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Genetic variability and heritability studies for seed cotton yield, yield attributing and fibre quality traits in upland cotton (*Gossypium hirsutum* L.)

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Abstract

Ninety six cotton germplasm collections were evaluated for genetic variability, heritability and genetic advance for fifteen quantitative traits during *Kharif* 2017 at Main Agricultural Research Station, Raichur. Analysis of variance revealed significant differences for all the quantitative traits under study except Upper Half Mean Length (UHML), micronaire and seed cotton yield per plant. A wide range was observed for plant height, number of sympodia per plant, sympodial length at ground level, number of bolls per plant, ginning outturn and seed cotton yield per plant. High GCV and PCV were recorded for traits *viz*., number of monopodia, sympodial length at ground level, sympodial length at fifty per cent of plant height and number of bolls per plant. High heritability coupled with high genetic advance as *per cent* of mean was observed for all the traits which indicated that selection could be effective for improvement in these traits except for fibre quality characters, ginning outturn and seed cotton yield per plant.

Keywords: Cotton, germplasm, variability, heritability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV)

Introduction

Cotton is a major fibre crop of global importance addressed as “King of fibre crops” or “White Gold”. Commercial cotton is grown in 77 countries and 123 countries are involved in the cotton related activities. It is the most important commercial crop contributing nearly 65 per cent of the total raw material needs of the textile industry in India. Though India has the largest cotton area in the world with 12.3 million hectares and has been the leading producer from 2015-16 with 28.5 million bales of raw cotton produced in 2017-18, its productivity (504 kg/ha) has remained lower than the global average of 792 kg/ha (Johnson, 2018) [10].

Germplasm, which is a prerequisite for any breeding programme, serves as a valuable source of material as it provides scope for building of genetic variability. Successful breeding program depends on the complete knowledge and understanding of the genetic diversity within and among genetic resources of the available germplasm and enable plant breeders to choose parental sources that will generate diverse populations for selection. The lack of genetic diversity is implicated in the slowing of progress in developing new cotton cultivars with improved yield, stress resistance or quality potential (Ismail *et al.*, 2008) [8].

The demand of cotton fibre will be fulfilled by developing new genotypes with desired characters by applying various breeding techniques. Selection is effective when magnitude of variability in the breeding population is enough. The identification and use of genotype with higher genetic potential is a continuous requirement for the production of better cotton. Efforts are going on to enhance the yield as well as the fibre quality. To achieve these objectives comprehensive studies to understand the genetic mechanism to control the plant characters under different environmental conditions is necessary (Ahsan *et al.*, 2015) [2].

In the process of identification of superior genotypes, seed cotton yield coupled with various quality traits are considered to be beneficial character. Several yield contributing traits such as plant height, number of monopodia, number of sympodia, sympodial length, number of bolls per plant, and boll weight are responsible for the improvement in seed cotton yield (Adsare and Salve, 2017) [1]. The information on the estimates of variability with respect to yield and its heritable components in the material with which the breeder is working is prerequisite for any breeding programme. Hence, it becomes necessary to split the total variability into heritable and non-heritable components with the help of certain genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA).

The present study was conducted to understand the genetic variation of different *Gossypium hirsutum* accessions for fifteen yield, yield attributing and fibre quality traits and to analyse its heritable components of the actual variability for making selections for breeding program.

