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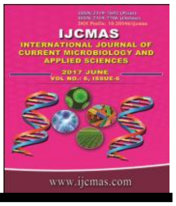

Original Research Article

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Genetic Variability and Heritability Study in F_2 Population of *Gossypium barbadense* L. Cotton for Yield and its Components

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ABSTRACT

Keywords

Heritability,
Genetic variability
PCV,
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The success of most crop improvement programs depends upon the genetic variability and heritability of desirable traits. The genetic variability and heritability study was carried out in F2 population of Suvin X BCS 23-18-7 cross, at College of Agriculture, UAS Darwad during Kharif 2016-17. The highest range of variation was observed in F2 population for seed cotton yield per plant (5.5 g - 259 g) followed by plant height (30 -205 cm) and lint yield per plant (2 - 89.5 g) while lint index (1.87 - 8.68) recorded lowest range of variation. Respectively PCV and GCV per cent were recorded higher (> 20 %) for number of monopodia per plant (46.08 and 26.09), number of sympodia per plant (27.86 and 21.99), boll weight (25.69 and 22.99) and seed cotton yield (32.80 and 20.51) while moderate (10 - 20 %) for plant height (17.56 and 14.16) and lint yield (13.09 and 11.43) but high PCV and moderate GCV observed for number of bolls per plant (25.40 and 14.19). Higher heritability (> 60 %) was observed for plant height, number of sympodia per plant, seed index, ginning outturn, lint index, boll weight and seed cotton yield per plant. Whereas, days to first flowering, number of monopodia per plant, number of bolls per plant and seed cotton yield per plant were recorded moderate (30 - 60 %) heritability. Similarly, Genetic advance over mean high (> 20 %) for plant height, number of monopodia per plant, number of sympodia per plant, lint yield per plant, lint index, boll weight and seed cotton yield per plant while moderate (10 - 20%) for number of bolls per plant, seed index and ginning outturn. But, only days to first flowering (3.35) recorded lower GAM. Traits which showing high heritability coupled with moderate to high GAM (plant height, number of sympodia per plant, seed index, ginning outturn, lint index, boll weight and seed cotton yield per plant), supports for recovery of desirable lines through selection.

Introduction

Cotton, the “king of fibre” known for its desirable properties is also called “White Gold” due to its global importance in agriculture as well as industrial economy, in India providing direct employment to around 35 million people. Of the four cultivated species worldwide, two diploid (2n=2x=26) A genome species (*G. arborium* and *G. herbacium*) and two AD genome (2n=4x=52) species (*G. hirsutum* and *G. barbadense*), were independently domesticated and cultivated for their fibers (Wendel *et al.*, 1999). Pima cotton or Egyptian cotton, *Gossypium barbadense* is known for its finest fibre properties being cultivated in less than 2% in the world (Chen *et al.*, 2007), it is just because of low yielding ability, higher susceptibility to sucking pests and boll worms. In India, long and extra-long staple cotton is widely grown in South Zone states of Tamil Nadu, Andhra Pradesh and Karnataka as the climatic requirement for growing this cotton are more conducive and there has been a heavy demand for this cotton in the recent past in textile industry. To meet industrial requirement there is urgent need to improve yield potential in *G. barbadense*. Attempts have been made to identify high yielding extra-long staple *G. barbadense* genotypes with desirable fibre property. In the process of identification of genotypes, seed cotton yield coupled with superior fibre quality properties are considered as the prime factors.

Seed cotton yield is a complex trait governed by several yield contributing characters such as plant height, number of monopodia, number of sympodia, number of bolls, number of fruiting points per plant. In cotton, genotypic and phenotypic variation for different agronomic and fibre quality characters such as plant height, number of monopodia, number of sympodia, number of bolls, number of fruiting points per plant, seed index, lint index, micronaire value and seed cotton yield has been extensively studied by several workers (Ahuja and Tuteja, 2000; Neelam and Potdukhe, 2002; Sakthi *et al.*, 2007; Dhamayanathi *et al.*, 2010; Choudki *et al.*, 2012 and Raza *et al.*, 2016). Since 1970, several extra-long staple inter-specific (*G. hirsutum* x *G. barbadense*) hybrids such as Varalaxmi (first inter-specific hybrid developed by Katharki), DCH-32, NHB-12, HB-224 and TCHB-213 developed at various institutes were widely cultivated all over the country. However, due to the genetic deterioration of promising released varieties/hybrids, new genotypes with improved fibre properties are desirable to meet the demand in Indian textile industry. The genetic improvement of any crop is dependent upon the existence of initial genetic variability among the populations, and the best method for genetic variability create in sexually (seed) propagated crop is through wide hybridization or crossing between genetically diverse parents. Hence, present study was conducted to create genetic variability by crossing diverse parents selected within *G. barbadense* and analyzed extent of genetic variability generated in their F2 population for seed cotton yield and its component traits.

