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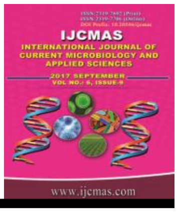

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Genetic variability and Heritability Study in F_2 Segregants of *Desi* Cotton for Yield and its Component Traits

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ABSTRACT

Keywords

Phenotypic coefficient of variance, Genotypic coefficient of variance, Heritability and genetic advance as per cent of mean.

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The success of most crop improvement programs depends on variability and heritability of desirable traits. An investigation was carried out during *kharif* 2016 at Botanical garden, University of Agricultural Sciences, Dharwad, India to assess the extent of variability generated by hybridization and to estimate the heritability and genetic advance as percent of mean for seed cotton yield and its component traits in F_2 generation of cross QTP 16 × ASa 151. The segregating population thus obtained was evaluated for eight quantitative traits. A wide range was observed for traits plant height, number of sympodia per plant, number of bolls per plant and seed cotton yield per plant. High phenotypic coefficient of variation and genotypic coefficient of variation were recorded for traits number of sympodia per plant, number of bolls per plant and seed cotton yield per plant. High heritability coupled with high genetic advances was recorded for all traits under consideration except for traits ginning outturn, seed index and seed cotton yield per plant in the F_2 population. Seed cotton yield per plant recorded moderate heritability couple with high genetic advance as per cent of mean.

Introduction

Cotton, the king of fiber 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. 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.

Materials 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. arboretum* species. The experimental material for the present study involved F_2 cross which was developed by selfing F_1s developed by crossing two genetically diverse genotypes viz. *QTP 16 × ASa 151.* 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 practices (Anon., 2016) 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_1s 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 Chaudhary (1977). The genotypic and phenotypic coefficient of variation was computed according to Burton and Devane (1953). Heritability in broad sense was estimated as the ratio of genotypic to phenotypic variance and expressed in percent (Hanson *et al.*, 1956). This was worked out as per the formula proposed by Johnson *et al.*, (1955).

Results and Discussion

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 16 × ASa 151 was evaluated for the extent of variability released in the F_2 generation. The results are presented in table 1 and are depicted in figures 1 and 2.

The PCV for the traits was recorded as plant height(21.29), number of sympodia per plant(38.15), number of bolls per plant(50.37), boll weight(16.90), number of locules per boll(14.20), seed cotton yield per plant(51.35), ginning outturn(8.94), seed index(9.32) and lint index(16.07).

The GCV for the traits was recorded as plant height(19.51), number of sympodia per plant(33.26), number of bolls per plant(44.46), boll weight(15.50), number of locules per boll(12.88), seed cotton yield per plant(38.88), ginning outturn(8.43), seed index(8.74) and lint index(14.63).

The PCV and GCV are classified as suggested by Sivasubramanian and Menon (1973), 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.*, (2015) and Shakti *et al.*, (2007).

Table.1 *Genet*ic variability in the F_2 population of cross QTP 16 × *ASa 151*

	PH	NS	NB	BW	NL	GOT	SI	LI	SCY
Mean	185.76	17.09	34.66	2.16	3.34	31.98	6.78	3.21	73.80
Minimum	100.00	5.00	6.00	1.42	3.00	22.27	5.15	2.00	14.00
Maximum	305.00	39.00	98.00	3.11	4.00	40.00	8.34	4.99	196.00
PV	1564.45	42.51	304.76	0.13	0.23	8.18	0.40	0.27	1436.37
EV	250.60	10.20	65.20	0.02	0.04	0.91	0.05	0.05	613.20
GV	1313.85	32.31	239.56	0.11	0.19	7.27	0.35	0.22	823.17
PCV	21.29	38.15	50.37	16.90	14.20	8.94	9.32	16.07	51.35
GCV	19.51	33.26	44.66	15.50	12.88	8.43	8.74	14.63	38.88
$h^2_{(bs)}$	83.98	76.01	78.61	84.14	82.26	88.90	88.00	82.86	57.31
GAM	36.83	59.72	81.55	29.29	24.07	16.37	16.89	27.43	60.63

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
$h^2_{(bs)}$ – 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

