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Research Note

Studies on genetic variability correlation and path analysis in upland cotton

M. Gnanasekaran*, K. Thiyagu and M. Gunasekaran

TNAU, Cotton Research Station, Srivilliputtur-626 135

E-Mail: gnanasekaran79@gmail.com

Abstract

The research work for studying genetic variability, heritability and genetic advance as well as correlation and path coefficient analysis for 13 traits with sixty seven genotypes of upland cotton was carried out during winter 2017 at Cotton Research Station, Srivilliputtur, Tamil Nadu Agricultural University, India. The variability studies indicated that the high estimate of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for seed cotton yield per plant. High phenotypic coefficient of variation and moderate genotypic coefficient of variation was observed for the number of monopodia per plant. High heritability observed for the number of monopodia per plant, the number of bolls per plant, seed index, lint index, ginning percentage, 2.5% span length, uniformity ratio, bundle strength, fibre fineness and seed cotton yield per plant. The number of monopodia per plant, the number of bolls per plant, bundle strength, fibre fineness and seed cotton yield per plant shows high heritability coupled with high genetic advance over mean indicating the preponderance of additive gene action in the inheritance of these traits. The correlation study revealed that plant height, the number of monopodia per plant, the number of sympodia per plant and the number of bolls per plant had a significant positive association with seed cotton yield per plant. Path analysis indicated that the number of bolls per plant and seed index have maximum positive direct effect on seed cotton yield per plant.

Key words

Cotton, correlation, heritability, path analysis, seed cotton yield variability.

Cotton is one of the most important commercial crops and popularly known as the “White Gold”. It is an industrial commodity of worldwide importance. India has been the traditional home of cotton and cotton textiles. Cotton provides numerous useful products and supports millions of jobs as it moves from field to fabric. It occupies the place of pride in Indian agriculture and economy by earning valuable foreign exchange which accounts for 60% of total foreign exchange earnings through export of lint and value added cotton products. Eventhough India has achieved self sufficiency in cotton production, the area under cotton cultivation is decreases day by day and also the productivity of cotton in India is very low compared to the other cotton growing countries. Therefore, it is essential to develop a new high yielding cultivars with good fibre quality parameters to improve the production level

(Jatoi *et al.*, 2011). Genetic variability is pre-requisite for plant breeders to exercise selection and the phenotypic and genotypic coefficients of variation were estimated using genotypic and phenotypic variances respectively. The coefficient of variation indicated only the extent of existing variability for various traits, but that does not give any information about the heritable portion of it. Therefore, the heritability accompanied by estimates of genetic advance and genetic advance over mean were also estimated. Heritability itself provides no indication about the genetic progress that would result from selection. However, at a fixed selection pressure, the amount of advance varies with magnitude of heritability. Many investigations had studied heritability for seed cotton yield and other traits (Dhamayanathi *et al.*, 2010; Eswari *et al.*, 2017 and Gnanasekaran *et al.*, 2018). Further,

the efficiency of selection in any breeding programme mainly depends upon the knowledge of association of the characters. Phenotypic correlation indicated the extent of the relation between two characters while genotypic correlation provides an estimate of inherent association between the genes controlling them. The cause for negative effect of the trait is very essential for formulating selection indices by path analysis (Gururajan and Sunder, 2004; Gite *et al.*, 2006). Hence the present study was planned to assess the genetic variability, correlation and path analysis for various yield and yield contributing characters in a set of genotypes. Such informations may be fruitful in formulating efficient selection programme for synthesis and development of new cotton genotypes with improved yield and its contributing traits.

The experiment was conducted in the research field of the Cotton Research Station, Tamil Nadu Agricultural University, Srivilliputtur during the winter 2017. The mean maximum and minimum temperature prevailed during the cropping period was 31.5°C & 24.2°C respectively and an average rainfall of 740.0mm which was received in 24 rainy days. The experimental site is located at 9° 5'N latitude, 77° 6'E longitudes and an altitude of 137.92m above the mean sea level. The crop has grown in sandy clay loam soil texture with pH of 8.2.