Materials and Methods

Suvin and BCS23-18-7 phenotypically diverse (Table 1 and Fig. 1) genotypes belongs to finest fibre quality cotton species of *Gossypium barbadense*, were selected as a parents for creating genetic variability for fibre quality traits and seed cotton yield during Kharif 2014-15 from Agriculture Research Station, UAS Dharwad. Developed F1 by crossing Suvin X BCS23-18-7 during Summer 2014-15 and generated F2 by slfing F1 during Kharif 2015-16. The genetic variability and heritability for seed cotton yield and its component traits in F2 population was carried out during Kharif 2016-17 at College of Agriculture, UAS, Dharwad, Karnataka. Geographically, experimental field is located at 15°29'46.8"North latitude and 74°59'11.3" East longitude at an altitude of 678 m above mean sea level with an average rainfall about 722.73 mm. The soil type of the experimental block was vertisol with a pH in the range of 7 to 7.5 and plots were homogeneous with respect to soil nutrient status. Before sowing, seeds were treated with Imidacloprid to protect the crop from the incidence of sucking pests during early growth stage. Seeds were hand dibbled in rows of 8 m length with spacing of 90 cm between rows and 40 cm between plants. Agronomic managements were followed according to recommended package of practices for irrigated conditions of the south zone. Observations were recorded on randomly selected 19 plats in Suvin and BCS 23-17-8 and 36 plants in F1 and all the 1329 F2 plants for seed cotton yield and its component traits viz., days to first flowering, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, ginning outturn (%), seed index (g) and lint index (g). The mean and variance were analyzed based on the formula given by Singh and Choudhary (1977) and the genetic components of variation was estimated with the help of given formula.

Phenotypic variance

The individual observation made for each trait on F2 population is used for calculating the phenotypic variance.

Phenotypic variance ($\sigma^2 p$) = Var F2

Where, Var F2 = variance of F2 population

Environmental variance

The average variance of parents and their corresponding F1 is used as environmental variance for single crosses.

$$\text{Environmental variance } (\sigma^2 e) = \frac{(\sigma^2 p_1) + (\sigma^2 p_2) + (\sigma^2 F_1)}{3}$$

Where,

$\sigma^2 p1$ = Variance of parent P1
$\sigma^2 p2$ = Variance of parent P2
$\sigma^2 F1$ = Variance of cross F1

Genotypic variance

Genotypic variance ($\sigma^2 g$) = $\sigma^2 p - \sigma^2 e$

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 e$ = Environmental variance

Both genotypic and phenotypic coefficients of variation were computed as per the method suggested by Burton and Devane (1953). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were classified as suggested by Sivasubramanian and Menon (1973) that are, low (< 10 %), moderate (10 - 20 %) and high (> 20 %). The heritability percentage was classified as low (0-30%), moderate (30–60%) and high (> 60%) by Robinson *et al.*, (1949). Genetic advance was computed by using the formula given by Robinson *et al.*, (1949) and genetic advance over mean was calculated by given formula. The genetic advance as per cent mean was categorized as low up to 10 per cent, 10 to 30 per cent consider as a moderate and more than 20 per cent noticed as a high (Johnson *et al.*, 1955).

$$\text{Genetic advance over mean} = \frac{\text{Genetic advance}}{\text{Mean}} \times 100$$

Results and Discussion

The genetic variability is a prerequisite for any crop improvement program. Pedigree methods of selection from F_2 onwards from cross between genetically diverse parents has been known to be one of the effective means of generates and maintaining genetic variability. Heritability is generally ratio of the genotypic variance to phenotypic variance.

The higher heritability values generally are the reflection of closed value of respective phenotypic and genotypic variances and also indicate that selection of this character is useful in improving plant type. Heritability by itself does not provide indication of the amount of genetic progress that would results from selecting the best individuals, rather it depends on the amount of genetic variance. Therefore, genetic advance and genetic advance over mean gain importance in providing an idea of the amount of progress that can be achieved by selection.

Therefore, present study was attempted to evaluate genetic variability, heritability and GAM in F_2 population of intraspecific cross of *G. barbadense*. Statistical analysis revealed the presence of considerable level of genetic variability for all the characters under this study (Table 2).

