The Pharma Innovation

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Genetic variability studies for yield attributing traits among elite genotypes of cotton (*Gossypium hirsutum* L.) under rain-fed situation

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Abstract
Cotton (*Gossypium hirsutum* L.) is an important fiber crop in India due to its many uses is considered white gold. Genetic variability studies among the parental lines assist us in the selection and pattern of crossing and deducing the gene action underlying the expression of different yield attributing traits under rain-fed situation as most of the cotton-growing areas in our country are rain-fed areas. The current study was performed at the agricultural research station Hebballi under the University of Agricultural Sciences Dharwad. Analysis of the experiment showed significant variation among different parental lines. Different genetic variability parameters, heritability, genetic advance, genotypic and phenotypic coefficient of variation. There is no significant variation for plant height(cm), number of monopodia, number of nodes, stem diameter and shoot dry weight and remaining all other traits studied showed variation. The highest GCV and PCV was observed in the case of Boll weight(g) followed by lint index(g). Study on heritability and genetic advance depicted that boll weight has high heritability followed by plant height. Genetic advance for plant height(cm) followed by biomass(g). There was significant variability among different parental lines for yield attributing trains under the rainfed situation. Selection of different parental lines to study the genetics of different traits can be done through this study.

Keywords: genetic variability, heritability, genetic advance, GCV and PCV

Introduction
Cotton is a significant fiber crop grown globally in tropical and sub-tropical regions around the world accounting for more than 60 countries. Cotton fiber has many uses, as a result of which its s considered as white gold and queen of fiber plants (Divya *et al.* 2014) [5]. Cotton being an often-cross pollinated crop, the advancement of exploitation of heterosis is as comparable as that of maize crop. Cotton production is highest during the year 2020 in India (www.statista.com). As the country's textile industry is principally cotton-based, contributes to the GDP of the country on behalf of agriculture and industrial sectors. Cotton's contribution to India's export of textiles and apparel accounts for 23%. During the year 2019-20 Cotton production in India was 36.04 million bales, each bale accounting for 170 kgs (www.ibef.com). To meet the needs and demands of the growing population, the quality and production and productivity of cotton are to be improved. Assessment of genetic variability among the parental lines assists in the selection of superior genotypes for the crossing program. The range of yield attributing traits, integrity and reliability of the cotton parental lines used for different crossing programs can be known.

Materials and Methods
The experiment was conducted at Hebballi agricultural research station which is at the north transitional zone that is zone 8 of Karnataka at an altitude of 678 meters above the sea level situated between the latitude of 25017' N, longitude of 71046' E respectively. Parental lines that have been utilized for the development of various experimental populations with line X tester crosses were sown in randomized completely block design They are Sahana, RAH-221, L-761, R-132, 1-2-1, 8-1-2, LH-2076, IC-6, DC-12-111, LRA 5166 ARBH-813 and RAH-100. Entries were sown in two rows of 5 m length at a spacing of 90 x 20 centimeters respectively. 10 plats were chosen randomly at maturity in each accession in two replications and data was collected on plant height(cm), number of monopodia, number of sympodia, sympodial length at 50% plant height(cm), number of nodes, interboll distance(cm), stem diameter(cm), number

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of bolls per plant, number of seeds per boll, boll weight(g), seed index(g) Lint index (g) ginning outturn (%), Halo length (mm), Seed cotton yield (g/plant), Root dry weight (g) Shoot dry weight (g) Root to shoot dry weight ratio, Biomass/plant (g). Windostat 2.1 software was utilized for the analysis of variance using the mean values collected from the data (Panse and Sukhtame, 1995) [3]. The mean sum of squares from the variance table was utilized for calculating phenotypic and genotypic variances (Lush, 1940) [2]. Heritability, genetic advance, genetic advance as a percentage over mean were calculated according to the formula given by Johnson *et al.* (1955) [1].