Material and methods

1. **Genetic material and field procedure:** In the present investigation, an attempt was made to assess genetic variability parameters for yield, yield contributing and fibre quality traits. Ninety six germplasm lines of *Gossypium hirsutum* cotton including forty seven diverse lines (45 IC and 2 EC lines) from Central Institute for Cotton Research (CICR), Nagpur and forty nine advanced breeding lines indigenously bred and developed in Main Agricultural Research Station (MARS), Raichur were evaluated for the study, along with two already identified and released varieties from AICRP cotton section at MARS, Raichur *viz.*, SUJAY (SCS-793) and BGDS-1063 which were used as checks in the trial. These genotypes were grown in two rows of 6m length with 75cm × 30cm spacing at Main Agricultural Research Station field, Raichur during *Kharif* season of 2017-18 using augmented design. Recommended package of practices and plant protection measures were adapted to raise a good crop.
2. **Recording observations:** At maturity, five random plants were selected from each genotype and observations were recorded for fifteen traits *viz.,* plant height (cm), number of monopodia per plant, number of sympodia per plant, sympodial length at ground level (cm), sympodial length at fifty per cent plant height (cm), inter-nodal distance (cm), number of bolls per plant, boll weight (g), upper half mean length (mm), fibre strength (g/tex), micronaire value (µg/inch), ginning out turn (%), seed index (g), lint index and seed cotton yield per plant (g). The lint samples obtained by ginning 100 grams of each seed cotton of all ninety six samples along with the two checks were then subjected to quality evaluation at Quality Evaluation Unit (QEU), Mahyco, Jalna, Maharashtra.
3. **Statistical analysis:** Analysis of variance of the recorded data was calculated according to the method of Federer (1977) [6] to compare the mean differences among cotton genotypes for seed cotton yield per plant and its other components. Genotypic and phenotypic coefficients of variance were calculated using the method suggested by Burton and Devane (1953) [3]. Broad sense heritability (h^2) for all the fourteen characters was estimated using the formula given by Hanson *et al.*, (1953) [7]. Genetic advance (GA) was estimated using the formula given by Johnson *et al.* (1955) [9].

Results and discussions

Analysis of variance revealed significant difference among genotypes for all the quantitative traits except for upper half mean length (UHML), micronaire and seed cotton yield per plant and infers existence of considerable genetic variability among the genotypes (Table 1). The *per se* performance and the range of variations observed among the traits are furnished in Table 2 showcasing wide range of variation recorded for all the traits under study which in turn is very important for the plant breeders and selection is effective when magnitude of variability in the breeding population is high enough

Table 1: Analysis of variance for yield, yield attributing and fibre quality traits in cotton (*Gossypium hirsutum* L.) genotypes

Source	Block	Entry	Check	Genotype	Check vs. Genotype	ERROR
Df	5	97	1	95	1	5
PH	3294.443**	243.518*	64.419	390.197*	111.012	53.193
NM	2.724*	0.235*	0.052	0.235*	0.678	0.134
NS	873.122**	27.533**	2.542	26.324**	598.817**	7.923
SLG	193.129**	46.128*	23.519	54.629*	15.601*	14.512
SLFPH	78.729*	30.872*	14.963	33.731*	0.023	8.187
IND	4.108**	0.585*	0.163	0.765*	0.161	0.251
NBP	68.113**	19.033*	27.080*	18.830*	40.502**	4.307
BW	59.809*	15.586*	12.201	17.542*	10.118	10.598
UHML	0.873	1.010	0.067	0.897	5.399	1.188
FS	1.934*	0.905*	0.083	0.907*	1.014	2.589
MIC	0.465	0.171	0.120	0.186	0.181	0.134
GOT	33.857**	11.946*	0.534	13.532*	5.172	6.601
SI	1.447*	0.878*	0.007	0.893*	0.597	0.157
LI	0.905*	0.472*	0.026	0.513*	0.002	0.166
SCYP	6.584	18.720	0.031	18.498	11.184	15.071

* Significant at 5% (P = 0.05) ** Significant at 1% (P = 0.01)
PH- Plant height (cm) **NM**- Number of monopodia **NS**- Number of sympodia **SLG**- Sympodial length at ground level (cm)
SLFPH- Sympodial length at 50% plant height (cm) **INL**- Inter-nodal length (cm) **NBP**- Number of bolls per plant
BW- Boll weight (g) **UHML**- Upper half mean length (cm) **FS**- Fibre strength (g/tex) **MIC**- Micronaire (µg/inch)
GOT- Ginning outturn (%) **SI**- Seed index (g) **LI**- Lint index (g) **SCYP**- Seed cotton yield per plant (g)

Table 2: Mean and range performance for different characters among *Gossypium hirsutum* L. genotypes

S. No.	Character	Mean	Range	
			Minimum	Maximum
1	Plant height (cm)	114.0	78.0	165.0
2	Number of monopodia per plant	0.8	0.2	1.8
3	Number of sympodia per plant	19.8	14.2	29.0
4	Sympodial length at ground level (cm)	28.6	12.4	67.8
5	Sympodial length at 50% plant height (cm)	28.4	13.6	46.0
6	Inter nodal distance (cm)	4.1	2.2	6.6
7	Number of bolls/plant	19.0	10.4	27.6
8	Boll weight (g)	4.4	3.28	5.19
9	Upper Half Mean Length (mm)	28.7	27.4	32.8
10	Fibre strength (g/tex)	23.1	21.4	26.5
11	Micronaire (µg/inch)	3.8	3.0	5.3
12	Ginning outturn (%)	33.4	23.42	42.70
13	Seed index (g)	7.8	5.78	10.56
14	Lint index	3.9	2.10	6.89
15	Seed cotton yield per plant (g)	34.6	26.3	44.0