The experimental material comprised of fifty intra *hirsutum* hybrids, its parents and two checks namely Cotton Hybrid SVPR 1 and Mallika Non Bt. The F₁s were developed by crossing five female parents *viz.*, CPD 1501, BGDS 1055, TSH 321, CCH 15-1 and SHM 55 with ten male parents *viz.*, TCH 1819, CNH 19, COD 5-1-2, GSHV 177, SCS 1207, Suraj, African I-2, TCH 482-7, TCH 484-4 and

TCH 486-2 in a Line x Tester mating fashion. Thus, the sixty seven genotypes were raised during winter 2017-18. Experimental materials were raised in two replications in a randomized block design (RBD) with double rows of 4.5m length and spacing of 100cm between rows and 45cm between plants. Recommended agronomic practices and need based plant protection measures were followed to obtain good crop stand.

Data were recorded from five selected plants in each entry for thirteen characters *viz.*, plant height (cm) (PH), the number of monopodia per plant (NM/P), the number of sympodia per plant (NSy/P), the number of bolls per plant (NB/P), boll weight (g) (BW), seed index (SI), lint index (LI), ginning percentage (GP), seed cotton yield per plant (g) (SCY/P), 2.5% span length (mm) (SL), bundle strength (g/tex) (BS), fibre fineness (µg/inch) (FF) and uniformity ratio (%) (UR). Observations on five fibre quality traits in each replication were recorded with ten grams of lint sample by High Volume Instrument (HVI) in ICC mode.

The means for all the observed parameters were worked out and were further subjected to Analysis of variance (ANOVA) according to Johnson *et al.* (1955). The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer (1981). Heritability (h²) in the broad sense was calculated according to the formula given by Allard (1960). Genetic advance was estimated by the following formula given by Burton (1953) from the heritability. Correlation coefficients at phenotypic and genotypic level were calculated as per procedure given by Al-Jibouri *et al.* (1958). Path analysis was carried out as suggested by Dewey and Lu (1959).

Table 1. Analysis of variance for various yield components and fibre quality traits

Source of Variation	DF	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	2.5% SL	UR	BS	FF	SCY/P
Replication	1	2.39	0.17	0.01	22.92	0.04	2.01	0.24	3.40	0.02	0.15	0.79	0.001	0.00001
Genotypes	66	62.76*	0.18*	2.18*	35.03*	0.43*	2.41*	0.75*	9.47*	7.50*	7.68*	11.93*	0.651*	0.0013*
Error	66	26.36	0.03	0.77	4.02	0.14	0.53	0.10	1.69	0.31	0.53	0.23	0.049	0.0001

Greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant. Thus, the primary objective of germplasm conservation is to collect and preserve the genetic variability in indigenous collection of crop species to make it available to present and future generations. The analysis of variance (**Table. 1**) revealed significant differences among the genotypes for all the characters studied indicating that the data generated from the above diverse material will yield reliable informations. The results pertaining to genetic parameters *viz.*, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h²) and genetic advance over mean for all the thirteen characters are furnished in **Table 2**. High estimate of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for seed cotton

yield per plant (26.65% and 25.09%). High phenotypic coefficient of variation and moderate genotypic coefficient of variation was observed for the number of monopodia per plant (20.31%, 17.6%) whereas the moderate estimates of PCV and GCV were estimated for traits like the number of bolls per plant (17.27% and 15.39%), lint index (11.43% and 10.05%), bundle strength (10.5% and 10.3%) and for fibre fineness (13.94% and 12.92%). Plant height (6.19%, 3.95%), the number of sympodia per plant (8.15%, 5.63%), ginning percentage (6.51%, 5.43%), 2.5% span length (6.81%, 6.54%), uniformity ratio (4.23%, 3.95%) exhibited low PCV and GCV which indicated that the characters were highly influenced by the environmental factors. The phenotypic coefficient of variation which measures the total variation was found to be greater than the genotypic coefficient of variation for all

