (seed cotton yield (kg/ha): $h^2 = 82.2$, GAM = 58.05%, plant height: $h^2 = 66.9$, GAM = 33.86%, number of bolls per plant: $h^2 = 80.50$, GAM = 51.59%, boll weight: $h^2 = 86$, GAM = 25.28%) exhibited high heritability coupled with high genetic advance except number of monopodial branches per plant ($h^2 = 26.10$, GAM = 25.75%) and number of sympodial branches per plant ($h^2 = 10.80$, GAM = 23.71%) with low heritability coupled with high genetic advance indicates prevalence of additive gene effects. The genotypic and phenotypic correlation coefficient estimates for plant height (0.2997, 0.2377), number of monopodial branches per plant (0.3283, 0.1940), number of sympodial branches per plant (0.2094, 0.0845), number of bolls per plant (0.9093, 0.9146) and boll weight (0.4116, 0.3979) were exhibited positive correlation with all the traits how-

ever very strong correlation was observed for number of bolls per plant and boll weight with total seed cotton yield. Path coefficients shown that number of bolls per plant (0.9219, 0.9155) and boll weight (0.3984, 0.3876) found to be most important trait for seed cotton yield as it is showing positive direct and indirect effects at both genotypic and phenotypic level.

Keywords Cotton, Correlation coefficients, Heritability, Path coefficients, Variability.

Introduction

Cotton is one of the promising cash crops often referred as “white gold” and king of fibers, being a principal raw material for flourishing textile industry plays very important role in national economy. According to the cotton corporation of India limited in 2014–15 area under cotton cultivation was 128.19 lakh ha with production of 380 lakh bales (cotton advisory board). However, the average productivity of cotton (504 kg/ha) in India is the lowest among cotton growing nations of the world (cotton advisory board). Currently *Gossypium* includes 50 species, four of which are cultivated, 44 are wild diploids and two are wild tetraploids. Out of the four cultivated species, *Gossypium hirsutum* L. and *Gossypium barbadense* L. commonly called as new world cottons are tetraploids ($2n = 4x = 52$), whereas *G. herbaceum* L. and *Gossypium arboreum* L. are diploids ($2n = 2x = 26$) and are commonly called as old world cottons.

Genetic variability has been considered a pivotal

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Table 1. List of upland cotton genotypes used in the investigation.

Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes
1	RAS-158	51	RAS-10 N.S	101	ARB-18
2	RAS-11	52	IPS-11	102	RAS-132-33
3	RAS-360	53	RAS-11 B-3	103	RAS-127
4	IPS-12	54	RAS-416	104	RAS-146
5	IPS-18	55	RAS-35 (B)	105	ARB-18-18
6	RAS-554	56	RAS-515-22	106	RAS-373
7	RAS-387	57	RAS-311	107	RAS-105
8	RAS-331-4	58	RAS161	108	RAS-168
9	RAS-336	59	RAS-343	109	RAS-71-97
10	RAS-324-115	60	RAS-35 (B)	110	ARB-78
11	RAS-314	61	RAS-248	111	RAS-34 (B)
12	RAS-577-22	62	RAS-67-57	112	ARB G × Plant
13	RAS-17 N-S	63	RAS-321	113	RAS-120
14	RAS-152	64	RAS-515	114	RAS-517-22
15	RAS-89	65	RAS-13-112	115	SD-27
16	RAS-517-21-3	66	RAS-35-48-3	116	RAS-135
17	RAS-364	67	RAS-47	117	RAS-323
18	RAS-628	68	RAS-64	118	3 × 2 F8
19	RAS-348	69	RAS-371	119	RAS-33
20	IPS-55	70	RAS-347	120	RAS-33 O.P.S
21	RAS-146	71	RAS-361	121	RAS-145
22	PH-132	72	RAS-120	122	RAS-27
23	RAS-112	73	RAS-608	123	RAS-54
24	RAS-74-113	74	RAS-336	124	AR-29
25	RAS-515	75	RAS-355	125	504-82-76-150
26	IPS-20	76	RAS-407	126	RG-187
27	RAS-311	77	RAS-522	127	RAS-400
28	IPS-32	78	RAS-369	128	504-48-76.O.P.S
29	ARB-49	79	RAS-311	129	RAS-48-O.P.S
30	IPS-23	80	RAS-120	130	ARB-43 (B)
31	RAS-152	81	RAS-393	131	ARB-43 (N)
32	RAS-350	82	RAS-308	132	RAS-376
33	RAS-318	83	RAS-511	133	RAS-663
34	RAS-389	84	RAS-351	134	RAS-678
35	ARB-115	85	504-48.76	135	RAS-682
36	ARB-78	86	ARB-115	136	RAS-657
37	RAS-382	87	RAS-362	137	RAS-679
38	IPS-42	88	RAS-98	138	RAS-656
39	RAS-399	89	RAS-118	139	RAS-658
40	RAS-305	90	504-48.76	140	RAS-661
41	RAS-303	91	RAS-654	141	RAS654
42	RAS-18	92	ARB-116	142	RAS-662
43	RAS-118	93	508-831	143	RAS-165 O.P.S
44	RAS-248	94	RAS-329	144	RAS-680
45	RAS-378	95	Vinur		
46	RAS-15	96	CMFS O.P.S		
47	RAS-67	97	ARB-47-114		
48	RAS-384	98	RAS-352		
49	RAS-35-48.3	99	RAS-92		
50	RAS-331-4	100	RAS-222		

factor in improving crop productivity. Domestication of crops has resulted in narrowing the genetic base in almost all major crops including cotton. So it is es-

sential to evaluate large number of available germplasm to develop superior genotypes. Correlation studies provides information about yield con-

Table 2. Estimates of genetic variability parameters for yield, yield attributing traits in cotton (*G. arboreum*) genotypes. h^2 (%)—Heritability in broad sense, GAM = Genetic advance as percent mean. X_1 : Plant height (cm), X_2 : Number of monopodial branches per plant, X_3 : Number of sympodial branches per plant, X_4 : Bolls per plant, X_5 : Boll weight (g), X_6 : Seed cotton yield (kg/ha).

Charac- ters	Min	Range Max	Mean $\pm$ SE	Coefficient of variability		h^2 (%)	GAM (%)
				PCV (%)	GCV (%)		
X_1	52.5	171.0	97.9 $\pm$ 7.62	19.16	15.67	66.9	33.86
X_2	0.5	5.0	2.89 $\pm$ 0.657	37.36	19.09	26.1	25.75
X_3	5.0	23.5	15.12 $\pm$ 8.38	83.08	27.32	10.8	23.71
X_4	8.0	34.0	19.51 $\pm$ 1.47	24.26	21.77	80.5	51.59
X_5	1.3	2.4	1.95 $\pm$ 0.057	11.13	10.32	86	25.28
X_6	264.7	1666	836.92 $\pm$ 66.7	26.74	24.25	82.2	58.05

tributing characters, this information is useful to plant breeder in selection of elite genotypes from diverse genetic population and path analysis helps in revealing the nature of association (direct or indirect) among the yield attributing characters.

Materials and Methods

The present experiment was conducted during *rabi* of 2012-13 in rainfed situation with 144 *G. arboreum* genotypes (Table 1) in 12×12 simple lattice design with two replications to study the variability, correlation and path analysis among the yield and its attributing characters. The genotypes were planted with spacing of 90×60 cm and necessary agronomic practices were taken time to time. The observations were

recorded on six quantitative traits viz. plant height (cm), number of monopodial branches per plant, number of sympodial branches per plant, number of bolls per plant, boll weight (g), and seed cotton yield (kg/ha).

