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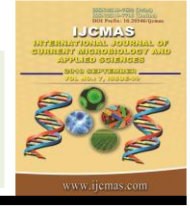

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Estimation of Genetic Variability Parameters in F_2 Population of *Gossypium hirsutum* L. for Yield, Yield Attributes and Fiber Quality Traits

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A B S T R A C T

Cotton is a crop of prosperity having a profound influence on men and matter. The assessment of genetic variability is prerequisite for organization of breeding programmes in any crop. Experiment on estimation of genetic variability parameters in F_2 population of cross a RHAP 24 × RHAP 15 was carried out at College of Agriculture, UAS Dharwad during *kharif* 2016-17. In the present investigation yield and yield attributes *viz.*, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight and seed cotton yield exhibited high PCV and GCV whereas, medium PCV and GCV was observed for plant height and maturity ratio. The fibre quality traits *viz.*, upper half mean length, fibre uniformity ratio, fibre strength, strength to length ratio and fibre elongation percentage exhibited low PCV and GCV. In the present study plant height, boll weight and seed cotton yield per plant exhibited high broad sense heritability coupled with high genetic advance as per cent mean (GAM). Simple selection is effective for the traits exhibiting high heritability and high genetic advance.

Introduction

Cotton (*Gossypium spp*.), the white gold has been principal commercial crop of world since time immemorial. Despite the increasing production of artificial fibres which was thought to threaten the existence of cotton some time back, it has flourished. Now, the world has turned its attention towards this crop as a natural fibre which is environment friendly and biodegradable. Till today the crop, cotton has maintained its prime place as king of fibre. Due to its global importance in agriculture as well as industrial economy, in India it provides direct employment to around 35 million people (Mohan Kumar and Katageri, 2017). Indian textile industry predominantly depends on cotton (60 %) and contributes around five per cent to the country's gross domestic product (GDP). Contribution to industrial production is 14 per cent and to exports earnings is 11 per cent, providing employment to over 51 million people directly and 68 million people indirectly (Mohan Kumar and Katageri, 2017).

There are four commercially cultivated cotton species for natural fibre. Among them, two are diploid (2n = 2x = 26) old world or Asiatic cotton *viz.*, *G. arboretum* (A_2) and *G. herbaceum* (A_1). Remaining two are allotetraploid (2n = 4x = 52) new world cotton *viz., G. hirsutum* (AD_1) and *G. barbadense* (AD_2) (Wendel *et al.,* 2009). Upland cotton *G. hirsutum* popularly known as medium and long staple cotton or Mexican cotton occupies 95 per cent of the world's cotton production.

Knowledge of the nature and magnitude of genotypic and phenotypic variability present in any crop species plays a vital role in formulating successful breeding programme for evolving superior cultivars. Creating genetic variability is pre-requisite for plant breeders to exercise selection, as a part of continuous variation is due to heredity (Ranganatha *et al.*, 2013). The phenotypic and genotypic coefficients of variation are 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 and genetic advance as per cent mean are also estimated. The present investigation was carried out to estimate the magnitude of genetic variability, heritability and genetic advance for yield, yield attributes and fibre quality traits in F_2 segregating population of cotton.

Materials and Methods

The present study was carried out in the Botanical garden, Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad. During *kharif* 2015. Two stabilized lines RHAP 24 and RHAP 15 of *G. hirsutum* were crossed to get F_1s. The line RHAP 24 is characterized with high fibre strength, high fibre length and low yield potential as compared to RHAP 15. Characteristics of parents for fiber quality traits and other qualitative traits are presented in Table 1 and Table 2. A dominant morphological marker, pubescence of leaf present on male parent (RHAP 15) was used to identify true F_1s. A large F_2 segregating population was developed by selfing of true F_1s during summer 2016.

In order to estimate the magnitude of genetic variability, heritability and genetic advance for yield, yield attributes and fibre quality traits, in the present investigation a total of 278 F_2 individuals along with parents and F_1s were raised during *kharif* 2016. 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 6 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 15 plant from parents, 10 plants from F_1s and all the 278 F_2 individuals for seed cotton yield, yield attributes and fiber quality traits *viz.*, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), ginning outturn (%), seed index (g) lint index (g), seed cotton yield per plant (g). upper half mean length (mm), fiber uniformity ratio in percentage, fiber strength (g tex^{-1}), strength to length ratio, fiber elongation per cent, maturity ratio and micronaire (µg $inch^{-1}$). The mean and variance were analyzed based on the formula given by Singh and Choudhary (1977) and the genetic components of variation were estimated with the help of given formula.

Phenotypic variance

The individual observation made for each trait on F_2 population was used for calculating the phenotypic variance.