Statistically range is a difference between highest to lowest, breeders generally used to know the existing range of variability for interested traits in the working population. For seed cotton yield per plant recorded highest range (5.5 - 259 g) followed by plant height (30 - 205 cm), lint yield per plant (2 - 89.5 g), number of bolls per plant (2 - 51 bolls), ginning outturn (19.84 - 53.13 %), days to first flowering (60 -88 days) and number of sympodia per plant (2 - 25) while lint index (6.81) recorded lowest range.

Of the 1329 F2 plants 147 plants were recorded higher yield than F1 (158 g/plant), plant number F-692 recorded highest 259 g (63.88 % superior over F1), followed by F-463 recorded 251 g (58.82 % more than F1), F-984 recorded 242.5 g (53.44 % more than F1) and F-908 shown 238.5 g (50.91 % greater than F1). These results confirmed that, the genetic variation can be created through hybridization between diverse parents. There were many reports available on this aspect, most related study of Yanal *et al.,* (2013) reported presence of wide range for seed cotton yield (441.81- 2175.7 kg / ha) in 54 G barbadense lines (53 F5 lines + suvin check). The coefficients of variation expressed in percentage at phenotypic and genotypic levels (PCV and GCV) have been used to compare the variability observed among the different characters. The number of monopodia per plant (46.08), number of sympodia per plant (27.86), number of bolls per plant (25.40), lint yield per plant (33.68), boll weight (25.69) and seed cotton yield (32.80) recorded higher PCV (> 20 %), whereas plant height (17.56), seed index (10.23) and lint index (13.09) were recorded moderate PCV (10 - 20 %), but days to first flowering (5.14) and ginning outturn (7.14) recorded low PCV (< 10 %).

Similarly for GCV, number of monopodia per plant (26.09), number of sympodia per plant (21.99), boll weight (22.99) and seed cotton yield (20.51) recorded higher, whereas plant height (14.16), number of bolls per plant (14.19) and lint index (11.43) observed moderate GCV, and remaining two traits viz., seed index (8.28) and ginning outturn (6.73) shown less GCV. The narrow difference between genotypic coefficient of variation and phenotypic coefficient of variation indicates that characters were less affected by environment, and comparison between GCV and PCV depicted in figure 2.

Traits number of monopodia per plant, number of sympodia per plant, boll weight and seed cotton yield were recorded higher PCV and GCV. Similarly in F4 populations of upland cotton Raza *et al.,* (2016) reported higher GCV and PCV for seed cotton yield per plant and number of monopodia per plant, and moderate for plant height. Dhamayanathi *et al.,* (2010) reported higher GCV and PCV for days to 50 per cent flowering, bolls per plant, ginning outturn and seed cotton yield per plant in 24 pima cotton genotypes.

Table.1 Characteristics of parents

Varieties	Fiber length (mm)	Fiber fineness (Mic)	Fiber strength (g/tex)	Seed cotton yield (gm/plant)
Suvin	37-39	3.0-3.3	46-48	81 - 95
BCS 23-18-7	29-31	3.4-3.5	26-29	135 - 148

Table.2 Genetic variability in F2 population

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
F_2 mean	72.91	126.54	2.47	11.82	28.57	37.42	9.37	33.44	4.72	3.96	111.83
Minimum	60.00	30.00	0.00	2.00	2.00	2.00	4.48	19.84	1.87	2.00	5.50
Maximum	88.00	205.00	7.00	25.00	51.00	89.50	12.11	53.13	8.68	9.83	259.00
Range	28.00	175.00	7.00	23.00	49.00	87.50	7.63	33.28	6.81	7.83	253.50
P_1 mean	78.84	147.21	4.79	17.37	25.74	32.31	11.73	33.26	5.85	3.85	97.18
P_2 mean	68.22	118.06	1.72	16.17	37.17	29.46	8.95	33.49	4.50	3.14	116.90
F_1 mean	73.64	126.97	3.69	15.61	39.72	53.32	9.55	33.75	4.86	3.97	158.04
σ^2e	9.59	172.81	0.88	4.08	36.23	87.31	0.32	0.63	0.09	0.21	819.20
σ^2p	14.04	493.92	1.29	10.83	52.65	158.88	0.92	5.70	0.38	1.03	1345.13
σ^2g	4.44	321.11	0.41	6.75	16.42	71.58	0.60	5.07	0.29	0.83	525.94
h^2	31.66	65.01	32.05	62.31	31.19	45.05	65.54	88.90	76.22	80.10	39.10
PCV	5.14	17.56	46.08	27.86	25.40	33.68	10.23	7.14	13.09	25.69	32.80
GCV	2.89	14.16	26.09	21.99	14.19	22.61	8.28	6.73	11.43	22.99	20.51
GA	2.44	29.76	0.75	4.22	4.66	11.70	1.29	4.37	0.97	1.68	29.54
GAM	3.35	23.52	30.43	35.75	16.32	31.26	13.81	13.07	20.56	42.39	26.42

