



# CORRELATION AND CAUSATION STUDIES FOR SEED COTTON YIELD AND ITS CONTRIBUTING TRAITS IN COTTON (*GOSSYPIMUM HIRSUTUM* L.)

C. Praveen Sampath Kumar<sup>1</sup>, S. Raju<sup>1</sup>, R. Ebenezer Babu Rajan<sup>1</sup>, Darling B. Sujj<sup>2</sup>  
and Ajish Muraleedharan<sup>3</sup>

<sup>1</sup>Depart. of Genetics and Plant Breeding, Faculty of Agr., Annamalai University, Annamalainagar 608 002, India.

<sup>2</sup>Depart. of Agricultural Extension, Faculty of Agriculture, Annamalai University, Annamalainagar 608 002, India.

<sup>3</sup>Department of Horticulture, Faculty of Agriculture, Annamalai University, Annamalainagar 608 002, India.

## Abstract

Thirty cotton genotypes were subjected to study the association among the seed cotton yield and yield contributing traits. Fourteen characters *viz.*, days to fifty percent flowering (X1), plant height at maturity (X2), number of sympodial branches per plant (X3), number of bolls per plant (X4), single boll weight (X5), seed index (X6), Ginning out turn (X7), lint index (X8), lint yield (X9), biological yield per plant (X10), 2.5 percent span length (X11), micronaire (X12), bundle strength (X13) and seed cotton yield per plant (X14) were studied. The genotypic correlation revealed that seed cotton yield had positive significant association with lint yield followed by number of bolls per plant, single boll weight and plant height at maturity while positive non significant with biological yield and bundle strength. The characters *viz.*, lint yield, number of bolls per plant and single boll weight had exerted their maximum positive direct effect towards seed cotton yield, which was very close to its genetic correlation coefficient. Hence, these characters could be declared as choice of characters for seed cotton yield improvement.

**Key words :** Cotton, correlation and causation.

## Introduction

Cotton is a natural fiber of vegetable origin, like linen, jute or hemp and composed of cellulose. The cotton is a variety of plants of the genus *Gossypium*, belonging to the Malvaceae family. Out of about 50 species of cotton plants in the world, only four have been domestically cultivated for cotton fibers. *Gossypium hirsutum* and *Gossypium barbadense* are the most commonly cultivated species of cotton in the world. *Gossypium hirsutum* variety is the most important agricultural cotton, accounting for more than 90% of world fiber production

The first cotton fabric dates back to approximately as early as 3,200 B.C., as per evidence from the excavation and by fragments of cloth found at the Mohenjo-Daro archaeological site on the banks of the River Indus. The cultivation and manufacturing of cotton fabric had been practiced in India since pre-historic times. From India, cotton textiles probably travelled to Mesopotamia. The trade in cotton is assumed to have been started around Rome at the time of Alexander the Great, in the 4<sup>th</sup> century B.C.

Cotton Mills Federation has projected the cotton requirement for 2025 at 60 million bales (Deshpande *et al.*, 2008). Therefore, one of the main objectives of cotton improvement program is to breed varieties and hybrid cultivars with high seed cotton yield and superior quality of fibre. Cotton hybrids are always being utilized to give an extra push to yield and quality potential.

In the state of Tamil Nadu, cotton is cultivated both under irrigated and rainfed condition. The textile industry of the state is mainly based on extra long staple with high bundle strength of cotton to the extent of 89%. All the four cultivated species of cotton, namely *Gossypium hirsutum*, *Gossypium barbadense*, *Gossypium arboreum* and *Gossypium herbaceum* are grown in this state along with their intra and inter-specific hybrids. Among the southern states of India which grow *Gossypium barbadense* genotypes, the climate of Tamil Nadu is conducive for *Gossypium barbadense* hybrids and varieties. Tamil Nadu produces only one sixth of its cotton requirements and the balance is met by purchases from up-country markets.