Phenotypic variance (σ^2_p) = Var F_2

Where,

Var F_2 = variance of F_2 population

Environmental variance

Since the replication is not possible for F_2 population, the average variance of parents and their corresponding $F_1$was used to estimate the environmental variance.

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

Where,

$\sigma^2 p_1$ = Variance of parent P_1

$\sigma^2 p_2$ = Variance of parent P_2

$\sigma^2 F_1$ = Variance of cross F_1

Genotypic variance

Genotypic variance $(\sigma^2_g) = \sigma^2_p - \sigma^2_e$
σ^2_p = Phenotypic variance
σ^2_e = Environmental variance

Genetic advance (GA)

Genetic advance as per cent mean was categorized as low, moderate and high as given by Johnson *et al.*, (1955).

$GA = h^2 K \sigma_p$

Where,

h^2 = Heritability in broad sense

K = Selection intensity which is equal to 2.06 at 5 per cent intensity of selection

σ_p = Phenotypic standard deviation

Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{\bar{x}} \times 100$$

Where,

GA = Genetic advance
$\bar{x}$ = General mean of the character

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). The genetic advance was computed by using the formula given by Robinson *et al.*, (1949). The genetic advance as per cent mean was categorized as low up to 10 per cent, 10 to 20 per cent consider as a moderate and more than 20 per cent noticed as a high (Johnson *et al.*, 1955).

Results and Discussion

Variability is the prerequisite for organization of breeding programmes and its estimates helps in realization of response to selection as the progress in breeding depends upon its amount, nature and magnitude of variability (Singh and Narayanam, 2013).

In the present investigation, majority of the traits registered a wide range of variability is presented in Table 3. The graphical representation of PCV, GCV, heritability and GAM in F_2 segregating generation of cotton is depicted in Figure 1. 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 yield and yield attributes *viz*., number of monopodia per plant (35.07 %), number of sympodia per plant (31.03 %), number of bolls per plant (45.70 %), boll weight (28.39 %) and seed cotton yield (56.19 %) exhibited high PCV. Correspondingly the traits, number of monopodia per plant (26.33 %), number of sympodia per plant (22.21 %), number of bolls per plant (29.68 %), boll weight (22.83 %) and seed cotton yield (51.93 %) exhibited high GCV whereas, medium PCV and GCV was observed for plant height and maturity ratio. However, fibre quality traits *viz*., upper half mean length, fibre uniformity ratio, fibre strength, strength to length ratio and fibre elongation percentage exhibited low PCV and GCV. Similar findings were observed by Tuteja *et al*., (2008), Choudki *et al*., (2012), Vineela *et al*., (2013), Dhivya *et al*., (2014), Fakhar *et al*., (2015), Nagaraju (2016) and Mohan Kumar and Katageri (2017).

The ratio of genotypic variance to the phenotypic variance or total variance is known as heritability. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1981). In the present investigation high heritability was recorded for traits, plant height (64.58 %), boll weight (64.64 %), ginning outturn (78.26 %) seed cotton yield per plant (85.43 %), upper half mean length (77.86 %) fiber strength (63.45 %), fiber elongation per cent (64.44 %) and maturity ratio (81.23 %). Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. The genetic advance is the measure of genetic gain under selection. The success of trait under selection depends on genetic variability, heritability and selection (Allard, 1960). Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al*., 1955).

Table.1 Characteristics of parents for fibre quality traits (Summer 2015)

Genotype	UHML	FUR	FS	FEL	MIC	MR	S/L
RHAP-24	30.40	91.90	31.10	6.60	3.23	0.55	1.02
RHAP-15	25.10	84.50	23.20	6.90	3.54	0.55	0.92

Where, UHML- Upper Half Mean Length of fibre in mm, FUR- Fibre Uniformity Ratio in per cent, FS- Fibre Strength in g tex^{-1}, FEL-Fibre Elongation in percent, MIC- Micronaire value in µg inch^{-1}, MR- Maturity Ratio, S/L- Strength over the Length ratio.