X_1 - Days to first flowering
X_2 - Plant height
X_3 - Number of monopodia per plant
X_4 - Number of sympodia per plant
X_5 Number of bolls per plant
X_6 - Lint yield per plant (g)
X_7 - Seed index
X_8 - Ginning outturn (%)
X_9 - Lint index
X_{10} - Boll weight
X_{11} - Seed cotton yield
σ^2e - Environment variance
σ^2p - phenotypic variance
σ^2g - Genotypic variance
h^2 - heritability
PCV- phenotypic coefficient of variation
GCV- Genotypic coefficient of variation
GA- Genetic advance
GAM- Genetic advance over mean

Fig.1 Phenotypic appearance of parents

Suvin BCS 23-18-7

Fig.2 Comparison between PCV and GCV

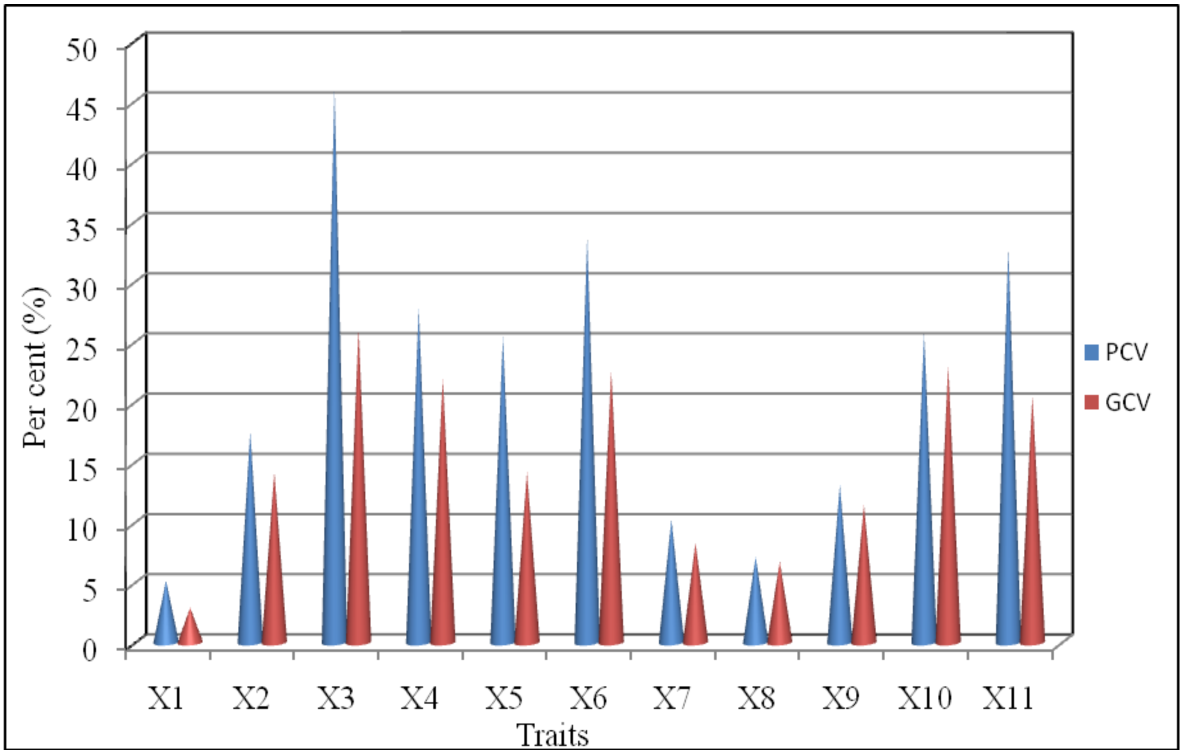
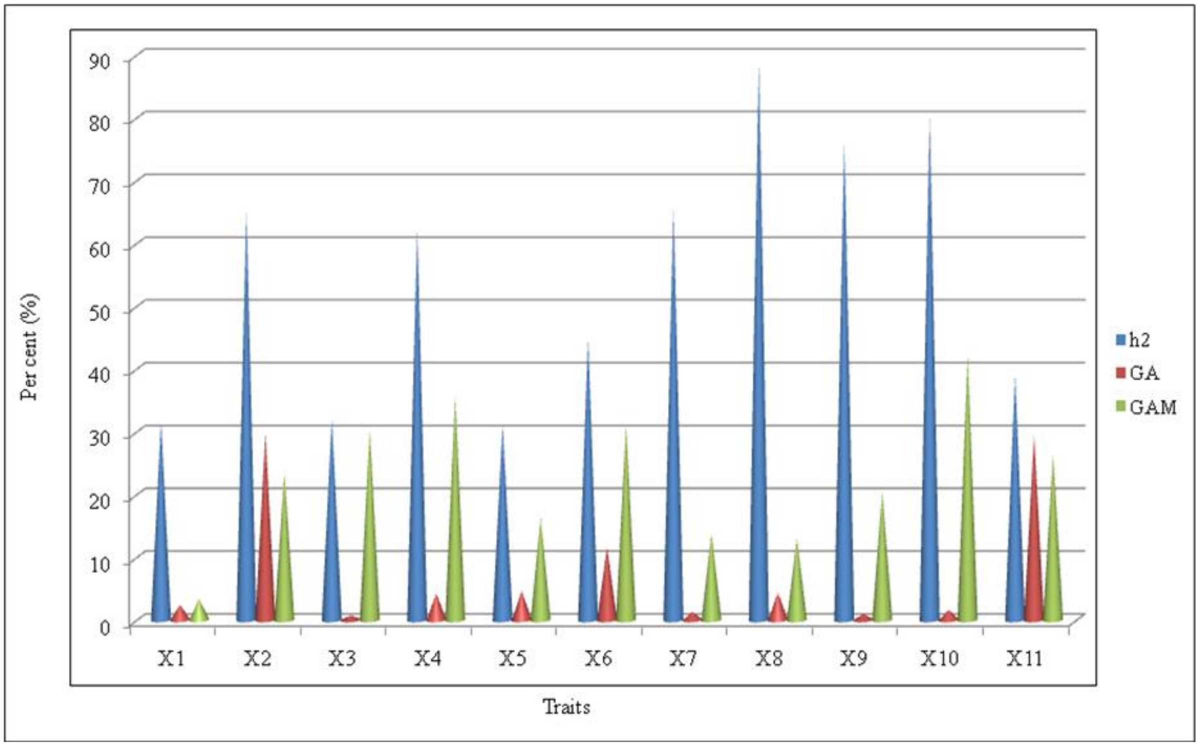