Table 2. Genetic components of variance for various quantitative traits

Characters	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	2.5% SL	UR	BS	FF	SCY/P
PCV	6.19	20.31	8.15	17.27	10.8	12.1	11.43	6.51	6.81	4.23	10.5	13.94	26.65
GCV	3.95	17.6	5.63	15.39	7.7	9.7	10.05	5.43	6.54	3.95	10.3	12.92	25.09
h ²	40.85	75.12	47.73	79.39	50.88	64.2	77.27	69.67	92.05	87.1	96.2	85.93	88.67
GA	5.62	0.5	1.19	7.23	0.56	1.6	1.04	3.39	3.75	3.64	4.89	1.05	0.05
GAM	5.21	31.42	8.02	28.24	11.32	16	18.2	9.34	12.92	7.58	20.81	24.67	48.67

the characters indicated some degree of environmental influence on the traits. Selection for improvement of such traits may sometimes be misleading. These findings were also supported by Kulkarni *et al.*, 2011, Pujer *et al.*, 2014, Sunayana *et al.*, 2017 and Gnanasekaran *et al.*, 2018.

High heritability value was observed for characters like the number of monopodia per plant (75.12%), the number of bolls per plant (79.39%), seed index (64.20%), lint index (77.27%), ginning percentage (81.10%), 2.5% span length (92.05), uniformity ratio (87.10%), bundle strength (96.20%), fibre fineness (85.93%) and seed cotton yield per plant (88.67%). This finding was agreed with earlier finding of Pujer *et al.*, 2014, Eswari *et al.*, 2017 and Gnanasekaran *et al.*, 2018 have also reported similar results for the number of bolls per plant, 2.5% span length, bundle strength and seed cotton yield per plant. Sunayana *et al.*, 2017 have reported the same results for the number of bolls per plant (79.39%), seed index (64.20%), lint index (77.27%), ginning percentage (81.10%), and seed cotton yield per plant (88.67%). This suggested the greater effectiveness of selection and improvement to be expected for these characters in future breeding programmes as the genetic variance is mostly due to the additive gene action. Plant height, the number of sympodia per plant and boll weight showed moderate estimates of heritability. These results are in agreement with the results reported by Sunayana *et al.*, 2017 for plant height; Eswari *et al.* (2017) and Gnanasekaran *et al.* (2018) for the number of sympodia per plant; Rama Reddy and Sarma (2014) for boll weight. Heritability estimates along with genetic advance would be more useful in predicting yield under phenotypic selection than heritability estimates alone as suggested by Johnson *et al.* (1955) and Swarup and Chaugale (1962). If heritability is mainly due to non-additive gene effect, the expected genetic advance would be low, and if there is additive gene effect, a high genetic advance may be expected (Panse, 1957). In the present investigation high heritability coupled with high genetic advance as percentage of mean was observed for the number of monopodia per plant, the number of bolls per plant, bundle strength, fibre fineness and seed cotton yield per plant indicating the preponderance of additive gene action in the inheritance of these traits. Pujer *et al.* (2014), Eswari *et al.* (2017) and Sunayana *et al.* (2017) reported high heritability and high genetic advance as percentage of mean for the number of bolls per plant, seed cotton yield per plant revealed the influence of additive gene action for these traits. Hence the improvement of these traits can be made through

direct phenotypic selection. The traits such as ginning percentage (69.67 and 9.34%) and uniformity ratio (87.10 and 7.58%) in which high heritability accompanied by low genetic advance was recorded indicates the effect of non additive gene action and hence heterosis breeding may be rewarding for these traits. Siva Prasad *et al.* (2005) for ginning percentage and Pujer *et al.* (2014) for uniformity ratio reported the similar results.

Computation of correlation between yield and yield attributing traits is of considerable importance in plant selection. The genotypic and phenotypic correlation co-efficient between yield and its components were presented in **Table 3**. Of total traits studied, four traits namely, plant height (0.552), the number of monopodia per plant (0.321), the number of sympodia per plant (0.565) and the number of bolls per plant (0.733) had a significant positive association with seed cotton yield per plant. Hence, the selection for these traits will help in selecting genotypes with higher seed cotton yield per plant. Such positive association of seed cotton yield per plant with these traits was also observed by Pujer *et al.* (2014), Asha *et al.* (2015), and Sunayana *et al.* (2017). The close association between yield and yield attributing traits can be exploited in the selection programme which might be helpful in evolving high yielding genotypes. The traits like boll weight, seed index, lint index, ginning percentage, 2.5% span length, uniformity ratio, bundle strength and fibre fineness exhibited non-significant association with seed cotton yield. Similar results were reported by Srinivas *et al.* (2015) for ginning percentage and bundle strength; Sunayana *et al.* (2017) for lint index; Rao and Gopinath (2013) for 2.5% span length (mm), bundle strength (g/tex), fibre fineness ($\mu\text{g}/\text{inch}$) and uniformity ratio (%).

