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# ESTIMATION OF GENETIC PARAMETERS FOR YIELD AND FIBER QUALITY TRAITS IN UPLAND COTTON GENOTYPES (*GOSSYPIUM HIRSUTUM* L.)

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## ABSTRACT

The present investigation was undertaken to assess genetic variability, heritability, and genetic advance for 15 agronomic and fibre-related traits in thirty-six genotypes of upland cotton (Gossypium hirsutum L.). The experiment was conducted during the winter season of 2020 at the Cotton Research Station, Junagadh Agricultural University, India. Analysis of variance indicated the presence of highly significant differences among genotypes for all the traits studied, reflecting substantial genetic variability within the experimental material. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for number of bolls per plant, followed by number of monopodia per plant, seed cotton yield per plant, and number of sympodia per plant, suggesting the predominance of additive gene action and greater scope for selection. Furthermore, high heritability coupled with high genetic advance as percent of mean was observed for number of bolls per plant, number of monopodia per plant, seed cotton yield per plant, number of sympodia per plant, boll weight, lint index, fibre fineness, plant height, and seed index, indicating the effectiveness of direct selection for the improvement of these traits.

***Key words*:** Heritability, GCV, PCV, Genetic advance, Variability

## Introduction

Cotton is a globally important crop and a major source of natural fibre for the textile industry. Often referred to as "white gold" or the "king of fibres," it holds a significant position in the agricultural economy of India. Majority of plant trichomes are multicellular, but *Gossypium* spp. produce unicellular seed trichomes known as fibre, making cotton the leading cash crop with significant economic and social impact on Indian economy (Boopathi *et al.*, 2011). Cotton has long been considered the backbone of the non-food crop sector and contributes substantially to foreign exchange earnings through the export of lint and value-added products. Although India has achieved self-sufficiency in cotton production, a decline in the cultivated area and relatively low productivity compared to other cotton-growing countries remain major concerns. Therefore, the development of high-yielding cultivars with desirable fibre quality traits is essential to enhance overall productivity.

A crop improvement program's success is contingent upon the extent of genetic variability in the breeding material. In this regard, phenotypic and genotypic coefficients of variation are important tools for assessing the extent of variability present in different traits. However, these measures alone do not provide information about the transmissible (heritable) portion of variation. Hence,

**Table 1:** Analysis of variance for various characters in 36 genotypes of cotton.

| Source of variation | d.f. | Seed index (g) | Ginning (%) | Lint index (g) | Oil content (%) | 2.5 % Span length (mm) | Fibre strength (g/tex) | Source of variation |
|---|---|---|---|---|---|---|---|---|
| **Replications** | 2 | 0.01 | 0.01 | 0.03 | 0.01 | 0.01 | 0.01 | 0.015 |
| **Genotypes** | 35 | 15.35** | 3.66** | 1.60** | 0.18** | 9.06** | 15.25** | 1.17** |
| **Error** | 70 | 1.27 | 0.59 | 0.26 | 0.01 | 1.13 | 1.16 | 0.19 |

***Continue ...1***

| Source of variation | d.f. | Days to flowering | Days to boll opening | Plant height (cm) | Number of monopodia per plant | Number of sympodia per plant | Number of bolls per plant | Boll weight (g) | Seed cotton yield per plant (g) |
|---|---|---|---|---|---|---|---|---|---|
| **Replications** | 2 | 1.36 | 4.23 | 0.14 | 0.04 | 0.32 | 0.25 | 0.01 | 1.36 |
| **Genotypes** | 35 | 73.90** | 250.61** | 724.53** | 2.12** | 48.83** | 282.52** | 1.26** | 1768.21** |
| **Error** | 70 | 2.36 | 3.49 | 103.74 | 0.12 | 2.97 | 14.13 | 0.08 | 129.92 |

the estimation of heritability along with genetic advance and genetic advance as percent of mean is necessary to predict the effectiveness of selection.

Heritability alone cannot fully determine the expected genetic gain, as the response to selection also depends on the magnitude of genetic advance under a given selection pressure. Therefore, a combined assessment of variability parameters, heritability, and genetic advance provides a reliable basis for identifying traits amenable to improvement through selection. Such information is essential for developing efficient breeding strategies aimed at enhancing yield and associated traits in upland cotton (*Gossypium hirsutum L.*).

## Materials and Methods

Thirty-six genotypes of upland cotton (*Gossypium hirsutum* L.) were evaluated at the Cotton Research Station, Junagadh Agricultural University, during the winter season of 2020. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was grown in a single-row plot with a spacing of 120 cm between rows and 45 cm between plants. Recommended agronomic practices, including fertilizer application and plant protection measures, were followed to ensure proper crop growth. Observations on fifteen quantitative traits comprising phenological, yield, and fibre quality characters were recorded from five randomly selected plants per genotype per replication.

