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Variability, heritability and hereditary propel in upland cotton (Gossypium hirsutum L.)

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The analysis of variance study indicated the presence of significant difference among all the traits in *Gossypium hirsutum* accessions. The highest phenotypic coefficient of variation (GCV) and genotypic coefficient of variation (GCV) were recorded by seed index, plant height, lint index and boll weight. Genotypic co-efficient of variation had a similar trend as PCV. High heritability along with high genetic advance was observed in traits viz., number of sympodia per plant, single plant yields, seed index and micronaire value. The combinations of high heritability with high genetic advance will provide a clear base on the reliability of that particular character in selection of variable entries. Based on *per se* performance, the accessions MCU5, TCH1715, TCH1716 and G cot 16 were identified as potential donors for single plant yield (g), number of bolls per plant, 2.5% span length (mm) and bundle strength (g/tex). So these accessions may be utilized for crossing programme to improve a particular character in crop improvement.

Key words: Genetic variability, heritability, genetic advance, upland cotton.

INTRODUCTION

Cotton is an important fibre crop of global importance which is grown in tropical and subtropical regions of more than 60 countries of the world. Despite threat from synthetic fibre or manmade fibre, cotton retains its reputation as "queen of the fibre plants"". For multiple uses of lint and by-products, cotton is also referred to as "white gold". In any crop improvement programme, knowledge on nature of gene action and inheritance of traits is essential so as to choose a suitable breeding methodology in crop improve-ment (Vineela et al., 2013). Development of an effective breeding programme depends on the existence of genetic variability for various economic characters in the gene pool. Selection is effective only when there is enough magnitude of variability in the breeding population. An understanding of precise magnitude of variability present in a population is important in formulating the most appro-priate breeding technique for improvement of various characters. The present investigation was carried out with 54 *Gossypium hirsutum* lines of diverse origin to estimate their *per se* performance, variability, heritability and genetic

advance on the genetic architecture of 16 yield, yield components and fibre quality traits.

MATERIALS AND METHODS

The study was conducted in the Department of Cotton, Tamil Nadu Agricultural University, Coimbatore during winter 2010. Fifty four *G. hirsutum* cotton genotypes were planted in randomized block design with two replications. Uniform spacing of 90 x 45 cm and all the recommended field operations were carried out. In each replication five competitive plants were randomly selected and observations were recorded for 16 characters viz., days to 50% flowering, plant height (cm), internode length (cm), number of sympodia/plant, number of ovules/plant, number of bolls/plant, boll weight (g), number of seeds/plant, seed setting percentage, seed cotton yield/plant, lint index, seed index, ginning outturn (%), 2.5% span length (mm), bundle strength (g/tex) and fibre fineness.

Analysis of variance was carried out statistically utilizing the mean values (Panse and Sukhtame, 1995). The phenotypic and genotypic coefficient of variation was estimated using the formula suggested by Burton (1952) and expressed in percentage. The phenotypic and genotypic variances were calculated by utilizing the

Table 1. Mean and range performance for different characters among G. *hirsutum* accessions.

Characters	Mean	Minimum	Maximum
Days to 50% flowering	56.6	50.0	65.0
Plant height (cm)	108.8	78.0	147.0
Inter node length(cm)	5.4	4.0	6.5
No of Sympodia per plant	19.6	14.0	27.0
No of bolls per plant	23.6	19.5	38.5
Boll weight (g)	4.3	12.4	5.5
No of seeds per boll	27.4	23.0	35.5
No of ovules per flower	30.7	24.0	38.0
Seed setting percentage	89.6	71.5	100.0
Single plant yield (g / plant)	57.6	31.7	91.6
Lint index	5.7	4.0	7.9
Seed index	9.6	6.4	16.3
Ginning outturn (%)	37.3	30.8	46.1
2.5 % span length (mm)	28.4	24.3	34.0
Bundle strength (g / tex)	20.4	16.2	23.7
Micronaire value	4.3	3.5	5.2

respective mean sum of square from variance table (Lush, 1940). Heritability, expected genetic advance and genetic gain in the broad sense was calculated according to the formula suggested by Johanson et al. (1955).

RESULTS AND DISCUSSION

The *per se* performance of yield and fibre quality characters were recorded on 54 germplasm accessions and the range of variations observed in respect of all the 16 traits studied are presented in the Table 1. Based on *per se* performance, the accessions such as MCU 5, TCH1715, TCH1716 and G cot 16 in *G. hirsutum* were identified as potential donors which recorded highest mean values for single plant yield, number of bolls per plant, 2.5% span length (mm) and bundle strength

(g/tex). These accessions may be exploited for further improvement of the above traits by breeding programmes. Regarding the identifica-tion of donor for specific trait, the highest performer of that particular trait can be considered. Among the accessions, TCH 1715 (5.5 g of boll weight), RB 488 (46.1% of GOT) were expressed the highest *per se* for that particular traits. The culture TCH 1710 (34 mm, 23.1g/tex) recorded the highest 2.5% span length. So these acces-sions may be utilized for crossing programme to improve that particular character in crop improve-ment. Anjali was found to be compact type which can be utilized in development of genotype suitable for high density planting.