Fig.3 Comparison among heritability (h^2), genetic advance (GA) and GAM



Heritability (h2) as a ratio of genotypic to phenotypic variance indicates the effectiveness with which selection of genotypes can be based on phenotypic performance. Heritability of different traits were classified in to (> 60 %), high moderate (30 - 60 %) and low (< 30%) (Robinson *et al.*, 1949). Ginning outturn (88.90), boll weight (80.10), lint index (76.22), and lint yield per plant (71.58), seed index (65.54), plant height (65.01) and number of sympodia per plant (62.31), recorded higher heritability. Whereas, days to first flowering (31.66), number of monopodia per plant (32.05), number of bolls per plant (31.19) and seed cotton yield per plant (39.10) showed moderate heritability. Similar results were reported by many researchers, more relevant study of Dhamayanathi *et al.*, (2010) reported higher heritability for plant height, seed cotton yield per plant, boll weight and number of bolls per sympodia in 24 pima cotton genotypes.

Heritability estimates along with genetic advance over mean will be more useful in predicting the outcome of selecting the best individuals. The GAM (> 20 %) for different traits were observed viz., plant height (23.52), number of monopodia per plant (30.43), number of sympodia per plant (35.75), lint index (20.56), boll weight (42.39) and seed cotton yield (26.42). And the number of bolls per plant (16.32) lint yield per plant (31.26) and seed index (13.81), and moderate GAM (10 - 20 %) observed for ginning outturn (13.07), whereas, only days to first flowering was recorded low GAM of 3.35. And comparison among heritabillity, genetic advance and genetic advance over mean is depicted in figure 3. Choudki *et al.*, (2012) reported high GAM for seed cotton yield per plant and seed index in F11 generation of interspecific (*G. herbacium* X *G. barbadense*) cross. Ramesh (2016) evaluated recombinant inbred lines of inter specific hybrid (*G. hirsutum* X *G. barbadense*) and reported higher GAM for seed cotton yield per plant, number of monopodia per plant and bolls per plant, and moderate GAM for boll weight and lint index.

Because of the presence of higher heritability with a high genetic advance over mean for number of sympodia per plant, lint index, boll weight and seed cotton per plant (main yield contributing traits), chances of recovery for transgressive segregants for seed cotton yield is very high.

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