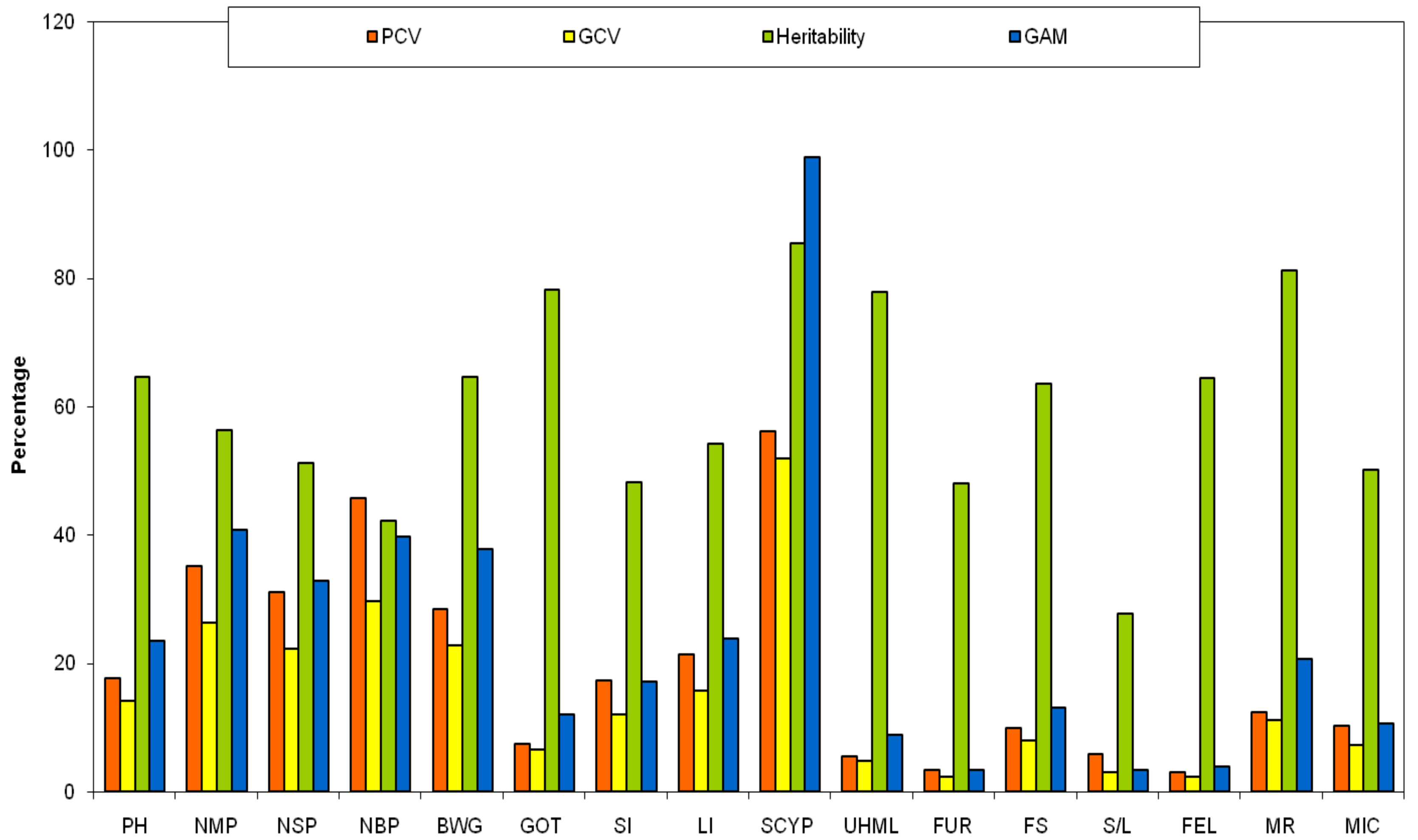
Table.2 Characteristics of parents for qualitative traits

RHAP 24	RHAP 15
• **Thin leaf** • **Medium maturity** • **Less pubescent** • **Susceptible to sucking pest** • **Good fibre quality**	• Thick leaf • Late maturity • High pubescent • Tolerant to sucking pest • Poor fibre quality

Table.3 Genetic variability parameters for 16 quantitative traits in F_2 populations derived from the cross RHAP 24 × RHAP 15

