

Genetic Variability, Correlation and Path Analysis in F₂ Generation of Interspecific Cross of *Gossypium arboreum* and *Gossypium herbaceum* for Yield and its Component Traits

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ABSTRACT

The success of most crop improvement programs depends on variability and heritability of desirable traits. A study on genetic variability, correlation and path coefficient analysis for seed cotton yield and its component traits in the F₂ population of cross QTP 5 × ASh 90 was conducted at Botanical garden, University of Agricultural Sciences, Dharwad during kharif 2016. The segregating populations thus obtained were evaluated for eight quantitative traits. A wide range of variability was observed for plant height, number of sympodia, number of bolls and seed cotton yield per plant. The two F₂ populations recorded high GCV, heritability and GAM estimates for seed cotton yield and number of bolls per plant. Seed cotton yield recorded significant positive correlation with number of bolls and number of sympodia per plant. Path coefficient analysis of seed cotton yield revealed the maximum direct contribution from number of bolls per plant and boll weight. The number of bolls per plant had maximum indirect contribution through number of locules per boll.

Key words: Phenotypic coefficient of variance, Genotypic Coefficient of Variance, Heritability, Genetic Advance as Per Cent of Mean, Correlation, Path Coefficient.

INTRODUCTION

Cotton, the king of fibre is one of the most momentous and important cash crops having profound influence on economics and social affairs of the country. It is also called “White Gold” due to its global importance in agriculture as well as industrial economy. It is the most important commercial crop contributing nearly 65 per cent of the total raw material needs of the textile industry in our

country. Creation of new variability, when the available natural variability gets exhausted or is limited is one of the basic endeavors of plant breeders. Hybridization is an important source of variability brought about by better reshuffling of genes. The magnitude of variability present in a crop species is of utmost importance as it provides the basis for effective selection.

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The variation present in a population is measured by phenotypic, genotypic coefficient of variation; heritability and genetic advance under selection help the plant breeder in selection of elite genotypes from diverse genetic populations. Improvement of yield, the most important target in many crops can be achieved by indirect selection through other easily observable characters. But this needs a good understanding of the association of different traits with seed cotton and association among themselves. The association, direct and indirect effects of different traits vary with breeding material and environment. Therefore the information on the association of various traits among themselves and with seed cotton yield provides useful information for successful breeding programme. In plant breeding correlation studies pave the way to know the association prevailing between highly heritable characters with most economic characters and give better understanding of the contribution of each trait in building up the genetic makeup of the crop. Practically all the metric traits in plants are interdependent and interrelated, if selection is practiced considering only one trait, naturally the others also would be affected. In such cases the knowledge of association between characters is quite helpful to plant breeders to formulate their selection strategy based on two or more traits simultaneously. Since, seed cotton yield and fibre quality traits are complex quantitative characters, direct selection may not be a reliable approach as these traits are influenced by environmental factors. Therefore, it becomes essential to identify the component characters through which yield improvement could be obtained. Though correlation gives information about the contributing component of these complex characters, it does not provide an exact picture of relative importance of direct and indirect contribution of the component characters. Path coefficient analysis is an important tool for partitioning the correlation coefficient into direct and indirect effects. Thus, correlation in combination with path analysis would give better insight into the cause and effect

relationship between different character pairs. Selection for a specific character is known to result in correlated response in certain other characters, generally plant breeders practice selection for one or two attributes at a time. Then it becomes important to know the effect of selection on other characters. Study of nature of association of component traits with seed cotton yield and among themselves in F_2 populations and study of the contribution of components towards seed cotton yield through path analysis provides an opportunity for indirect selection of these component traits to improve complex trait like yield.

MATERIAL AND METHODS

The material for the present study was generated in the Botany garden, Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad during *kharif* 2015 by crossing two stabilized lines of *G. arboreum* and *G. herbaceum* species. The experimental material for the present study involved F_2 cross which was developed by selfing F_1 s developed by crossing two genetically diverse genotypes viz. *QTP 5* \times *ASh 90*. The F_2 generation was raised during *kharif* 2016.