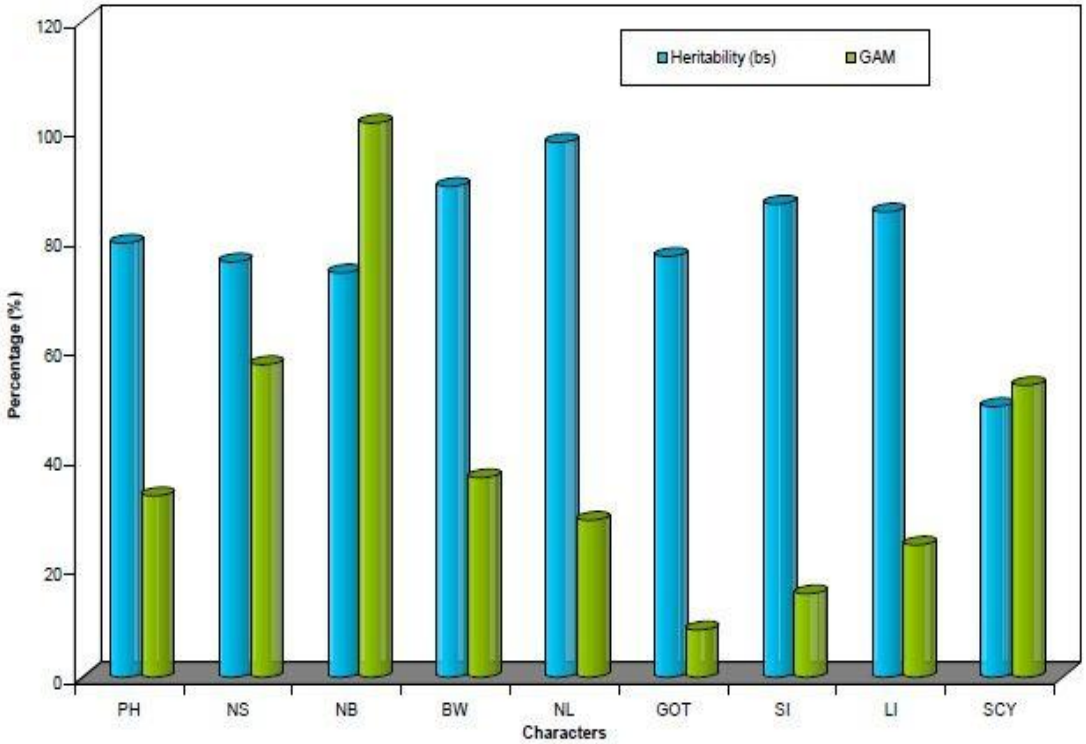

Fig. 1 : Heritability (bs) and GAM in F_2 population of cross *QTP 5 × ASh 90*

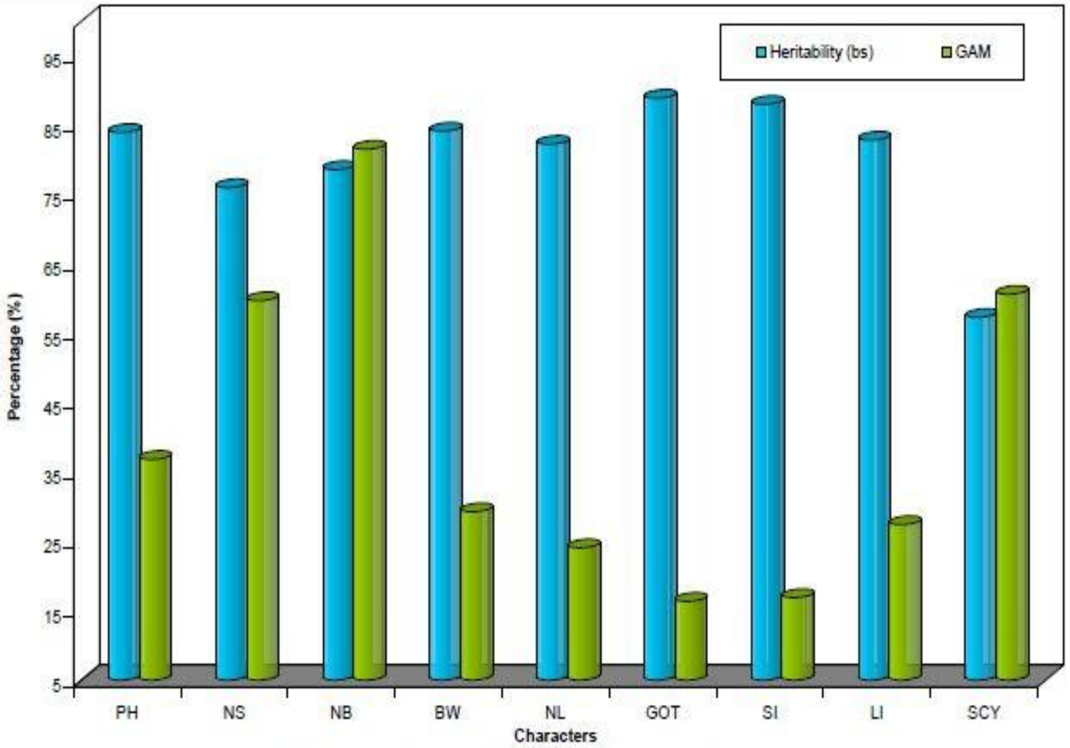

Fig. 2: Heritability (bs) and GAM in F_2 population of cross *QQTP 16 × ASa 151*

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.,* (2014).

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 selection (Johnson *et al.*, 1955), 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 (83.98%), number of sympodia per plant (76.01%), number of bolls per plant (78.61%), boll weight (84.14%), number of locules per boll (82.26%), seed cotton yield per plant (57.31%), ginning outturn (88.90%), seed index (88.00%) and lint index (82.86%).

The genetic advance as per cent of mean for the traits was recorded as plant height (36.83%), number of sympodia per plant (59.72%), number of bolls per plant (81.55%), boll weight (29.29%), number of locules per boll (24.07%), seed cotton yield per plant (60.63%), ginning outturn (16.37%), seed index (16.89%) and lint index (27.43%).

The heritability was classified as suggested by Robinson *et al.,* (1951), 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.,* (1955), 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.

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