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Vrinda Joshi
Department of Genetics and
Plant Breeding, College of
Agriculture, UAS, Dharwad,
Karnataka, India

BR Patil
Department of Genetics and
Plant Breeding, College of
Agriculture, UAS, Dharwad,
Karnataka, India

Genetic variability and heritability study in F₂ population for yield, yiled attributes and Fibre quality traits in cotton (*Gossypium hirsutum* L.)

Vrinda Joshi and BR Patil

Abstract
The success of most crop improvement programmes depends on variability and heritability of desirable traits. An investigation was carried out during *kharif* 2017 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 F₂ generation of cross RHAP-12 × RHAP-7. The segregating population thus obtained was evaluated for sixteen quantitative traits. A wide range of variation was observed for traits number of monopodia per plant, boll weight and seed cotton yield per plant. High phenotypic coefficient of variation and genotypic coefficient of variation were recorded for traits monopodia per plant, boll weight and seed cotton yield per plant. High heritability coupled with moderate to high genetic advance was recorded for all traits under consideration in the F₂ population. Most of the characters including seed cotton yield per plant recorded high heritability couple with moderate to high genetic advance as per cent of mean.

Keywords: variability, genetic advance, cotton and heritability

Introduction
Cotton (*G. hirsutum*) is an important fiber crop grown in India. It is often cross pollinated crop in which large amount of variation is observed for many important traits. The success of any breeding programme depends on the spectrum of genetic variability present in the population. In addition to genetic variability, knowledge on heritability and genetic advance helps the breeder to employ a suitable breeding strategy to achieve the objective. Burton (1952) [2] and Swarup and Chaugle (1962) [11] indicated that genetic variability together with the heritability estimates would give on the amount of genetic advance expected out of selection. Yield is a complex character which depends upon several component characters. Therefore, direct selection for yield is often not effective.

In cotton crop, genotypic and phenotypic variation for different quantitative and qualitative traits such as plant height, number of monopodia, number of sympodia, number of bolls per plant, seed index, lint index, micronaire value and seed cotton yield has been studied by several earlier research workers such as Neelam and Potdukhe (2002) [5], Sakthi *et al.* (2007) [8] and Dhamayanathi *et al.* (2010) [3].

The genetic improvement in cotton crop is depends on the existence of initial genetic variability among the populations. The initial variability and the degree of correlations amongst yield and yield attributes are of prime importance for developing superior genotypes of cotton. A study was conducted with the objective of evaluating the variability in *Gossypium hirsutum* genotypes for yield and yield attributes to analyze its heritable components of the actual variability for making selections for breeding programme.

Material 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* 2016 by crossing two stabilized lines of *G. hirsutum* (RHAP-12 and RHAP-7) species. The experimental material for the present study involved F₂ cross which was developed by selfing F₁s developed by crossing two genetically diverse genotypes viz. RHAP-12 X RHAP-7. The F₂ generation was raised during *kharif* 2017.

The mean and variance were analyzed based on the formula given by Singh and Choudhary (1977) [9]. Both genotypic and phenotypic coefficients of variation were computed as per the method suggested by Burton and Devane (1953) [1]. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were classified as suggested by Sivasubramanian and Menon (1973) [10] that are, low (< 10 %), moderate (10 - 20 %) and high (> 20 %). The

Correspondence
Vrinda Joshi
Department of Genetics and
Plant Breeding, College of
Agriculture, UAS, Dharwad,
Karnataka, India

heritability percentage was classified as low (0-30%), moderate (30–60%) and high (> 60%) by Robinson *et al.,* (1949) [7]. Genetic advance was computed by using the formula given by Robinson *et al.,* (1949) [7] 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) [4].

Results and Discussion
For most of the traits wider range of variability was observed because significant difference between parents for all these traits (Table 1). Previously many studies well beyond doubt it proved that higher variability is expected when diverse parents are used in generating segregating population (Aman 2016) [10].

The presence of variability coupled with higher PCV and GCV again supports presence of wider genetic variability in the F_2 population. The presence of higher, moderate and lower PCV for different traits was due to the higher, moderate and low range of variability in F_2 population respectively. For example traits like number of monopodia per plant, number of bolls per plant, boll weight and seed cotton yield per plant recorded higher PCV and GCV with higher range variability. Similarly plant height, number of symposia per plant, seed index, lint index and fibre strength recorded moderate PCV and GCV may be due to moderate range of variability. Most of the fibre quality traits except fibre strength indicated low

PCV and GCV indicating less variability for these traits. The narrow difference between genotypic coefficient of variation and phenotypic coefficient of variation indicated that characters were less affected by environment and variation is mainly due to genetic component. Comparison between GCV and PCV depicted in Fig. 1. Number of monopodia per plant, number of sympodia per plant, boll weight and seed cotton yield were recorded higher PCV and GCV, which indicated the presence of large amount of variation, it may be due to presence of significant difference between parents for these traits. Similarly in F_4 populations of upland cotton Raza *et al.* (2016) [6] 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) [3] 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