The analysis of variance showed highly signi-ficant differences among genotypes for all the

characters studied (Table 2) and infers existence of considerable genetic diversity among genotypes. Phenotypic variance, genotypic variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability in broad sense and genetic advance as percentage of mean which were estimated for 16 characters are shown in Table 3. The knowledge of nature and magnitude of variability available in the genotypes for different characters is an important prerequisite for making simultaneous selection over more number of characters to bring remarkable improvement in cotton. The analysis of variance study indicated the presence of significant difference among all the traits in the accessions. The heritable (genotypic) variation is usually masked by non-heritable variation creating

Table 2. Analysis of variance for the different characters among the germplasm accessions of *G. hirsutum*.

Source of variation	Degrees of freedom	Days to 50% flowering	Plant height (cm)	Inter node length (cm)	Number of sympodia / plant	Number of bolls / plant	Boll weight (g)	Number of sees / boll	Number of ovule / flower	Seed setting percentage	Single plant yield (g)	Lint index	Seed index	Ginning out turn (%)	2.5 % span length (mm)	Bundle strength(g /tex)	Micronaire value
Genotypes	53.0	10.4**	466.6**	0.7**	14.1**	18.3**	0.6*	10.8**	17.1**	90.4**	441.9**	1.3**	4.6**	21.1**	10.2**	6.1**	0.3**
Error	53.0	2.7	218.6	0.4	2.8	5.0	0.3	5.50	6.5	40.1	2.1	0.5	1.2	10.9	0.2	0.3	0.1

*,** Significant at 5 and 1% levels, respectively.

difficulty in exercising selection. Hence it becomes necessary to partition overall variability into heritable and non-heritable components to enable the breeders to plan for proper breeding programme. The plant height recorded the highest value for phenotypic variance (342.6) and the single plant yield recorded highest genotypic variance (219.9). The micronaire value exhibited the lowest phenol-typic variance (0.2) and in case of genotypic variance, the traits *viz*., inter node length, boll weight and micronaire value had recorded the lowest value (0.1). The co-efficient of phenotypic and genotypic variance were calculated for all the characters under study. The PCV ranged from 4.5 (days to 50% flowering) to 25.9% (single plant yield). The highest PCV was followed by seed index (17.7%), plant height (17.0%), lint index (17.0%) and boll weight (15.4%). Genotypic co-efficient of variation had a similar trend as PCV. The range varied from 3.5 (Days to fifty percent flowering) to 25.8 (Single plant yield). The maximum genotypic coefficient of variation (GCV) was observed for single plant yield (25.8) followed by seed index (13.5), number

of sympodia per plant (12.1), lint index (11.2) and number of bolls per plant (10.9), plant height (10.2). The lowest PCV (4.5%) and GCV (3.5) values was observed in days to 50% flowering. In the present study, there was a close correspond-dence between phenotypic and genotypic variance for days to 50% flowering, inter node length, boll weight, single plant yield, lint index, micronaire value and 2.5% span length indicating less environmental influence. But plant height, number of sympodia per plant, number of bolls per plant, number of seeds per boll, seed setting percentage and ginning outturn showed higher variation indicating the influence of environment on these characters. Since the variations are influenced by the magnitude of the units of measurements of different traits, a measure of coefficient of variation which is independent of the unit of measurement is more useful in comparing between populations. In *G. hirsutum* accessions PCV was higher than the GCV for all characters. From this, we can understand that the environment plays a major role on expression of all these traits leading to increase in the PCV more than GCV.

The highest PCV and GCV estimates were recorded for single plant yield indicating the presence of significant genetic variability in this character. Selection pressure can be applied on this character to isolate promising genotypes. Similar observations in cotton was reported by Dheva and Potdukhe (2002) and Preetha and Raveendran (2007).

Moderate PCV and GCV estimates were noticed for the characters such as plant height, number of sympodia per plant, number of bolls per plant, lint index and seed index. Girase and Mehetne (2002) and Harshal (2010) also reported the moderate PCV and GCV in various traits with the suggestion that these characters can be improved though rigorous selection. The characters such as days to 50% flowering, 2.5% span length and micronaire value exhibited low PCV and GCV which indicated that the breeds should go for source of high variability for these characters to make improvement. Similar suggestion were given by Kowsalya and Raveendran (1996), Do Thi Ha An et al. ((2006) in their conclusion. In a population, the observed variability is a

Table 3. Components of variance for yield and fibre quality characters of *G. hirsutum* accessions.