The analysis of variance was carried out using simple lattice design as suggested by Cochran and Cox [1], phenotypic and genotypic components of variances were estimated following Standard method [2]. Heritability in broad sense, genetic advance as percent of means were estimated [3]. The correlation coefficients were worked out to determine the degree of association of characters with yield and also among the yield components. Genotypic and phenotypic correlations were computed by using the formula

Table 3. Estimates of genotypic and phenotypic correlation in cotton (*G. arboreum*) genotypes. *Significant @ 5% level of significance. **Significant @ 1% level of significance. r_g —Genotypic correlation, r_p —Phenotypic correlation. X_1 : Plant height (cm), X_2 : Number of monopodial branches per plant, X_3 : Number of sympodial branches per plant, X_4 : Bolls per plant, X_5 : Boll weight (g), X_6 : Seed cotton yield (kg/ha).

Charac- ters	Levels	X_1	X_2	X_3	X_4	X_5	X_6
X_1	r_g	1	0.6477	0.4363	0.3961	-0.0949	0.2997
	r_p	1	0.3187**	0.2069**	0.3022**	-0.063	0.2377
X_2	r_g		1	0.3937	0.44	-0.1063	0.3283
	r_p		1	0.041	0.228***	-0.0181	0.1940
X_3	r_g			1	0.291	-0.1053	0.2094
	r_p			1	0.1022	-0.0147	0.0845
X_4	r_g				1	0.0099	0.9093
	r_p				1	0.0102	0.9146
X_5	r_g					1	0.4116
	r_p					1	0.3979
X_6	r_g						1
	r_p						1

Table 4. Estimates of direct and indirect effect of yield attributing characters on cotton (*G. arboreum*) yield. *Significant @ 5% level of significance, **Significant @ 1% level of significance, G–Genotypic level, P–Phenotypic level. X_1 : Plant height (cm), X_2 : Number of monopodial branches per plant, X_3 : Number of sympodial branches per plant, X_4 : Bolls per plant, X_5 : Boll weight (g), X_6 : Seed cotton yield (kg/ha).

Charac- ters	Levels	X_1	X_2	X_3	X_4	X_5	X_6
X_1	G	–0.0081	–0.0052	–0.0035	–0.0032	0.0008	0.2997
	P	–0.0134	–0.0043	–0.0028	–0.0041	0.0008	0.2377
X_2	G	–0.0187	–0.0289	–0.0114	–0.0127	0.0031	0.3283
	P	–0.0011	–0.0034	–0.0001	–0.0008	0.0001	0.1940
X_3	G	–0.0009	–0.0008	–0.002	–0.0006	0.0002	0.2094
	P	–0.0001	0.0000	–0.0004	0.0000	0.0000	0.0845
X_4	G	0.3651	0.4056	0.2682	0.9219	0.0091	0.9093
	P	0.2767	0.2088	0.0935	0.9155	0.0094	0.9145
X_5	G	–0.0378	–0.0424	–0.042	0.0039	0.3984	0.4116
	P	–0.0244	–0.007	–0.0057	0.004	0.3876	0.3979

given by Al-Jibouri et al. [4]. Correlation coefficients were compared against 'r' values given in [5] tables at (n–2) degrees of freedom at the probability levels of 0.05 and 0.01 to test their significance. Path analysis as carried out by using genotypic and phenotypic correlations coefficients to know the direct and indirect effects of the components on yield as illustrated by Dewey and Lu [6]. The data analysis are carried out using WINDOSTAT 9.2 software (Indostat services, Hyderabad).

Results and Discussion

Genetic variability parameters

Magnitude of genetic variability in a population decides effectiveness of selection. It was observed that genotypes under investigation shown high range of variability for all the six characters studied (seed cotton yield kg/ha) ranging from 264 to 1666, plant height (cm) ranging from 52.5 to 171, number of monopodial branches per plant were 0.5 to 5, where number of sympodial branches per plant ranging from 5.0 to 23.5, number of bolls per plant were ranging from 8.0 to 34.0 and boll weight [g] recorded range of 1.3 to 52.4 (Table 2) indicates existence of significant variability among the genotypes.