Heritability estimates along with genetic advance as per cent mean will be more useful in predicting the outcome of selecting the best individuals. In the present study plant height, sympodia per plant, seed index, lint index, boll weight, seed cotton yield, bolls per plant, ginning outturn, fibre strength, micronaire value, maturity ratio and fibre elongation recorded higher heritability with high to moderate GAM indicating the predominance of additive gene action, which enhances the early fixation of genes responsible for transgressive segregation through pedigree method of selection.
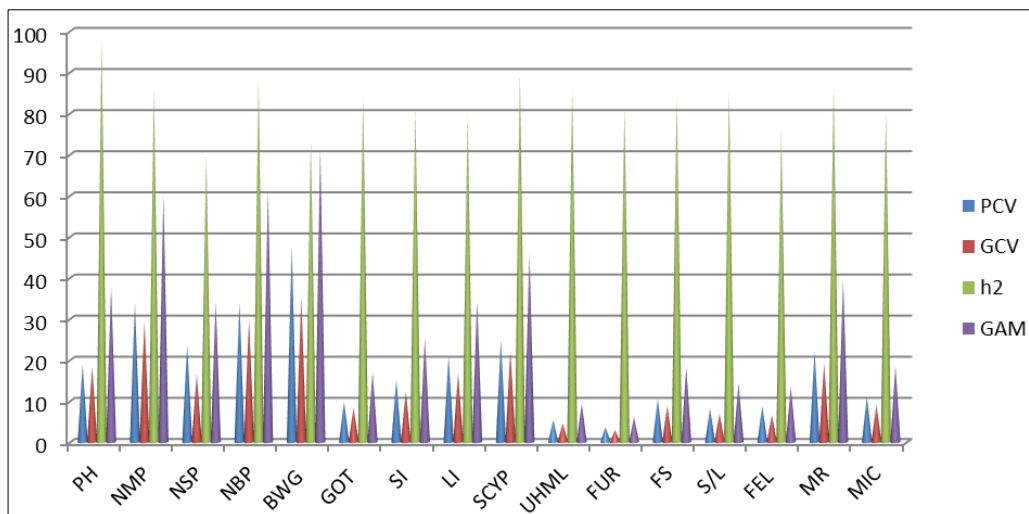

Fig 1: Comparison between PCV, GCV, heritability and GAM for yield, yield attributes and fibre quality traits in the F_2 population of cotton

Table 1: Mean, Range, Variance, GCV, PCV, h^2 and GAM for yield, yield attributes and fibre quality traits in the F_2 population of cotton

	Mean	**Max**	**Min**	**PCV**	**GCV**	**h^2**	**GA**	**GAM**
PH	143.76	205.00	70.00	18.80	18.37	97.75	54.41	37.85
NMP	2.89	7.00	1.00	33.99	29.25	86.06	1.74	60.26
NSP	10.65	20.00	4.00	23.60	16.53	70.05	3.63	34.06
NBP	18.29	46.00	6.00	33.91	29.90	88.20	11.27	61.60
BWG	3.37	7.83	1.00	47.66	34.90	73.23	2.43	71.90
GOT	33.53	40.33	25.10	9.86	8.29	84.11	5.73	17.09
SI	6.75	9.68	4.64	15.08	12.27	81.39	1.71	25.28
LI	3.43	5.38	2.14	21.03	16.75	79.67	1.18	34.51
SCYP	108.15	209.00	57.00	24.77	22.22	89.69	49.50	45.77
UHML	25.48	29.00	20.60	5.34	4.60	86.08	2.41	9.47
FUR	81.15	88.30	71.90	3.63	2.96	81.60	4.95	6.10
FS	23.32	31.20	18.50	10.55	8.85	83.84	4.25	18.23
S/L	0.91	1.28	0.75	8.13	6.94	85.37	0.13	14.30
FEL	4.31	5.40	3.30	8.71	6.59	75.71	0.58	13.58

MR	0.60	1.48	0.46	22.13	19.14	86.50	0.24	39.43
MIC	3.72	5.39	2.84	11.13	8.97	80.61	0.69	18.48

Where, PH-Plant Height (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 percent, SI- Seed Index, LI- Lint Index, SCYP- Seed Cotton Yield per Plant in grams, UHML- Upper Half Mean Length, FUR- Fiber Uniformity Ratio, FS- Fiber Strength, S/L- Ratio of strength to length, FEL-Fiber Elongation in percent, MR- Maturity Ratio, MIC- Micronair value in µg/inch.

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