The experiment was carried without replication as it was segregating material. The inter row spacing was 60 cm and inter plant spacing was 30 cm. Recommended package of practices¹ were followed to raise the crop. The observations were recorded on each plant in F_2 and 20 plants in each of the parents, F_1 s and checks for seed cotton yield and its component traits viz. plant height, number of sympodia per plant, number of bolls per plant, boll weight, number of locules per boll, seed cotton yield per plant, ginning outturn, lint index and seed index. The mean and variances were analyzed based on the formula given by Singh and Chaudhary⁹. The genotypic and phenotypic coefficient of variation was computed according to Burton and Devane³. Heritability in broad sense was estimated as the ratio of genotypic to phenotypic variance and expressed in percent⁵. This was worked out as per the formula proposed by Johnson *et al.*⁶. Simple correlations were computed by

using the formula given by Weber and Moorthy²⁴. Correlation coefficients were compared against Table 'r' values¹³ at (n-2) df at the probability levels of 0.05 and 0.01 to test their significance. Path coefficient analysis was carried out using the simple correlation coefficient to know the direct and indirect effects of the yield components on seed yield as suggested by Wright²⁵ and illustrated by Dewey and Lu¹². Scales for path coefficients as suggested by Lenka and Mishra were followed in the current study.

RESULTS AND DISCUSSION

Genetic variability, heritability, genetic advance as percent of mean

Creation of genetic variability is pre-requisite for plant breeders to exercise selection. The phenotypic and genotypic coefficients of variation were estimated using genotypic and phenotypic variances respectively. The coefficient of variation indicates only the extent of variability existing for various traits, but does not give any information about the heritable portion of it. Therefore, heritability accompanied by estimates of genetic advance as per cent of mean was estimated. In the present study, the cross *QTP 5* × *ASh 90* was evaluated for the extent of variability released in the F₂ generation.

The PCV for the traits was recorded as plant height(13.84), number of sympodia per plant(27.75), number of bolls per plant(52.37), boll weight(19.74), number of locules per boll(14.25), seed cotton yield per plant(52.38), ginning outturn(5.46), seed index(8.57) and lint index(13.79).

The GCV for the traits was recorded as plant height(12.33), number of sympodia per plant(24.19), number of bolls per plant(45.04), boll weight(18.70), number of locules per boll(14.09), seed cotton yield per plant(36.85), ginning outturn(4.79), seed index(7.97) and lint index(12.72).

The PCV and GCV are classified as suggested by Sivasubramanian and Menon¹⁰ low(0-10 %), moderate(11-20%) and high(> 21 %). Traits plant height, number of sympodia per plant, number of bolls per plant and seed cotton yield per plant recorded high PCV and

GCV estimates. A very high PCV and GCV for these traits indicate greater scope for selection for this trait to improve seed cotton yield. Traits boll weight, number of locules per boll and lint index recorded moderate PCV and GCV estimates. Traits ginning outturn and seed index recorded low GCV and PCV estimates. Low PCV and GCV estimates for these traits indicate a narrow range of variability for these characters and limited scope for selection.

The PCV values were invariably higher than GCV for all the characters as reported by Bayyapu *et al.*^{2,11} and Shakti *et al.*⁸. All the characters studied, recorded small difference between GCV and PCV except number of sympodia per plant, number of bolls per plant and seed cotton yield per plant which indicated that the characters were least affected by environment and selection for this trait based on the phenotype would be fruitful. Similar results of less difference between PCV and GCV were reported by Erande *et al.*⁴.

Although range can provide a preliminary idea about the variability but coefficient of variation is reliable as it is independent of unit of measurement. The extent of variability as measured by phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), also gives information regarding the relative amount of variation in different populations. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) showed variation for the characters studied in the present population.