In any selection programme, it may not be always

possible to select on the basis of yield alone for evolving superior yielding genotypes because yield is a complex character and is collectively influenced by many component characters. The inter-relationships between yield and yield contributing characters are estimated by correlation co-efficient analysis. Such association studies provide information on nature extent and direction of selection.

Further, the partitioning of correlation co-efficient into direct and indirect effects of yield components on yield will also throw more light on selection programme. Knowledge of association between yield and yield contributing characters would be of immense aid in plant breeding programme where simultaneous improvement in two or more characters is desired to be achieved.

### Materials and Methods

The present investigation was carried out in the Plant Breeding farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University. The experimental material comprised of 30 cotton genotypes collected from Central Institute for Cotton Research, Coimbatore.

These promising genotypes were sown in the second week of June. The experiment was laid out in a Randomized Block Design with three replications with spacing of 75 cm between the rows and 30cm between plants within row in 40 cents area. Recommended agronomic practices and need based plant protection measures were adopted.

Five plants at random in each replication were chosen and labeled for recording observations and the mean of five plants were used for statistical analyses. The data on the following yield and yield components and quality parameters were recorded. The characters *viz.*, days to fifty percent flowering (X1), plant height at maturity (X2), number of sympodial branches per plant (X3), number of bolls per plant (X4), single boll weight (X5), seed index (X6), Ginning out turn (X7), lint index (X8), lint yield (X9), biological yield per plant (X10), 2.5 percent span length (X11), micronaire (X12), bundle strength (X13) and seed cotton yield per plant (X14). The genotypic and phenotypic correlation co-efficients were calculated from the mean of the three replications of each genotype by adopting the method suggested by Al-Jibouri *et al.* (1958). Path-coefficient analysis was also done as per the method suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

### Results and Discussion

Correlation study indicates the degree of interdependence of plant characters which forms an important tool in selection of pertinent genotype. Most of

the plant breeding programmes are aimed at augmentation of yield, which is an intricate character dependent on many other component characters which are further related among them. The estimates of phenotypic and genotypic correlations coefficients among the fourteen traits are discussed below.

In the present study, the genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients. This can be interpreted as a strong inherent genotypic relationship between the characters studied though their phenotypic expression was impeded by environmental influence. The phenotypic and genotypic correlation coefficients among different characters revealed that seed cotton yield per plant had exhibited significant positive association with lint yield followed by number of bolls per plant, single boll weight and plant height at maturity. Similar results were reported by Khan *et al.*, (2010) and Ashok Kumar *et al.*, (2010) for number bolls per plant and single boll weight this indicated that association between these traits could be utilized for increasing seed cotton yield. This corroborates with the findings of Kaushik *et al.*, (2006) thus suggesting that selection pressure applied for increasing the aforementioned traits would eventually increase the seed cotton yield.

However, correlation of yield and its components alone are not adequate in any selection programme. The inter relationship among the individual character may ultimate influence the yield.

In the present study, significant negative association observed between days to fifty percent flowering with plant height at maturity and bundle strength at both levels while it had significant negative association with number of bolls per plant at genotypic level. Plant height at maturity had exhibited significant positive association with number of bolls per plant and biological yield at both levels. Number of bolls per plant and single boll weight had showed significant positive association with lint yield and biological yield at phenotypic and genotypic levels. This is in corroboration with the earlier reports of Shazia *et al.*, (2010), Desalegn *et al.*, (2009) and Sharma *et al.*, (2005).

Seed index recorded significant positive association with lint index and bundle strength at phenotypic and genotypic levels while it had significant positive association with 2.5 per cent span length and significant negative association with ginning out turn at genotypic level. Ginning out turn had significant positive association with lint index at both levels while lint yield recorded significant positive association with biological yield at phenotypic and genotypic levels. Biological yield revealed