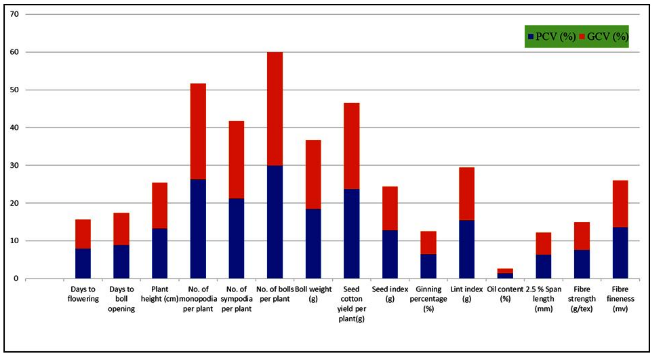

**Fig. 1:** Graphical representation of phenotypic and genotypic coefficient of variation for various characters of cotton.

Oil content was determined using Nuclear Magnetic Resonance (NMR) technique following Tiwari *et al.*, (1974). The 2.5% span length (mm) was measured from a 100 g seed cotton sample using standard fibre testing procedures. Fibre strength (g/tex) was measured using a stelometer at 3.2 mm gauge length and expressed as tenacity. Fibre fineness was measured as micronaire value (mv), expressed in micrograms per inch ($10^{-6}$ g/inch), where higher values indicate coarser fibres and lower values indicate finer fibres.

Analysis of variance (ANOVA) was performed to assess the significance of differences among genotypes as per Panse and Sukhatme (1985). The GCV and PCV were calculated as per the formula proposed by Burton (1952) categorized as low (<10%), medium (10-20%) and high (>20%). Heritability and genetic advance estimated by formula given by Allard (1960), genetic advance classified as low (<10%), medium (10-20%) and high (>20%) and Categorization of a range for heritability estimation was given by Searle (1965) like low (<40%), moderate (40-60%), high (40-80%) and very high (>80%). Derived parameters were computed using the following standard equations:

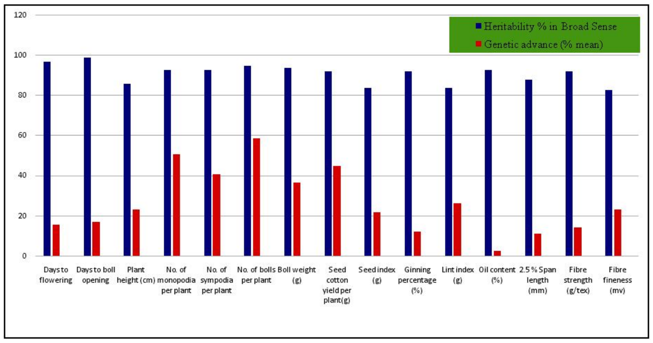

**Fig. 2:** Graphical representation of heritability and genetic advance expressed as percent of mean for various characters of cotton.

**Table 2:** Mean, phenotypic range, $\sigma^2_g$, $\sigma^2_p$, $\sigma^2_e$, GCV %, PCV %, heritability, genetic advance, genetic advance per cent of mean for fifteen characters of cotton.

| Character | Mean±SE | Range | | $\sigma^2_g$ | $\sigma^2_p$ | $\sigma^2_e$ | PCV (%) | GCV (%) | HBS | GA | GAM |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Min. | Max. | | | | | | | | |
| **Days to flowering** | 63.11±0.87 | 56.00 | 76.67 | 23.84 | 24.63 | 0.79 | 7.86 | 7.73 | 96.81 | 9.90 | 15.68 |
| **Days to boll opening** | 106.99±1.06 | 97.00 | 135.67 | 82.37 | 83.54 | 1.17 | 8.84 | 8.48 | 99.00 | 18.57 | 17.35 |
| **Plant height (cm)** | 117.62±5.80 | 88.63 | 154.67 | 206.93 | 241.51 | 34.68 | 13.21 | 12.23 | 86.00 | 27.43 | 23.32 |
| **No. of monopodia per plant** | 3.21±0.20 | 1.33 | 5.00 | 0.77 | 0.70 | 0.04 | 26.23 | 25.43 | 93.00 | 1.63 | 50.76 |
| **No. of sympodia per plant** | 19.03±0.98 | 12.20 | 26.00 | 15.29 | 16.28 | 0.99 | 21.20 | 20.54 | 93.00 | 7.80 | 41.01 |
| **No. of bolls per plant** | 32.40±2.13 | 18.30 | 67.60 | 89.46 | 94.17 | 4.70 | 29.96 | 29.96 | 95.00 | 18.99 | 58.63 |
| **Boll weight (g)** | 3.41±0.16 | 2.47 | 5.17 | 0.39 | 0.42 | 0.03 | 18.35 | 18.35 | 94.00 | 1.25 | 36.62 |
| **Seed cotton yield per plant(g)** | 102.49±43.30 | 55.90 | 162.07 | 546.09 | 589.40 | 43.30 | 23.69 | 22.80 | 92.00 | 46.33 | 45.21 |
| **Seed index (g)** | 8.69±0.43 | 7.00 | 12.00 | 1.03 | 1.22 | 0.19 | 12.69 | 11.64 | 84.00 | 1.91 | 21.98 |
| **Ginning percentage (%)** | 35.24±0.64 | 30.77 | 39.23 | 4.69 | 5.12 | 0.42 | 6.42 | 6.14 | 92.00 | 4.27 | 12.54 |
| **Lint index (g)** | 4.74±0.29 | 3.77 | 7.20 | 0.45 | 0.53 | 0.09 | 15.41 | 14.09 | 84.00 | 1.26 | 26.57 |
| **Oil content (%)** | 18.26±0.06 | 17.66 | 18.87 | 0.05 | 0.06 | 0.01 | 1.35 | 1.30 | 93.00 | 0.47 | 2.59 |
| **2.5 % Span length (mm)** | 27.75±0.60 | 24.40 | 31.40 | 2.65 | 3.02 | 0.38 | 6.26 | 5.86 | 88.00 | 3.14 | 11.29 |
| **Fibre strength (g/tex)** | 29.62±0.61 | 25.43 | 34.43 | 4.69 | 5.08 | 0.38 | 7.61 | 7.31 | 92.00 | 4.29 | 14.48 |
| **Fibre fineness (mv)** | 4.60±0.25 | 3.53 | 5.73 | 0.32 | 0.39 | 0.06 | 13.59 | 12.41 | 83.00 | 1.07 | 23.34 |