It is not the magnitude of variation but the extent of heritable variation, which matters most for achieving gains in selection programme. The coefficient of variation indicates only the extent of variation for a character and does not discriminate the variability into heritable and non-heritable portion. The heritability worked out in broad sense would suggest how far the variation is heritable and selection is effective. Though the heritability estimates are the true indicators of genetic potentiality of the genotypes which can be used as a tool for selection⁶ changes in the

values of the heritability due to fluctuations of the environmental factors detract for total dependence on such estimates. However, heritability estimates when considered in conjunction with the genetic advance as per cent of mean form a reliable tool for selection.

The heritability for the traits was recorded as plant height(79.37%), number of sympodia per plant(75.96%), number of bolls per plant(73.95%), boll weight(89.78%), number of locules per boll(97.81%), seed cotton yield per plant (49.49%), ginning outturn(%76.96), seed index (86.51%) and lint index(85.08%).

The genetic advance as per cent of mean for the traits was recorded as plant height (33.18%), number of sympodia per plant (57.15%), number of bolls per plant (101.34%), boll weight (36.50%), number of locules per boll (28.71%), seed cotton yield per plant (53.40%), ginning outturn (8.66%), seed index (15.27%) and lint index (24.17%).

The heritability was classified as suggested by Robinson *et al.*⁷ (low (0-30 %), moderate (31-60 %) and high (> 61 %). All the traits under the present study recorded high heritability except seed cotton yield per plant which recorded moderate heritability estimate. High heritability provides the evidence that larger proportion of phenotypic variance has been attributed to genotypic variance, and reliable selection could be made for these traits on the basis of phenotypic expression.

The GAM was categorized, as suggested by Johnson *et al.*⁶ low (0-10 %), moderate (11-20 %) and high (> 20 %). All the traits under the present study recorded high genetic advance as per cent of mean except ginning outturn and seed index which recorded moderate genetic advance as per cent of mean. Traits plant height, number of sympodia per plant, number of bolls per plant, boll weight and lint index recorded high heritability coupled with high genetic advance as per cent of mean. Traits ginning outturn and seed index recorded high heritability coupled with moderate genetic advance as per cent of mean. Traits number of sympodia and number of bolls per plant which were important for improvement of seed cotton yield recorded high heritability coupled

with high genetic advance as per cent of mean so indirect selection for this can be practiced to improve seed cotton yield.

Association of seed cotton yield with various seed cotton yield attributing traits

The phenotypic correlation of seed cotton yield with various component traits in this population are presented in Table 2.

At phenotypic level, seed cotton yield per plant was positively and significantly associated with number of bolls per plant (0.9047), number of locules per boll (0.7979) and plant height (0.2074). Similar results were reported by Neelima²⁰, Kaushik *et al.*¹⁵, Ladole and Meshram¹⁶, Gururaj¹⁴ and Leela Pratap *et al.*¹⁷. Number of bolls per plant exhibited significant positive association with seed cotton yield in the population under consideration. It indicated the possibility of yield improvement by selection of genotypes with high number bolls.

Association among the various seed cotton yield attributing traits:

Plant height exhibited positive and significant association with number of sympodia per plant (0.5347). Boll number showed negative and significant association with boll weight (-0.2845). Ginning Outturn (0.5201) and seed index (0.7020) had exhibited positive and significant association with lint index.

Direct and indirect effects of various components traits on seed cotton yield per plant:

The direct and indirect effects of various components traits on seed cotton yield per plant are presented in Table 2 and depicted in Fig. 1.

The direct effect of number of bolls per plant on seed cotton yield per plant was positive and high (0.9338). The indirect contribution of number of bolls per plant via boll weight was negative and moderate (-0.2657). The trait boll weight exhibited high positive direct effect on seed cotton yield per plant (0.3541). The direct and indirect effects of all other component traits on seed cotton yield were negligible. Similar reports were reported by Rahul *et al.*²², Pujer *et al.*²¹, Srinivas *et al.*²³, Bayyapu *et al.*^{2,11} and Muhammad *et al.*¹⁹.