**Table 1:** Phenotypic and Genotypic correlation among various characters in 30 cotton genotypes.

Character		X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	P	1.000	-0.317*	0.154	-0.349	0.046	-0.227	0.138	-0.026	-0.218	-0.272	-0.159	0.056	-0.350*	-0.295
	G	1.000	-0.330*	0.158	-0.351*	0.059	-0.287	0.153	-0.072	-0.219	-0.276	-0.167	0.135	-0.380*	-0.297
X2	P		1.000	-0.105	0.401*	0.050	0.019	-0.235	-0.155	0.242	0.378*	0.065	0.123	0.138	0.395*
	G		1.000	-0.110	0.415*	0.040	0.061	-0.256	-0.262	0.252	0.404*	0.057	0.085	0.165	0.410*
X3	P			1.000	0.080	-0.030	0.159	0.018	0.172	0.101	0.156	0.027	0.005	0.165	0.103
	G			1.000	0.083	-0.047	0.213	0.028	0.293	0.105	0.161	0.028	0.062	0.172	0.106
X4	P				1.000	0.072	0.090	-0.174	-0.028	0.821*	0.411*	0.135	-0.007	0.030	0.874*
	G				1.000	0.083	0.111	-0.183	-0.040	0.825*	0.417*	0.140	-0.035	0.032	0.875*
X5	P					1.000	0.232	-0.082	-0.115	0.432*	0.401*	0.220	-0.001	0.232	0.432*
	G					1.000	0.222	-0.139	-0.213	0.525*	0.529*	0.291	-0.296	0.309	0.536*
X6	P						1.000	-0.272	0.355*	0.087	0.195	0.225	-0.000	0.421*	0.195
	G						1.000	-0.367*	0.594*	0.114	0.257	0.362*	-0.026	0.523*	0.240
X7	P							1.000	0.379*	0.096	-0.085	-0.102	-0.047	-0.311	-0.237
	G							1.000	0.716*	0.095	-0.094	-0.083	-0.126	-0.348	-0.249
X8	P								1.000	0.039	-0.059	0.074	0.001	0.009	-0.081
	G								1.000	0.083	-0.087	0.091	-0.030	-0.024	-0.140
X9	P									1.000	0.544*	0.200	-0.042	0.043	0.928*
	G									1.000	0.555*	0.213	-0.120	0.051	0.933*
X10	P										1.000	0.380*	-0.088	0.271	0.604
	G										1.000	0.405*	-0.101	0.309	0.613
X11	P											1.000	-0.042	0.537*	0.205
	G											1.000	-0.131	0.632*	0.215
X12	P												1.000	-0.027	-0.041
	G												-1.000	-0.065	-0.093
X13	P													1.000	0.172
	G													1.000	0.190
X14	P														1.000
	G														1.000

\* Significant at 5 per cent level

P – Phenotypic correlation

G – Genotypic correlation

**Table 2:** Path co-efficient analysis showing direct and indirect effects of yield component characters on seed cotton yield.

Character	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	-0.0055	-0.0208	0.0037	-0.0930	0.0078	-0.0087	-0.0294	0.0010	-0.1382	-0.0104	0.0107	0.0002	-0.0142
X2	0.0018	0.0632	-0.0026	0.1099	0.0053	0.0018	0.0493	0.0038	0.1595	0.0152	-0.0036	0.0001	0.0062
X3	-0.0008	-0.0069	0.0236	0.0219	-0.0062	0.0065	-0.0054	-0.0042	0.0666	0.0060	-0.0018	0.0001	0.0064
X4	0.0019	0.0262	0.0019	0.2647	0.0109	0.0034	0.0352	0.0005	0.5220	0.0157	-0.0090	-0.0006	0.0012
X5	-0.0003	0.0025	-0.0011	0.0218	0.1318	0.0067	0.0267	0.0031	0.3323	0.0199	-0.0188	-0.0004	0.0116
X6	0.0016	0.0038	0.0050	0.0294	0.0292	0.0305	0.0706	-0.0086	0.0721	0.0096	-0.0234	-0.0004	0.0196
X7	-0.0008	-0.0161	0.0006	-0.0484	-0.0183	-0.0112	-0.1926	-0.0104	0.0599	-0.0035	0.0053	-0.0002	-0.0131
X8	0.0004	-0.0165	0.0069	-0.0107	-0.0281	0.0181	-0.1378	-0.0146	0.0525	-0.0032	-0.0058	-0.0005	-0.0009
X9	0.0012	0.0159	0.0024	0.2184	0.0692	0.0034	-0.0182	-0.0012	0.6327	0.0209	-0.0138	-0.0002	0.0019
X10	0.0015	0.0255	0.0038	0.1103	0.0697	0.0078	0.0181	0.0012	0.3513	0.0377	-0.0262	-0.0001	0.0116
X11	0.0009	0.0036	0.0006	0.0371	0.0384	0.0110	0.0159	-0.0013	0.1349	0.0152	-0.0647	-0.0002	0.0237
X12	-0.0007	0.0053	0.0014	-0.0092	-0.0390	-0.0007	0.0242	0.0004	-0.0757	-0.0038	0.0085	0.0016	-0.0024
X13	0.0021	0.0104	0.0040	0.0084	0.0407	0.0159	0.0671	0.0003	0.0324	0.0116	-0.0409	-0.0001	0.0376