Characters	Mean of P_1	Variance of P_1	Mean P_2	Variance of P_2	Mean of F_1	Variance F_1	Mean of F_2	Maximum in F_2	Minimum in F_2	PCV (%)	GCV (%)	h^2 (bs) (%)	GA	GAM
PH	140.00	174.22	166.30	260.23	166.90	99.43	126.88 ± 1.34	190.00	70.00	17.67	14.20	64.58	29.82	23.50
NMP	3.10	0.54	2.90	0.54	3.10	0.32	2.96 ± 0.06	7.00	0.00	35.07	26.33	56.36	1.21	40.72
NSP	13.10	12.10	17.90	4.10	15.80	3.29	11.76 ± 0.22	23.00	5.00	31.03	22.21	51.24	3.85	32.75
NBP	48.50	267.61	69.20	211.51	52.60	168.93	42.30 ± 1.159	96.00	6.00	45.70	29.68	42.19	16.80	39.72
BWG	2.99	0.20	3.64	0.94	4.45	0.29	4.09 ± 0.07	7.17	1.30	28.39	22.83	64.64	1.54	37.81
GOT	31.12	1.47	35.98	1.64	35.70	1.43	35.62 ± 0.16	39.71	29.00	7.41	6.56	78.26	4.26	11.95
SI	7.72	0.60	10.22	1.34	8.42	1.21	8.27 ± 0.085	12.10	5.80	17.21	11.94	48.14	1.41	17.06
LI	3.48	0.08	5.77	0.77	4.68	0.46	4.60 ± 0.59	7.62	2.55	21.38	15.74	54.16	1.12	23.86
SCYP	140.00	1100.00	242.40	1702.04	228.40	1412.71	174.72 ± 5.88	428.00	20.00	56.19	51.93	85.43	172.78	98.88
UHML	31.23	0.42	24.52	0.83	25.52	3.14	27.23 ± 0.09	31.20	22.00	5.50	4.85	77.86	1.07	8.82
FUR	83.61	5.69	81.78	4.25	80.96	3.58	86.04 ± 0.18	93.10	77.10	3.42	2.37	48.00	2.91	3.38
FS	32.89	3.39	24.01	0.81	24.70	0.93	28.95 ± 0.17	34.70	23.10	9.97	7.94	63.45	4.72	13.03
S/L	1.05	0.00	0.98	0.00	0.97	0.01	1.06 ± 0.003	1.21	0.94	5.74	3.02	27.71	0.03	3.28
FEL	5.28	0.01	5.34	0.00	5.31	0.00	5.23 ± 0.009	5.90	4.70	2.94	2.36	64.44	0.27	3.91
MR	0.55	0.00	0.67	0.00	0.51	0.00	0.57 ± 0.004	0.90	0.43	12.32	11.10	81.23	0.12	20.61
MIC	3.10	0.10	4.08	0.07	3.05	0.02	3.48 ± 0.02	4.68	2.48	10.27	7.27	50.10	0.37	10.60

Where, PH-Plant Height in cm, NMP- Number of Monopodia per Plant, NSP- Number of Sympodia per Plant, NBP- Number of Bolls per Plant, BWG- Boll Weight in Grams, GOT- Ginning Outturn in per cent, SI- Seed Index, LI- Lint Index, SCYP- Seed Cotton Yield per Plant in grams, UHML- Upper Half Mean Length in mm, FUR- Fibre Uniformity Ratio in per cent, FS- Fibre Strength in g tex^{-1}, S/L- Strength over the Length ratio, FEL-Fibre Elongation in per cent, MR- Maturity Ratio and MIC- Micronaire value in µg $inch^{-1}$.



PH-Plant Height in cm, **NMP**- Number of Monopodia per Plant, **NSP**- Number of Sympodia per Plant, **NBP**- Number of Bolls per Plant, **BWG**- Boll Weight in Grams, **GOT**- Gining Outturn in *per cent*, **SI**- Seed Index, **LI**- Lint Index, **SCYP**- Seed Cotton Yield per Plant in grams, **UHML**- Upper Half Mean Length in mm, **FUR**- Fiber Uniformity Ratio in *per cent*, **FS**- Fiber Strength in g tex^{-1}, **S/L**- Strength over the Length ratio, **FEL**-Fiber Elongation in *per cent*, **MR**- Maturity Ratio and **MIC**- Micronaire value in µg $inch^{-1}$

Fig. 1. Graphical representation of PCV, GCV , Heritability and GAM in segregating generation of *G. hirsutum*

High genetic advance as per cent of mean (GAM) was recorded for the traits, plant height (23.50 %), number of monopodia per plant (40.72 %), number of sympodia per plant (32.75 %), number of bolls per plant (39.72 %), boll weight (37.81 %), lint index (23.86 %), seed cotton yield per plant (98.88 %) and maturity ratio (20.61 %).

In the present study plant height, boll weight and seed cotton yield per plant exhibited high broad sense heritability coupled with high genetic advance as per cent mean (GAM). The results indicated that simple selection is easy and effective to improve these traits. These results are in agreement with the reports made by Gitte *et al.*, (2007), Choudki *et al.,* (2012), Tuteja *et al.*, (2006), Muhammad *et al.*, (2015), Ahsan *et al.*, (2015) and Nagaraju (2016).

The traits, number of monopodia, numer of sympodia and number of bolls per plant exhibited medium heritability and high GAM. High heritability and medium genetic advance was observed for the traits, fibre strength, upper half mean length, fibre elongation and maturity ratio. The results indicated that inheritance of these traits is complex traits. These results are in agreement with the reports made by Choudki *et al.*, (2012), Tuteja *et al.,* (2006) and Nagaraju (2016).

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