Table 1: Genetic variability in the F₂ population of cross QTP 5 × Ash 90

	PH	NS	NB	BW	NL	GOT	SI	LI	SCY
Mean	194.88	17.85	26.24	2.30	3.35	36.35	6.95	4.01	57.63
Minimum	110.00	7.00	10.00	1.31	3.0	29.66	5.23	2.81	10
Maximum	290.00	31.00	76.00	3.37	4.0	39.78	8.3	7.4	156
PV	727.97	24.54	188.85	0.21	0.23	3.94	0.36	0.31	911.11
EV	150.20	5.90	49.20	0.021	0.005	0.91	0.05	0.05	460.20
GV	577.77	18.64	139.65	0.19	0.22	3.03	0.31	0.26	450.91
PCV	13.84	27.75	52.37	19.74	14.25	5.46	8.57	13.79	52.38
GCV	12.33	24.19	45.04	18.70	14.09	4.79	7.97	12.72	36.85
h ² _(bs)	79.37	75.96	73.95	89.78	97.81	76.96	86.51	85.08	49.49
GAM	33.18	57.15	101.34	36.50	28.71	8.66	15.27	24.17	53.40

PH – Plant height

NS – Number of sympodia per plant

NB – Number of bolls per plant

BW - Boll weight

SCY – Seed cotton yield

GCV – Genotypic coefficient of variation

h²_(bs) – Broad sense heritability

GAM – Genetic advance as percent of mean

NL– Number of Locules per boll

GOT – Ginning outturn

SI – Seed index

LI – Lint index

PV – Phenotypic variance

GV – Genotypic variance

PCV – Phenotypic coefficient of variation

Table 1: Correlation analysis in F₂ population of cross QTP 16 × Ash 90

	PH	NS	NB	BW	NL	GOT	SI	LI	SCY
PH	1.0000	0.5347**	0.1804*	0.1030	0.1658*	0.0785	-0.0529	0.0043	0.2074**
NS		1.0000	0.1068	-0.0035	0.1287	-0.0237	0.0024	0.0343	0.1041*
NB			1.0000	-0.2845**	0.7336**	0.1582*	-0.0400	0.0364	0.9047**
BW				1.0000	0.0452	-0.0682	0.0346	0.0140	0.0875
NL					1.0000	0.1812*	0.0585	0.1242	0.7978**
GOT						1.0000	0.0787	0.5201**	0.1801*
SI							1.0000	0.7020**	-0.0232
LI								1.0000	0.0674
SCY									1.0000

Table 2: Path analysis in the F₂ population of cross QTP 5 x Ash 90

	PH	NS	NB	BW	NL	GOT	SI	LI	PCC with SCY
PH	-0.0192	-0.0103	-0.0035	-0.0020	-0.0032	-0.0015	0.0010	-0.0001	0.2074**
NS	0.0026	0.0049	0.0005	0.0000	0.0006	-0.0001	0.0000	0.0002	0.1041*
NB	0.1685	0.0998	0.9338	-0.2657	0.6850	0.1477	-0.0374	0.0340	0.9047**
BW	0.0365	-0.0012	-0.1007	0.3541	0.0160	-0.0241	0.0123	0.0050	0.0875
NL	0.0153	0.0119	0.0676	0.0042	0.0922	0.0167	0.0054	0.0114	0.7978**
GOT	0.0032	-0.0010	0.0065	-0.0028	0.0075	0.0413	0.0033	0.0215	0.1801
SI	0.0005	0.0000	0.0004	-0.0003	-0.0005	-0.0007	-0.0088	-0.0062	-0.0232
LI	0.0000	0.0001	0.0001	0.0000	0.0002	0.0008	0.0011	0.0015	0.0674