Residual effect = 0.0620

significant positive phenotypic and genotypic correlation with 2.5 per cent span length. 2.5 per cent span length exhibited significant positive phenotypic and genotypic correlation with bundle strength. These results are in conformity with that of Preetha and Raveendran (2007) and Kaushik *et al.*, (2006).

As the number of independent variables influencing a particular dependent variable are increased, there is bound to be certain amount of inter independence. Due to their mutual association, the development of dependent variable and their indirect effect exerted through other characters arises inevitably as an integral part of growth pattern. Under such complex situations, the total correlation would be insufficient to explain the association and for effective manipulation of the characters. Path analysis furnishes a method of partitioning the correlation coefficient into direct and indirect effects and measures the relative importance of factors involved. The result of such analysis is discussed below.

The estimated residual was 0.0620. Among the yield component characters, lint yield had recorded maximum positive direct effect on seed cotton yield per plant followed by number of bolls per plant, single boll weight, plant height at maturity, biological yield, bundle strength, seed index, number of sympodial branches per plant, and micronaire. Similar results were earlier reported by Ashok Kumar and Ravikesavan (2010). Negative direct effect of ginning out turn followed by 2.5 per cent span length, lint index and days to fifty percent flowering towards seed cotton yield per plant was recorded in the present inquiry. Similar results were earlier reported by Thiyagu *et al.*, (2010).

In addition to direct effect, maximum positive indirect effects of plant height at maturity, number of bolls per plant, single boll weight, biological yield and 2.5 per cent span length via lint yield and the traits plant height at maturity, lint yield and biological yield via number of bolls per plant were observed on seed cotton yield per plant. Maximum negative indirect effects of days to fifty per cent flowering and micronaire via lint yield and the traits lint index, days for fifty per cent flowering, number of sympodial branches per plant, and lint yield via ginning out turn were noticed on seed cotton yield per plant. Similar results were reported by Remzi Ekinici *et al.*, (2010); Gumber *et al.*, (2005).

It is inferred that the pattern of path co-efficient observed in the present study is in agreement with the correlation obtained. In general, the characters, plant height at maturity, number of bolls per plant, single boll weight and lint yield exhibited positive significant correlation and recorded high direct effect with seed cotton

yield. Hence, these traits could well be given prime importance while selection for high yielding genotypes. Similar results were earlier reported by Rasheed and Murtaza, (2009) Sharama *et al.*, (2005); Naveed *et al.*, (2004); Muthuswamy *et al.*, (2004).

The characters such as days to fifty percent flowering, number of bolls per plant, single boll weight, biological yield and 2.5 per cent span length recorded variable performance for direct and indirect effect and more similarly for correlation coefficient. Hence, selection for such characters could be positioned to later generation until there is favorable and constant association of genes controlled the characters.

From the character association and causation studies, it may be concluded that the characters namely, plant height at maturity, number of bolls per plant, single boll weight, lint yield might be applied with selection pressure to improve seed cotton yield.

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