The inter correlation between the quantitative yield contributing traits *viz.*, Plant height with the number of monopodia per plant, the number of sympodia per plant, the number of bolls per plant, seed index, 2.5% span length and bundle strength: The number of monopodia per plant with the number of sympodia per plant, boll weight, seed index and lint index: The number of sympodia per plant with the number of bolls per plant and seed index: Boll weight with seed index, lint index and fibre fineness were positive and significant indicating the possibility of simultaneous improvement of these traits. Similar results were reported by Sakthi *et al.* (2007), Kalpande *et al.* (2008) and Rao and Gopinath (2013). Ginning percentage has a significant negative

Table 3. Genotypic and phenotypic correlations of various quantitative traits

Characters	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	2.5% SL	UR	BS	FF	SCYP
PH	1.000	0.328*	0.841*	0.588*	-0.045	0.365*	-0.162	-0.610*	0.381*	-0.233*	0.233*	-0.004	0.552*
		0.202*	0.600*	0.386*	0.137	0.142	-0.080	-0.267*	0.191	-0.164	0.121	0.082	0.325*
NM/P		1.000	0.258*	0.171	0.364*	0.326*	0.371*	0.056	0.089	-0.123	0.077	0.119	0.321*
			0.205*	0.142	0.184	0.267*	0.319*	0.036	0.094	-0.112	0.070	0.098	0.295*
NSy/P			1.000	0.627*	0.181	0.347*	-0.022	-0.412*	0.146	-0.170	0.108	0.035	0.565*
				0.435*	0.160	0.204*	-0.007	-0.257*	0.112	-0.125	0.060	0.050	0.390*
NB/P				1.000	0.203*	0.098	-0.010	-0.151	-0.004	-0.027	-0.053	0.078	0.733*
					0.110	0.087	0.032	-0.084	0.007	-0.060	-0.044	0.086	0.604*
BW					1.000	0.911*	0.885*	0.036	-0.080	0.118	-0.033	0.280*	0.105
						0.397*	0.516*	0.114	-0.095	0.094	-0.014	0.234*	0.068
SI						1.000	0.626*	-0.388*	0.242*	0.041	0.341*	0.155	0.010
							0.628*	-0.479*	0.220*	0.019	0.282*	0.134	0.026
LI							1.000	0.471*	-0.125	0.180	0.013	0.264*	0.054
								0.376*	-0.090	0.153	0.006	0.238*	0.046
GP								1.000	-0.426*	0.171	-0.365*	0.115	0.048
									-0.363*	0.150	-0.318*	0.090	0.021
2.5% SL									1.000	-0.467*	0.791*	-0.179	-0.033
										-0.391*	0.742*	-0.177	-0.023
UR										1.000	0.057	0.315*	0.058
											0.058	0.246*	0.046
BS											1.000	-0.259*	0.049
												-0.221*	0.053
MIC												1.000	0.103
													0.089

* Significant at 5% level. The values in bold are phenotypic correlation

inter correlation with the number of sympodia per plant and seed index. Similar results also reported by Rao and Gopinath (2013) for seed index. The fibre quality traits exhibited positive inter correlation among themselves and some of these showing significance like 2.5% span length with bundle strength: Uniformity ratio with fibre fineness whereas 2.5% span length had a significant negative inter

correlation with uniformity ratio and ginning percentage. These findings are in accordance with the results of Rao and Gopinath (2013). Hence, the selection based on plant height, the number of monopodia, the number of sympodia, the number of bolls per plant, along with quality traits 2.5% span length and bundle strength will bring about breakthrough in cotton yields.