Residual effect = 0.2155

PH – Plant height

NS – Number of sympodia per plant

NB – Number of bolls per plant

BW - Boll weight

SCY – Seed cotton yield

* - Significant at 5 per cent level of probability

** - Significant at 1 per cent level of probability

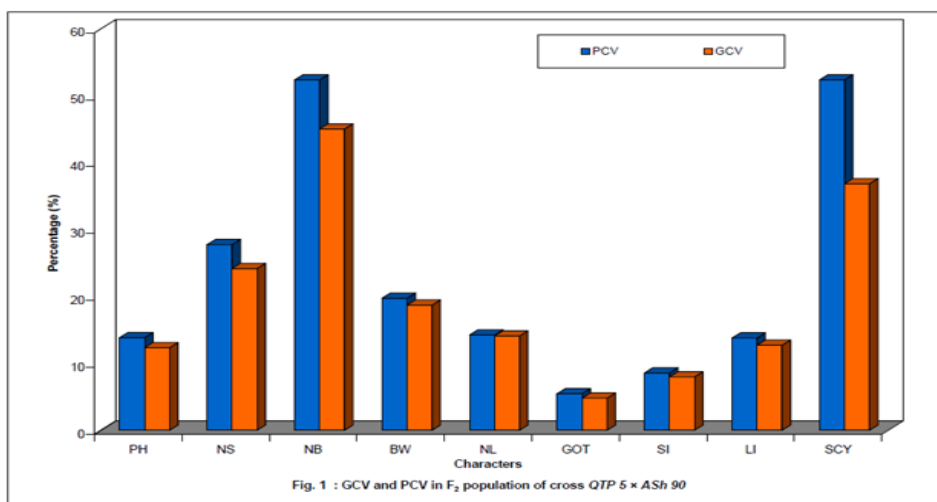
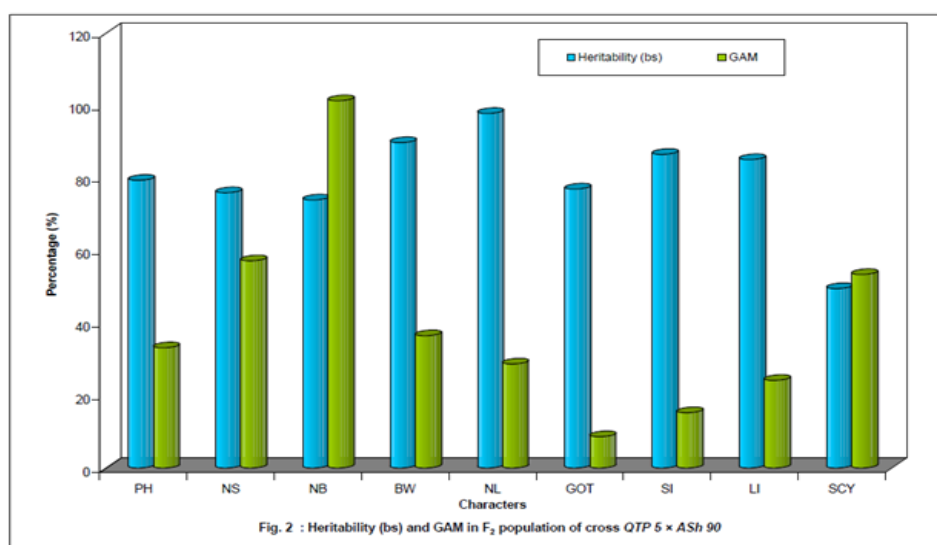
NL- Number of Locules per boll

GOT – Ginning outturn

SI – Seed index

LI – Lint index

PCC - Phenotypic correlation coefficient

Fig. 1 : GCV and PCV in F₂ population of cross QTP 5 × ASH 90Fig. 2 : Heritability (bs) and GAM in F₂ population of cross QTP 5 × ASH 90

CONCLUSION

In the present study a wide range of variability was observed for all the traits under consideration which indicated that parents chosen were diverse enough. All the traits exhibited high heritability except seed cotton yield. Correlation and path analysis revealed high and significant correlation of seed cotton yield with number of bolls and number of sympodia per plant and these also exhibited high heritability so selection based on these traits would be fruitful and can bring an improvement in the seed cotton yield.

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