The phenotypic coefficient of variance, genotypic coefficient of variance, broad sense heritability, genetic advance and genetic advance as percentage of mean for all the eleven traits are presented in Table 3. Since the coefficient of variation is independent of the measuring units it is more useful in comparing the population. It is apparent from the Table 3 that there is almost perfect relation between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) as indicated by higher values of PCV compared to GCV for all the characters and large difference observed between PCV and GCV for characters *viz.* sympodial length at fifty per cent plant height, inter-nodal distance, UHML, micronaire, ginning outturn and lint index which indicates the influence of the environment in the expression of these characters. Similar results were reported by Adsare and Salve (2017) [1], however contrary with Ahsan *et al.* (2015) [2].

Table 3: Estimation of variability parameters for yield, yield attributing and fibre quality traits in 98 cotton (*Gossypium hirsutum* L.) genotypes

S. No.	Character	Coefficient of Variation		h^2 (%)	GA (%)	GAM (%)
		GCV (%)	PCV (%)			
1	Plant height (cm)	15.67	16.95	85.51	34.02	29.85
2	Number of monopodia per plant	51.37	77.59	43.83	0.56	70.06
3	Number of sympodia per plant	13.57	13.83	96.19	5.42	27.41
4	Sympodial length at ground level (cm)	25.68	26.30	95.34	14.48	51.65
5	Sympodial length at 50% plant height (cm)	20.59	22.65	82.66	10.95	38.57
6	Inter-nodal distance (cm)	17.02	21.03	65.54	1.16	28.39
7	Number of bolls/plant	21.40	21.61	98.10	8.29	43.67
8	Boll weight (g)	11.17	12.64	78.04	1.62	36.88
9	Upper Half Mean Length (mm)	3.27	8.16	16.11	0.59	2.70
10	Fibre strength (g/tex)	4.01	5.71	49.45	1.34	5.82
11	Micronaire (µg/inch)	5.89	11.43	26.60	0.23	6.26
12	Ginning outturn (%)	7.69	10.94	49.44	0.44	11.14
13	Seed index (g)	10.41	11.55	81.36	1.50	19.35
14	Lint index	14.46	17.78	66.13	0.94	24.22
15	Seed cotton yield per plant (g)	11.03	11.23	96.40	3.88	11.23

GCV - Genotypic coefficient of variance **PCV** - Phenotypic coefficient of variance **h^2** - Broad sense heritability
GA - Genetic advance **GAM** - Genetic advance as per cent of mean

High GCV and PCV were observed for number of monopodia per plant (51.37 and 77.59), sympodial length at ground level (25.68 and 26.30), sympodial length at fifty per cent of plant height (20.59 and 22.65) and number of bolls per plant (21.40 and 21.61) indicating the presence of significant genetic variability in these characters. Selection pressure can be applied on these characters to isolate promising genotypes. Similar findings were reported by Dinakaran *et al.* (2012) [5], Vineela *et al.* (2013), Srinivas *et al.* (2014) and Chaudhari *et al.* (2017) [4]. Characters like plant height (15.67 and 16.95), number of sympodia per plant (13.57 and 13.83), boll weight (11.17 and 12.64), seed index (10.41 and 11.55), lint index (14.46 and 17.78) and seed cotton yield per plant (11.03 and 11.23) recorded moderate GCV and PCV, whereas inter-nodal length (17.02 and 21.03) showed moderate value of GCV and high value of PCV which suggests that these characters can be improved though rigorous selection. Similar outcomes were suggested by Preetha and Raveendran (2007), Kulkarni *et al.* (2011) and Suresh *et al.* (2017). Low GCV and PCV were observed for UHML (3.27 and 8.16) and fibre strength (4.01 and 5.71), whereas low value of GCV and moderate value of PCV were shown by ginning outturn (7.69 and 10.94) and micronaire (5.89 and 11.43) in parallel to the results stated by Dinakaran *et al.* (2012) [5], Pujer *et al.* (2014) and Shao *et al.* (2016).