Results and discussion
Fiber quality traits, the overall performance of seed cotton yield of the 12 elite cotton lines and different genetic parameters were recorded (Table 1). Analysis of variance showed that there is significant variation among the genotypes for traits such as number of sympodia, sympodial length at 50% plant height, inter boll distance, number of bolls per plant, boll weight, seed index, lint index, halo length, seed cotton yield per plant, root dry weight, root to shoot dry weight ratio ad biomass of the plant (Table 2). Plant breeders utilize this variation to make an effective selection. Other traits such as number of monopodia, number of nodes, stem diameter, number of seeds per boll and shoot dry weight showed non-significant variation (Table 2). Among the elite cotton lines, variability for seed cotton yield was significant as these came from different sources. The highest seed cotton yield, number of bolls per plant and boll weight were recorded for LRA 5166, SAHANA, ARBH-813, RAH 100 RAH 221 and the lowest yield under rainfed situation was observed in DC -12-111 and 1-2-1 respectively (Table 3). Halo length was found to be maximum in LRA 5166 and Sahana genotypes. These lines with the highest mean values can be further utilized in other breeding programs as donors for contributing specific yield-related trait improvement and enhancement. Accessions with high mean values in two different seasons can be used as potential donors for the improvement of different traits indifferent crossing programs. Sahana, LRA 5166, are found to have compact type plant architecture that can be used for high-density planting. The highest variation was for plant height (1348.50) but it was found to be non-significant, followed by seed cotton yield per plant (81.43) and was significant. Phenotypic variation was found to be highest for the trait seed cotton yield per plant (61.85) followed by biomass (47.54). Genotypic variance is highest for plant height (40.49) followed by biomass (28.86) respectively. The lowest phenotypic variance was found for stem diameter (0.06) followed by trait number of monopodia (0.55). The lowest genotypic variance was observed in trait stem diameter (0.02) followed by the number of seeds per boll (0.18) respectively. The difference in genotypic and phenotypic variances indicate that there exist remarkable differences between the elite cultivars in their response to environmental conditions which in turn reflects the nature of their stability and suitability to the rainfed situation. The heritable variation must be separated from non-heritable variation as it enhances the effectiveness of selection. It assists breeder to choose and plan suitable plant breeding program. In contrast to the Loci showing dominance and dominance gene action involved in the development of the hybrids, additive gene action assists in maintaining the integrity, the heritability of the quantitative traits, reliability and stability of the genotypes. PCV values ranged from 3.02 (number of seeds per boll) to 94.55 (boll weight) and GCV values from 1.54 (number of seeds per boll) to 89.16 (boll weight) the difference between the PCV and GCV values is less indicating the less influence of environment. PCV values for all the traits were high when compared to GCV values indicating the influence of environment over the expression of the trait.

Table 1: Salient features of Parental used in the present study

Sl. No	Parental genotypes	Salient features
1	SAHANA	High yielding released variety, tolerant to bollworm, suitable for irrigated and rainfed conditions.
2	ARBH-813	Long staple pre-release variety suitable for rainfed condition.
3	RAH-100	High yielding released variety, higher number, and medium sized bolls, suitable for irrigated condition.
4	RAH-221	High yielding genotype, high boll number with small boll size and poor fibre properties.
5	LRA-5166	High yielding released variety with drought tolerance.
6	IC-6	High yielding variety suitable for rain-fed regions.
7	DC -12-111	Long staple variety, grown in poor soils.
8	1-2-1	High boll number Long fine fiber but poor yielder in drought and salinity prone soils.
9	LH-2076	High yielding variety, suitable for most of the soil types in India.
10	8-1-2	Moderately resistant to drought and salinity and deep root system.
11	R-132	High yielding and large boll size.
12	L-761	Low drought susceptibility index and high yielding.

*Significant at 5%

Table 2: ANOVA for quantitative characters in parental genotypes

Source of variation	Df	Plant height (cm)	Number of monopodia	Number of sympodia	Sympodial length at 50% plant height (cm)	Number of nodes	Interboll distance (cm)	Stem diameter (cm)	Number of bolls per plant	Number of seeds per boll	Boll weight (g)
Replications	1	92.70	0.26	0.35	35.52*	0.12	0.01	0.07*	11.34*	11.53*	0.20*
Treatments	11	1348.50	0.38	13.76*	44.25*	13.74	1.24*	0.09	14.38*	27.84	0.87*
Error	11	122.00	0.21	4.56	18.45	4.83	0.84	0.04	1.06	1.63	0.51

Source of variation	Df	Seed index (g)	Lint index (g)	GOT (%)	Halo length (mm)	Seed cotton yield (g/plant)	Root dry weight (g)	Shoot dry weight (g)	Root to shoot dry weight ratio	Biomass / plant (g)
Replications	1	2.73	5.60	4.26*	3.47	20.54	3.76	60.37	26.89*	61.4
Treatments	11	14.65*	27.97*	12.27*	24.0*	81.43*	20.52*	44.60	43.82*	76.40*
Error	11	6.20	4.41	1.62	2.46	42.28	16.2	33.44	11.41	18.68

*Significant at 5%

Table 3: Study of significant traits of different parental genotypes

Sl. No.	Entry Name	Seed cotton yield (g/plant)	Boll weight (g)	Number of bolls per plant	Halo length (mm)
1	RAH 100	42.48	5.95	29.98	32.93
2	RAH 221	41.99	5.52	28.70	32.70
3	LH 2076	41.78	5.42	27.67	31.50
4	L-761	41.42	4.89	26.35	27.98
5	DC -12-111	37.93	4.87	25.22	27.90
6	LRA 5166,	47.80	6.64	34.66	34.70
7	SAHANA,	46.46	6.22	31.26	33.90
8	ARBH-813,	43.40	5.58	30.90	32.95
9	IC 6	42.13	5.54	30.21	29.76
10	R-132	39.77	5.42	29.88	32.50
11	8-1-2	39.54	5.21	29.22	31.97
12	1-2-1	37.92	5.10	28.11	30.86

