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.

**Keywords**
Heritability, Genetic variability, PCV, GCV and GAM

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**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 species...
viz., *G. hirsutum* (AD₁) and *G. barbadense* (AD₂) (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 *F₂* 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 *F₁*’s. 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 *F₁*’s. A large *F₂* segregating population was developed by selfing of true *F₁*’s 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 *F₂* individuals along with parents and *F₁*’s 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 *F₁*’s and all the 278 *F₂* 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 *F₂* population was used for calculating the phenotypic variance.

Phenotypic variance \( (\sigma_{p}^{2}) = \text{Var } F_{2} \)
Where,

\[ \text{Var } F_2 = \text{variance of } F_2 \text{ population} \]

**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.

\[
\text{Environmental variance (} \sigma^2_e \text{)} = \frac{(\sigma^2_{p1}) + (\sigma^2_{p2}) + (\sigma^2_{F1})}{3}
\]

Where,

\[ \sigma^2_{p1} = \text{Variance of parent } P_1 \]
\[ \sigma^2_{p2} = \text{Variance of parent } P_2 \]
\[ \sigma^2_{F1} = \text{Variance of cross } F_1 \]

**Genotypic variance**

Genotypic variance (\( \sigma^2_g \)) = \( \sigma^2_p - \sigma^2_e \)

\[ \sigma^2_p = \text{Phenotypic variance} \]
\[ \sigma^2_e = \text{Environmental variance} \]

**Genetic advance (GA)**

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

\[ \text{GA} = h^2 K \sigma_p \]

Where,

\[ h^2 = \text{Heritability in broad sense} \]
\[ K = \text{Selection intensity which is equal to 2.06 at 5 per cent intensity of selection} \]
\[ \sigma_p = \text{Phenotypic standard deviation} \]

Genetic advance as per cent of mean (GAM)

\[ \text{GAM} = \frac{\text{GA}}{\bar{x}} \times 100 \]

Where,

\[ \text{GA} = \text{Genetic advance} \]
\[ \bar{x} = \text{General mean of the character} \]

**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                   | Thick leaf                  |
| Medium maturity             | Late maturity               |
| Less pubescent              | High pubescent              |
| Susceptible to sucking pest | Tolerant to sucking pest    |
| Good fibre quality          | Poor fibre quality          |
Table 3 Genetic variability parameters for 16 quantitative traits in F₂ populations derived from the cross RHAP 24 × RHAP 15

| Characters | Mean of P₁ | Variance of P₁ | Mean P₂ | Variance of P₂ | Mean F₁ | Variance F₁ | Mean of F₂ | Variance F₂ | Maximum in F₂ | Minimum in F₂ | PCV (%) | GCV (%) | h² (bs) | GA | GAM |
|------------|------------|----------------|---------|----------------|---------|-------------|------------|-------------|---------------|---------------|---------|---------|---------|----|-----|
| PH         | 140.00     | 174.22         | 166.30  | 260.23         | 166.30  | 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    | 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   | 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   | 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    | 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   | 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    | 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    | 4.60 ± 0.59   | 7.62       | 2.55        | 21.38         | 15.74         | 51.16   | 1.12    | 23.86   |    |     |
| SCYP       | 140.00     | 1100.00        | 242.40  | 1702.04        | 228.40  | 1412.71      | 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       | 7.41          | 6.56          | 78.26   | 4.26    | 11.95   |    |     |
| FUR        | 83.61      | 5.69           | 81.78   | 4.25           | 80.96   | 3.58         | 86.04 ± 0.18 | 93.10       | 7.41          | 6.56          | 78.26   | 4.26    | 11.95   |    |     |
| FS         | 32.89      | 3.39           | 24.01   | 0.81           | 24.70   | 0.93         | 28.95 ± 0.17 | 34.70       | 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    |    |     |
| 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    |    |     |
| 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    |    |     |
| 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    |    |     |

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.
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, number 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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