The relative values of genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) gives idea about magnitude of variability in population. Results shown that (Table 2) rela-

tive values GCV were lower than PCV for all the six characters indicates influence of environment in observed variability and variability was not only due to genotypes. Hence necessary care must be taken during selection of those characters. The findings of Sambamurthy et al. [7] and [8] also reported greater PCV values than GCV values for all those characters. Seed cotton yield (kg/ha) exhibited higher magnitude of GCV (24.25%) and PCV (26.76%) along with number of sympodial branches per plant (GCV = 27.32%, PCV = 83.08%) and bolls per plant (GCV = 21.77%, PCV = 24.26%). Similarly, the researcher Nataraj Gururaj [9] and [10] reported large amount GCV and PCV values for these characters. Whereas, number of monopodial branches shown higher PCV (37.36%) coupled with moderate GCV (19.09%). However plant height (GCV = 15.67%, PCV = 19.16%) and boll weight (GCV = 10.32%, PCV = 11.13%) shown moderate GCV and PCV values. In agreement with this moderate GCV and PCV values for plant was reported by Hafiz et al. [11] and Dahiphale et al. [12].

Heritability (broad sense) and genetic advance being most important selection parameters, simultaneous use of both the parameters found more helpful in predicting the gain under selection. Heritability (< 40 : low, 40–60 : medium, 61–80 : high and > 80 : very high) and genetic advance as percent mean (< 10 : low, 10–20 : medium and > 20 : high) scales were based on Singh and Narayanan [13]. Results showed that plant height ($h^2 = 66.9\%$, GAM = 33.86%), seed cotton yield (kg/ha) ($h^2 = 82.2\%$, GAM = 58.05%), bolls

per plant ($h^2 = 80.5\%$, $GAM = 51.59\%$) and boll weight ($h^2 = 86\%$, $GAM = 25.28\%$) exhibited high heritability with high genetic advance, indicates heritability is due to additive gene effects and selection for these characters will be effective. These findings are supported by similar reports of Prasad et al. [14]. However number of monopodial branches per plant ($h^2 = 26.1\%$, $GAM = 25.75\%$) and number of sympodial branches per plant ($h^2 = 10.8\%$, $GAM = 23.71\%$) shown low heritability coupled with high genetic advance indicates these traits governed by additive gene effects and low heritability may attributed to high influence of environment and selection would be effective. These results are in conformity with the results reported by Deshmukh et al. [15].

Correlation and path analysis

In general, results showed higher magnitude genotypic correlation than phenotypic correlation for all the characters except boll weight (Table 3). This indicated that there was an inherent association among the characters. At genotypic level seed cotton yield (kg/ha) was positively associated with all the characters ($X_1 = 0.2997$, $X_2 = 0.3283$, $X_3 = 0.2094$, $X_4 = 0.9093$, $X_5 = 0.4116$) hence these attributes are predominant and may contribute considerably towards higher seed cotton yield (kg/ha). Similar findings were reported by earlier reporters [16—18]. Genotypic correlation among the yield components like plant height, number of monopodial branches per plant, number of sympodial branches per plant, bolls per plant registered the positive correlation with all the traits except bolls weight, however bolls per plant were shown least positive significance (0.0099) with boll weight. Correlation at phenotypic level revealed that all the ($X_1 = 0.2377$, $X_2 = 0.1940$, $X_3 = 0.0845$, $X_4 = 0.9146$, $X_5 = 0.3979$) characters were positively associated with seed cotton yield (kg/ha). Similarly Ahmad et al. [19] and Muhammad et al. [20] reported the positive association of these characters with seed cotton yield (kg/ha). Among the yield attributing traits, plant height shown significant positive association with number of monopodial branches per plant (0.3187), number of sympodial branches (0.2069) and bolls per plant (0.3022), however it was negatively associated with boll weight (-0.063). Number of monopodial branches

per plant exhibited positive correlation with number of sympodial branches per plant (0.041) and significantly with bolls per plant (0.228). However, boll weight was negatively associated with plant height (-0.0630), number of monopodial branches per plant (-0.1053), number of sympodial branches (-0.0147) except bolls per plant (0.0102). Similar results were reported by Patel et al. [21] and Erande et al. [22].

