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Genetic Advancement, Variability and Heritability in Upland Cotton (*Gossypium hirsutum* L.)

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Abstract: Cotton is one of the major sources of natural fibre at global scale. A field research experiment was carried out in the Plant Breeding and genetics Department, Cotton Research Institute Anyang Henan, China to examine the genetic advance, genotypic, phenotypic and environmental coefficient of variation, and heritability during 2017. Cotton genotypes such as 705230, 705240, 705242, 705244, 705252, 705360, 705366, 705368, 705398, 705441, 705482 and 705542 were used as experimental material. The present research indicated that a significant variation was present between the traits. The largest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was displays by the seed cotton yield per plant, number of bolls per plant and seed index, PCV had same swerve as GCV. Highest amount of heritability and uttermost genetic advance was found in the seed cotton yield per plant (26.3), number of bolls per plant, lint index, the co-efficient of accession and phenotype variance was estimated for various parameters under survey. The GCV ranged from 27.3% (single plant yield) to 3.7 (days to 50% flowering). The largest phenotypic coefficient of variation was by seed index (18.9%), boll weight (14.3%), lint index (16.0%), and plant height (15.0%). The association of the high genetic advance and high heritability supply clear image of the parameters in the selection procedure.

Keywords: Genetic advance, upland cotton, heritability, genetic variability.

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1 Introduction

Upland Cotton (*Gossypium hirsutum* L.) is one of the most important fibre and textile crops of global importance (Anderson and Rajasekaran, 2016) which is cultivated in subtropical and tropical regions of more than 60 different countries (Chen et al., 2007; Vineela et al., 2013; Feng et al., 2017). Cotton is also famous for its named as "king of the fibre plants". It has many uses in the form of lint fibers and as cotton byproducts. Upland cotton is also known as to "pure white gold" (Kumar and Katageri, 2017). In crop improvement strategies various breeding techniques are used, and identification and utilizing the genetic material with wide genetic potential is considered as essential for the production of improved cotton cultivars against different stresses (Fang et al., 2017; Hussain et al., 2017; Luo et al., 2016; Rauf et al., 2016; Singh et al., 2018). Fiber quality is key determinant of cotton price and its products (Abdullaev et al., 2017). Technological development is not sufficient to meet the challenge to improve cotton fiber quality, which is limited by the narrow genetic base of modern cultivars. This is mainly due to prevailing negative association among the key fiber quality traits and major agronomic parameters in cotton (Clement et al., 2012; Gapare et al., 2017; Zeng and Meredith, 2009). Research activities are in progress to increase the production as well as improve quality traits of cotton (Ma et al., 2018).

Information on nature of inheritance and genetic characters is indispensable in selecting desirable breeding techniques in crop improvement (Sun et al., 2017; Vineela, 2013). Evolution of effective breeding techniques based on genetic variability of yield related traits in the available gene pool is vital in future breeding program (Clement et al., 2015). Identification of genetic variability in plant population is of great significance to explain the most appropriate breeding methods for the improvement of different parameters (Chandnani et al., 2017; Hinze et al., 2017; Sun et al., 2017).

Analysis of various cotton lines, from various origins, was conducted to assess their phenotypic performance, genetic advance, heritability, and variability. Various yield and fibre quality parameters were studied (Shakeel et al., 2012). Relative amount of heritable variation could be assessed by heritability (Magadum et al., 2012). To analysis for the proportion of phenotypic variance attributable to genetic variance, heritability will have to be estimated. This is also critical as it provides the basis for effective selection. The genetic variability along with heritability of a character will indicate the possibility and extent to which improvement is feasible through selection on phenotypic basis (Magadum et al., 2012). Heritability value alone may not clearly indicate the breeding value (Mishra P. K., 2015). Hence, combination with genetic advance over means is more effective and reliable in predicting the resultant effect of selection (Ramanjinappa et al., 2011; Eswari et al., 2018).