HBS: Heritability % in Broad Sense; GA: Genetic advance; GAM: Genetic advance (% mean)
Where, $\sigma^2_g$, $\sigma^2_p$ and $\sigma^2_e$ are the genotypic, phenotypic and environmental variance, respectively. GCV % and PCV % are genotypic and phenotypic coefficients of variation, respectively

**Ginning percentage (%):**

$$\text{Ginning (\%)} = \frac{\text{Weight of lint (g)}}{\text{Weight of seed cotton (g)}} \times 100$$

**Lint index (g):**

$$\text{Lint index} = \frac{\text{Seed index (g)} \times \text{Ginning (\%)}}{100 - \text{Ginning (\%)}}$$

**Fibre strength (g/tex):**

$$\text{Tencity (g/tex)} = \frac{\text{Breaking load (kg)} \times 11.8}{\text{Bundle weight (mg)}}$$

## Results and Discussion

The mean sum square due to genotypes showed the significance difference for all characters, suggesting considerable amount of variability existed among all the genotypes (Table 1). The number of bolls per plant, number of monopodia per plant, number of sympodia per plant, and seed cotton yield per plant all had the greatest GCV and PCV values. This indicated the little presence of wide genetic variation for these traits. According to estimations of the genotypic and phenotypic coefficients of variability, the phenotypic coefficient of variation values were significantly greater than those of genotypic coefficient of variation for all the traits studied, indicating the little effect of environment on the expression of characters studied. (Gauswami *et al.*, 2020; Chaudhari 2017 and Dahiphale *et al.*, 2015). Very high heritability estimates were observed for days to flowering, days to boll opening, number of bolls per plant, boll weight, number of monopodia, number of sympodia per plant, oil content, seed cotton yield, ginning percentage, fiber strength, 2.5% span length, plant height, seed index, lint index and fiber fineness indicating that these characteristics have a considerable level of heritable variation. (Batti *et al.*, 2020 and Gauswami *et al.*,). For seed cotton yield per plant, high estimates of genetic advance as a percentage of mean were found followed by plant height, number of bolls per plant, days to boll opening and days to flowering (Gnanasekaran *et al.*, 2020). The number of sympodia per plant showed moderate levels of genetic advancement as a percentage of the mean Afterwards, fiber fineness, boll weight, seed index, fiber strength, ginning percentage, and 2.5% span length (Joshi and patil 2018 and Batti *et al.*, 2020). Conversely, low genetic advance as per cent of mean were noted for the oil content. The number of bolls per plant, number of monopodia per plant, seed cotton yield per plant, number of sympodia per plant, boll weight, lint index, fiber fineness, plant height, and seed index all showed high heritability and high genetic advance as a percentage of mean, indicating the significant role of additive gene action in the inheritance of these characters and suggesting direct selection would be effective for improving these traits. (Bardak *et al.*, 2019; Batti *et al.*, 2020).

## Conclusion

It can be concluded from the present findings that additive gene action governs traits such as number of bolls per plant, followed by number of monopodia per plant, seed cotton yield per plant, number of sympodia per plant, boll weight, lint index, fibre fineness, plant height, and seed index, as these traits exhibited high heritability coupled with high genetic advance. Therefore, direct selection for these traits would be effective in improving yield and associated characteristics in upland cotton (*Gossypium hirsutum* L.).

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