Table 4: Variability parameters for different quantitative characters in parental genotypes

Variability parameters	Plant height (cm)	Number of monopodia	Number of sympodia	Sympodial length at 50% plant height(cm)	Number of nodes	Inter boll distance (cm)	Stem diameter (cm)	Number of bolls per plant	Boll weight (g)
Mean	84.33	1.37	11.71	35.37	18.89	6.12	1.30	16.15	4.06
Maximum	105.00	2.00	22.60	48.20	22.60	8.33	1.80	20.80	5.60
Minimum	59.00	0.40	8.80	23.80	14.40	4.40	1.00	12.40	2.40
Vg	40.49	0.21	4.6	12.9	4.45	0.20	0.02	6.67	13.10
Vp	46.08	0.55	9.16	31.35	9.28	1.04	0.06	7.72	14.73
PCV	8.05	54.38	25.85	15.83	16.13	16.66	19.61	17.20	94.55
GCV	7.55	33.85	18.32	10.15	11.17	7.31	12.16	15.98	89.16
h²bs (%)	87.87	38.74	50.22	41.15	47.98	19.23	38.46	86.27	88.94
GA (%)	12.29	0.59	3.13	4.75	3.01	0.40	0.20	4.94	7.03
GAM (%)	14.19	77.21	22.75	10.73	21.92	32.58	24.44	34.34	25.26

Variability parameters	Number of seeds per boll	Seed index (g)	Lint index (g)	GOT (%)	Halo length (mm)	Seed cotton yield (g/plant)	Root dry weight (g)	Shoot dry weight (g)	Root to shoot dry weight ratio	Biomass (g)
Mean	27.48	9.44	4.59	32.69	27.49	42.29	33.40	76.80	0.65	110.2
Maximum	31.00	10.48	6.09	39.28	32.00	60.59	38.40	123.40	0.72	161.8
Minimum	23.00	7.67	3.56	28.12	17.66	22.15	12.70	36.80	0.21	49.5
Vg	0.18	4.22	11.78	5.32	10.77	19.57	2.16	5.58	16.20	28.86
Vp	0.69	10.42	16.19	6.94	13.23	61.85	18.36	39.02	27.61	47.54
PCV	3.02	34.20	87.66	8.06	13.23	18.60	12.83	8.13	8.08	25.09
GCV	1.54	21.77	74.78	7.06	11.94	10.46	4.40	3.08	6.19	19.55
h²bs (%)	26.09	40.53	72.76	76.67	81.41	31.65	11.76	14.30	58.68	60.71
GA (%)	0.45	2.70	6.03	4.16	6.10	5.13	1.04	1.84	6.35	8.62
GAM (%)	51.31	18.40	21.56	33.92	25.42	6.30	5.06	4.13	14.50	11.29

GCV and PCV values calculated are independent of the unit of measurement hence they assist in the comparison and grouping of different individuals in a population or between the populations. PCV and GCV values were found to be highest for boll weight followed by lint index. Selection pressure exercising on these characters may assist in isolating desirable genotypes. Pradeep and Sumalini (2005) [4] reported the same regarding different genotypes. Characters like number of sympodial branches, number of nodes, number of bolls per plant, boll weight, lint index and ginning outturn showed high heritability and high genetic advance which reflects that those characters are governed by additive genetic variance Panse and Sukhatme (1995) [3]. Other characters like plant height, root to shoot dry weight depicted high heritability and moderate genetic advance indicating the predominance of additive and non-additive genetic variance. Hence selection of parental line for crossing to improve certain elite cultivars through these traits will be effective as high heritability with high genetic advance over mean indicates the predominance of reliable additive genetic variance and predicts the genetic gain in the next generation.

Based on the study the elite cultivars which are having high mean values, high heritability and high genetic advance overpopulation mean can be crossed with others to improve other genotypes in those respective traits. Table 4 depicts different genotypes mean values. Negative selection should be practised for the trait days to flowering as earliness is preferred. Significant variability, high heritability, high genetic advance over mean, high PCV and GCV values assist in selecting a suitable genotype as a parent in a crossing program for improvement.

References
1. Johnson CH, Robinson HF, Comstock RE. Biometrical studies of yield and segregating populations of Korean lespedza. *Agron. J.,* 1955;47:320-324.
2. Lush JL. Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters. Proc. Am. Soc. Anim. Prod 1940;33:293-301.
3. Panse VG, Sukhatme PV. Statistical methods for agricultural workers, 3rd Ed., ICAR, New Delhi, 1995, 58.

4. Pradeep T, Sumalini K. Studies on performance of genetic variability for plant type and productive traits in multiple crosses of cotton (*Gossypium hirsutum* L.). J Indian Soc. Cotton Improv 2005;16:59-66.
5. Dhivya R, Amalabalu P, Pushpa R, Kavithamani D. Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.) African journal of plant science 2014;8(1):1-5
6. www.ibef.com
7. www.statista.com