Yield being polygenic trait with low heritability in common and which is result of interactive effects of various traits. Hence it is advantageous to do selection based on the yield attributing traits rather than seed yield *per se* alone. In this regard estimation of direct and indirect effects of various components towards yield will help in recommending the suitable selection criteria. In the present study, at genotypic and phenotypic level (Table 4), number of bolls per plant ($G = 0.9219$, $P = 0.9155$) exhibited higher magnitude of direct effect which is followed boll weight ($G = 0.3984$, $P = 3876$). These traits found to principal components for seed cotton yield and selection should be based on these characters. In accordance, earlier reporters [23—25] reported similar findings. However plant height ($G = -0.0081$, $P = -0.0314$), number of monopodial branches per plant ($G = -0.0289$, $P = -0.0034$), and number of sympodial branches per plant ($G = -0.0289$, $P = -0.0034$), shown negligible negative direct effect towards seed cotton yield in consonance with the finding of Ahuja and Dhayal [26] and Alther and Singh [27]. Number of bolls per plant found to be most important trait for seed cotton yield as it is showing positive direct and indirect effects at both genotypic and phenotypic level.

Conclusion

It can be concluded from the studies that, the genotypes under evaluation exhibited significant variability for all the traits indicating the enormous scope for selection. GCV and PCV estimates indicated influence of environment in observed variability, hence necessary care should be taken while selection. Number of bolls / plant and boll weight were significantly correlated in positive direction and showing high direct and indirect effects with total seed cotton yield, hence these traits must be under focus in development of superior cotton cultivars or hybrids to break the yield

barriers or improvement of agronomic traits in desired direction.