Absolute traits under study except ginning outturn exhibited high magnitude of broad sense heritability (Table 3). Among the eleven characters studied, number of bolls per plant (98.10%) recorded the highest heritability closely followed by seed cotton yield per plant (96.40%), number of sympodia per plant (96.19%), sympodial length at ground level (95.34%) and plant height (85.51%). Number of monopodia per plant (43.83%), ginning outturn (49.44%) and fibre strength (49.45%) observed moderate estimates of heritability while UHML (16.11%) and micronaire (26.60%) exhibited low estimates of heritability. For efficient selection, we cannot completely rely upon heritability. Thus those characters which exhibit maximum heritability and high genetic advance as percentage of mean could be used as powerful tool in selection process. Such characters are controlled by the additive genes and less influenced by the environment (Panse and Sukhatme, 1995). The higher genetic advance as per cent of mean (GAM) were observed for plant height (29.85%), number of monopodia per plant (70.06%), number of sympodia per plant (27.41%), sympodial length at ground level (51.65%), sympodial length at fifty per cent of plant height (38.57%), inter-nodal length (28.39%), number of bolls per plant (43.67%), boll weight (36.88%) and lint index (24.22%). The moderate estimates of GAM were recorded for ginning outturn (11.14%), seed index (19.35%) and seed cotton yield per plant (11.23%) while UHML (2.70%), fibre strength (5.82%) and micronaire (6.26%) exhibited lower GAM.

High heritability along with high genetic advance as per cent of mean (GAM) were observed for plant height (85.51% and 29.85%), number of sympodia per plant (96.19% and 27.41%), sympodial length at ground level (95.34% and 51.65%), sympodial length at fifty per cent of plant height (82.66% and 38.57%), inter-nodal length (65.54% and 28.39%), number of bolls per plant (98.10% and 43.67%), boll weight (78.04% and 36.88%) and lint index (66.13% and 24.22%). The results were in accordance with that of Ahsan *et al.* (2015) [2] and Shao *et al.* (2016). This indicates that selection can be resorted for the improvement of these characters in the future crop improvement programmes. The heritability should be considered along with genetic advance as percent of mean, however it is not necessary that character showing high heritability will also express high genetic advance (Johnson *et al.*, 1955) [10]. Seed index (81.36% and 19.35%) and seed cotton yield per plant (96.4% and 11.23%) exhibited high heritability coupled with moderate GAM whereas moderate heritability coupled with high GAM was shown by number of monopodia per plant (43.83% and 70.06%) which were confirmed by Muhammad *et al.*, 2004. Potential accessions were identified for traits under study which could be utilised for future crop improvement programmes (Table 4).

Overall, the germplasm exhibited significant variability for most of the traits studied. Direct selection could be enforced for most of the yield attributing traits since they exhibited high range of variation. Also, the results revealed the influence of environment on the development of most of the characters under study was minor with high heritability and genetic gain which indicated that the selection can be resorted for the improvement of these characters in the future crop improvement programmes.

Table 4: Potential accessions for yield, yield attributing and fibre quality traits

S. No.	Character	Accessions
1	Plant height	IC 357870, RAH 14412, IC 291448
2	Number of monopodia per plant	RAH 14304, RAH 14181, RAH 1469
3	Number of sympodia per plant	RAH 14234, RAH 1413, IC 357560
4	Sympodial length at ground level	IC 431986, RAH 14253, IC 357344
5	Sympodial length at 50% plant height	IC 431986, RAH 14253, IC 358894
6	Inter-nodal distance	IC 291317, IC 292032, IC 291342
7	Number of bolls/plant	RAH 14128, RAH 14289, IC 357210
8	Boll weight	IC 291223, IC 336105, RAH 14289
9	Upper Half Mean Length	IC 291572, RAH 14261, RAH 14261
10	Fibre strength	RAH 14110, RAH 14360, RAH 1432
11	Micronaire	RAH 14261, RAH 14324, RAH 14223
12	Ginning outturn	IC 291223, IC 357944, IC 357318
13	Seed index	IC 292032, RAH 1413, RAH 14360
14	Lint index	IC 292032, RAH 14201, IC 291966
15	Seed cotton yield per plant	RAH 14128, RAH 14289, IC 358355

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