Characters	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	h^2 (%)	A	GA as percentage of mean
Days to 50% flowering	6.6	3.9	4.5	3.5	58.5	4.0	7.0
Plant height (cm)	342.6	124.0	17.0	10.2	36.2	17.7	16.3
Inter node length(cm)	0.5	0.1	13.5	6.6	23.5	0.5	8.4
No of sympodia per plant	8.5	5.7	14.8	12.1	66.9	5.1	26.2
No of bolls per plant	11.7	6.7	14.4	10.9	57.2	5.2	21.8
Days to 50% flowering	6.6	3.9	4.5	3.5	58.5	4.0	7.0
Plant height (cm)	342.6	124.0	17.0	10.2	36.2	17.7	16.3
Boll weight (g)	0.4	0.1	15.4	8.4	29.8	0.5	12.1
No of seeds per boll	8.2	2.6	10.4	6.0	32.5	2.5	9.0
No of ovules per flower	11.8	5.3	11.2	7.5	44.5	4.0	13.1
Seed setting percentage	65.3	25.1	9.0	5.6	38.5	8.2	9.2
Single plant yield (g / plant)	222.0	219.9	25.9	25.8	89.1	39.0	27.3
Lint index	0.9	0.4	17.0	11.2	43.9	1.1	19.6
Seed index	2.9	1.7	17.7	13.5	58.0	2.6	27.1
Ginning outturn (%)	16.0	5.1	10.7	6.0	31.6	3.3	9.0
2.5 % span length (mm)	5.2	5.0	8.0	7.9	96.2	5.8	20.4

combined measure of genetic and environment causes, where as the genetic variability is the only estimate heritable from generation to generation. However, a measure of heritability alone does not give an idea about the expected gain in the next generation but it has to be considered in conjunction with genetic advance. The traits which expressed high heritability and high genetic advance as percentage of mean could be used as a powerful tool in selection process. According to Panes and Sukhatme (1995) such characters were found to be governed by additive genes and had minimum environment influence. The heritabi-lity estimates ranged from 23.5 (internode length) to 89.1% (single plant yield). The high heritability estimates of 89.1% were recorded by single plant yield followed by 2.5% span length (96.2 %) and bundle strength (91.8%) where as the low heritability was observed in inter node length (23.5%).

The high heritability was registered in the traits *viz.,* number of sympodia per plant, single plant yield, seed index, 2.5% span length and bundle strength. The inter node length exhibited low heritability in this investigation. For efficient selection, we cannot completely depend on heritability alone. The combinations of high heritability with high genetic advance will provide a clear base on the reliability of that particular character in selection of variable entries. The genotypic advance as percent of mean for 16 traits ranged from 7.0 to 27.3%. The higher genetic advance as percent of mean was recorded by single plant yield (27.3%) followed by seed index (27.1

%), number of sympodia per plant (26.2 %), number of bolls per plant (21.8 %). The lowest value of 7.0% was observed in the trait days to 50% flowering. High heritability along with high genetic advance was observed in traits *viz.,* number of sympodia per plant, single plant yields, seed index and micronaire value in *G. hirsutum* (Do Thi Ha An et al., 2008). These traits are highly reliable during selection. High heritability combined with moderate genetic advance was found in the 2.5% span length. It was in accordance with of Muhammad et al. (2004). Among the study materials some of the accessions were identified as potential donors for the improvement of different characters (Table 4). The accessions with high mean performance are generally preferred for all the traits except days to 50% flowering, since earliness is the preferred attribute and early flowering was taken into consideration. From the results of the present study, it can be concluded that direct selection can be done for most of the yield attributing traits since it exhibited high genetic variability and high range of variation. A high PCV over GCV for the characters studied indicated that environment influences the expression of these characters under study. High genetic advance, genetic gain and heritability were recorded for number of sympodia per plant, single plant yield, seed index, micronaire value and 2.5% span length indicated that selection can be resorted for the improvement of these characters in the future crop improvement programmes.

Table 4. Potential donors for yield and fibre quality traits.

S/N	Characters	Potential accessions
1	Days to 50% flowering	MCU-7, SVPR-3, TCH-1716, SVPR-2
2	Plant Height	SCS 102, T CH 1715, Okra narrow
3	Inter node length	MCU 5, RAC9740, SCS 102, F-1946
4	No. of Sympodia	PSCL VII, Okra narrow, RHC 1694, SCS 102
5	No. of ovules	NDLH 1588, TCH 1608
6	No. of Bolls	Okra Narrow, G cot-16, F-1946
7	Boll weight(g)	TCH 1715, MCU 13, LRA 5166
8	No. of seeds per boll	NDLH 1588, SVPR 4
9	Seed setting %	MCU 12, MCU 13, KC 3, TCH 1710
10	Single plant yield	MCU 5, MCU 12, Surabhi, SVPR 2, SVPR 4, KC 2, TCH 1715, TCH 1716, TCH 1732, TCH 1734, TCH 1744, G. COT-16, CCH 2117, Pusa 953, ARB 2001, RHC 1694, LH 1961, RB 488, GISV201, MHIS-5, MHIS-7, Sara 2,Giza 1461, Sumangala
11	Lint index	GISV 201, RAC 9544
12	Seed index	SVPR 4, L-752, TCH 1715
13	Ginning Out Turn	RB 488, TCH 1705
14	2.5 % span length	TCH 1608, CNH 152, TCH 1705, RAC 9740, TCH 1732, MCU 5, MCU 13, TCH 1710, TCH 1715, TCH 1716
15	Bundle strength	TCH 1710, TCH 1715, MCU 5, TCH 1732, TCH 1734, TCH
16	Micronaire value	1744 MHIS-7, MCU 7, CCH 2117, NDLH 1588

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