Table 4. Direct effects (diagonal) and indirect effects (off diagonal) of various traits on seed cotton yield at genotypic level

Characters	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	2.5% SL	UR	BS	FF	Correlation Co Efficient
PH	0.554	0.025	-0.437	0.578	0.026	0.378	0.307	-0.823	-0.607	0.212	0.342	-0.003	0.552
NM/P	0.181	0.076	-0.134	0.168	-0.207	0.677	-0.850	0.259	-0.143	0.112	0.115	0.067	0.321
NSy/P	0.466	0.020	0.519	0.616	-0.622	0.784	0.107	-0.906	-0.752	0.155	0.158	0.020	0.565
NB/P	0.326	0.013	-0.327	0.987	-0.118	0.503	0.048	-0.697	0.007	0.024	-0.078	0.045	0.733
BW	-0.063	0.028	-0.194	0.199	0.069	0.681	-0.412	0.166	0.128	-0.308	-0.348	0.159	0.105
SI	0.402	0.025	-0.180	0.096	-0.519	0.839	-0.123	-0.796	-0.284	-0.038	0.500	0.088	0.010
LI	-0.090	0.028	0.011	-0.010	-0.504	0.819	-0.985	0.480	0.299	-0.164	0.019	0.151	0.054
GP	-0.338	0.004	0.214	-0.148	-0.020	-0.095	-0.349	0.627	0.680	-0.156	-0.537	0.166	0.048
2.5% SL	0.211	0.007	-0.076	-0.004	0.046	0.242	0.623	-0.971	-0.596	0.425	0.162	-0.102	-0.033
UR	-0.129	-0.009	0.088	-0.026	-0.067	0.211	-0.899	0.792	0.745	-0.911	0.084	0.179	0.058
BS	0.129	0.006	-0.056	-0.052	0.019	0.750	-0.065	-0.690	-0.262	-0.052	0.469	-0.147	0.049
FF	-0.003	0.009	-0.018	0.076	-0.159	0.295	-0.314	0.030	0.286	-0.287	-0.380	0.568	0.103

Residual Effect = 0.4108

The study of path coefficients enable breeder to concentrate on the variable which show a high direct effect on seed cotton yield. The genotypic correlation coefficient of seed cotton yield with other yield contributing and fibre quality traits were further partitioned into direct and indirect effects (**Table 4**). It was indicated that the number of bolls per plant and seed index have maximum positive direct effect on seed cotton yield per plant and also correlation between these traits with seed cotton yield per plant is significant and it was followed by ginning percentage, fibre fineness, plant height, the number of sympodia per plant and bundle strength but the correlation between these four traits with seed cotton yield per plant is non-significant. Whereas the traits like lint index, 2.5% span length and uniformity ratio was negative direct effect and the number of monopodia per plant exhibited negligible levels of direct effect on seed cotton yield per plant. Therefore, a restricted selection model of direct selection for traits viz., the number of bolls per plant and seed index is suggested for obtaining yield improvement. In the present study, the number of bolls per plant exhibited positive indirect effect on seed cotton yield via seed index and plant height and a negative indirect effect via the number of sympodia per plant, boll weight and ginning percentage, whereas boll weight exhibited a positive indirect effect on yield via seed index, the number of bolls per plant, ginning percentage, fibre fineness and negative indirect effect via the number of sympodia per plant, lint index, uniformity ratio and bundle strength.

High heritability observed for the number of monopodia per plant, the number of bolls per plant, seed index, lint index, ginning percentage, 2.5% span length, uniformity ratio, bundle strength, fibre fineness and seed cotton yield per plant. The number of monopodia per plant, the number of bolls per plant, bundle strength, fibre fineness and seed cotton yield per plant shows high heritability coupled with high genetic advance over mean indicating the preponderance of additive gene action in the inheritance of these traits. Association analysis revealed that the simultaneous selection based on plant height, the number of monopodia, the number of sympodia, the number of bolls per plant, along with quality traits 2.5% span length and bundle strength will bring about breakthrough in cotton yields and needs to be postponing the selection for further/advanced generations.

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