References

1. Cochran WG, Cox GM (1957) Experimental designs. Jhon Wiley and Sons, New York, pp 611.
2. Burton, Devane (1953) Estimating heritability in tall fescue (*Festuca circuhinoceae*) from replicated clonal material. Agron J 45 : 478—481.
3. Allard RW (1960) Principles of plant breeding. John Wiley and Sons Inc, London, pp 75—98.
4. Al-Jibouri HA, Miller PA, Robinson HF (1958) Genetic and environmental variances and co-variances in an upland cotton cross of interspecific origin. Agron J 50 : 633—636.
5. Fisher RA, Yates F (1963) Statistical tables for biological, agricultural and medical research. Oliver and Boyd, London, pp 46—63.
6. Dewey DR, Lu KH (1959) A correlation and path coefficient analysis of components of crested wheat grass seed production. Agron J 51 : 515—518.
7. Sambamurthy JSV, Ratna Kumari S, Chamundeswari N (2004) Genetic variation in yield and yield components in desi cotton (*Gossypium arboreum* L.). J Cotton Res Develop 18 : 36—37.
8. Gumber RK, Chachal GS, Verma PK (2005) Genetic evaluation of *Gossypium arboreum* genotypes for yield and fiber quality. J Cotton Res Develop 9 : 44—48.
9. Nataraj S (2005) Genetic evaluation of cotton species under protective management, rainfed and saline situations. MSc (Ag) thesis. Univ Agric Sci, Dharwad, Karnataka, India.
10. Gururaj (2006) Genetic studies on compact and robust plant types of cotton (*Gossypium hirsutum* L.). MSc (Ag) thesis. Univ Agric Sci, Dharwad, Karnataka, India.
11. Hafiz GA, Abid M, Qurban A (2013) Genetic variability, heritability, genetic advance and correlation studies in cotton (*Gossypium hirsutum* L.). Int Res J Microbiol 4 : 156—161.
12. Dahiphale KD, Deshmukh JD, Bagade AB, Jadhav AB (2015) Studies on genetic variability, correlation and path coefficient analysis in cotton (*Gossypium hirsutum* L.). Int Trop Agric 33 : 23—29.
13. Singh P, Narayanan SS (2015) Biometrical techniques in plant breeding. Kalyani Publ, pp 153 :163.
14. Prasad U, Chengareddy V, Narisi Reddy A (2004) Studies on genetic variability in American cotton (*Gossypium hirsutum* L.). Int Symp on Strategies for Sustainable Cotton Production—A Global Vision. Crop Improve, pp 468.
15. Deshmukh VV, Mohod VK, Pande MK, Golhar SI (1999) Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.). PKV Res J 23 : 21—23.
16. Khan NU, Hassan G, Kumbhar MB, Parveen A, Aiman U, Ahmad W, Shah S, Ahmad S (2007) Gene action of seed traits and oil content in upland cotton (*G. hirsutum*). Sabrao J Breed Genet 39 : 17—30.
17. Ashok Kumar K, 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 Bas Appl Sci 4 : 5496—5499.
18. Farooq J, Anwar M, Riaz M, Farooq A, Mahmood A, Shahid MTH, Rafiq MS, Ilahi F (2014) Correlation and path coefficient analysis of earliness, fiber quality and yield contributing traits in cotton (*Gossypium hirsutum* L.). J Anim Pl Sci 24 : 781—790.
19. Ahmad W, Khan NU, Khalil MR, Parveen A, Aimen U, Saeed M, Samiullah, Shah SA (2008) Genetic variability and correlation analysis in upland cotton. Sarhad J Agric 24 : 573—580.
20. Muhammad ZA, Muhammad SM, Hidayatullah B, Abdul WS, Faiz HP, Abdul RC, Karim BS (2014) Genetic variability and correlation analysis of some upland cotton (*Gossypium hirsutum* L.) accessions. Int J Sci Engg Res 5 : 313—318.
21. Patel VK, Varghese S, Patel PG, Patel UG, Darji VB, Patel JS (2003) Character association for cotton seed oil content in different genotypes of cotton. J Maharashtra Agric Univ 28 : 203—205.
22. Erande CS, Kalpande HV, Deosarkar DB, Chavan SK, Patil VS, Deshmukh JD, Chinchane VN, Kumar Anil, Dey Utpal, Puttawar MR (2014) Genetic variability, correlation and path analysis among different traits in desi cotton (*Gossypium arboreum* L.). Afr J Agric Res 9 : 2278—2286.
23. Ekinci R, Sema Basbag O, Gencer (2010) Path coefficient analysis between seed cotton yield and some characters in cotton (*Gossypium hirsutum* L.). J Environ Biol 31 : 861—864.
24. Chandrashekhar A, Manjula SM, Patil SS, Madhura C, Basavaradder AB, Santosh HB (2016) Correlation and path coefficient analysis of yield component and fiber quality traits of upland cotton (*Gossypium hirsutum* L.). Int Agric Sci Res 6 : 171—176.
25. Muthu R, Kandasamy G, Jayarama M (2004) Correlation and path co-efficient analysis for yield and fiber quality traits in cotton (*G. hirsutum*). J Ind Soc Cotton Improve 29 : 17—20.
26. Ahuja SL, Dhayal LS (2007) Comparative characteristics and gene action in three petal-spotted mutants of *Gossypium hirsutum*. J Genet 86 : 81—84.
27. Alther AF, Singh RP (2003) Yield components analysis in upland cotton (*Gossypium hirsutum* L.). J Ind Soc Cotton Improve 28 : 151—157.