Current study was conducted to realize the genetic advancement, variability, and genetic variation among different accessions of upland cotton for yield, yield related parameter and quality traits. Heritability, genetic advance, genotypic, phenotypic, environmental variance and response to the selection were also calculated.

2. Materials and Methods

The study was designed to estimate the genetic variability, genetic advance, genotypic, phenotypic and environmental coefficients of variation and heritability. Field experiment was carried out in the Plant Breeding and Genetics Department, Cotton Research Institute, Anyang, Henan province, China during summer cotton season of 2017. Experimental material consisted of cotton accessions 705230, 705240, 705242, 705244, 705252, 705360, 705366, 705368, 705398, 705441, 705482, and 705542 which were arranged in randomized complete block design with three replications. Plants were grown at a distance of 30 cm (plant × plant) and 45 cm (row × row). All of the recommended cultivation practices were followed to provide stress free environment for plant growth. At the time of data collection from each replications 5 healthy plants were randomly selected for further examinations and data were recorded for sixteen parameters as, internode length (cm), plant height (cm), number of sympodial branches per plant, number of ovules, days to 50% of flowering, number of bolls per plant, number of seeds per boll, boll weight (g), lint index, ginning outturn percentage%, seed setting percentage%, 2.5% span length (mm), seed cotton yield, seed index, fiber fineness, and bundle strength or tenacity (g/tex).

Analysis of variance was calculated as described by (Steel and Torrie, 1962) using the mean values (Panse and Sukhatme, 1978). The phenotypic and genotypic co-efficient of variation was estimated using the formulas referred by (Yadav et al., 2015) and described as percentage. Genotypic and phenotypic variations were estimated using mean table (Lush, 1940). Expected genetic gain and genetic advance in the wide sense was estimated according to the equations described earlier (Johnson et al., 1955). The genetic advance, genetic variance, heritability, phenotypic variance, was estimated by using procedure of Falconer (Falconer, 1989).

Genetic variance (Vg) = (Genotype Mean Square (GMS) – Error Mean Square (EMS) (No. of Replications (r)

$$Vp=(Vg+Ve)/r \qquad [1]$$

Vp is Phenotypic Variance

Environmental variance = Error mean square (EMS)

Genotypic phenotypic and Environmental coefficient of variation was calculated as

$$GCV\ \%=\sqrt{(Vg/\bar{X})}\ \times 100 \qquad [2];$$

$$PCV\ \%=\sqrt{(Vp/\bar{X})}\ \times 100 \qquad [3];$$

$$ECV\ \%=\sqrt{(Ve/\bar{X})}\ \times 100 \qquad [4];$$

Whereas, GCV% = Genotypic Coefficient of Variation; Vp = phenotypic variance, Vg = Genotypic Variance; PCV = phenotypic coefficient of variation, Ve = environmental variability, ECV% = Environmental Coefficient of Variance;

Heritability (H2) estimated as $(H)^2=Vp/Vg$.

Table 1. Mean performance for various parameters among *G. hirsutum* accessions.

Parameter	Maximum	Minimum	Mean
Days to 50% flowering	63.0	49.0	54.5
Plant height (cm)	158.0	75.0	112.8
Internode length (cm)	6.7	3.0	5.2
No of Sympodial branch per plant	24.0	12.0	19.9
No of bolls per plant	35.5	20.5	25.6
Boll weight (g)	5.4	11.4	4.5
Number of seeds per boll	32.5	21.0	30.3
Number of ovules per flower	36.0	25.0	28.7
Seed setting percentage %	98.0	69.5	83.6
Single plant yield per plant (g)	89.6	29.7	57.6
Lint index	7.5	3.0	4.7
Seed index	12.3	5.4	8.6
Ginning outturn percentage %	43.1	28.8	39.3
2.5 % span length (mm)	32.0	23.3	26.4
Bundle strength (g/tex)	25.7	14.2	22.4
Micronaire value	5.2	3.8	3.3

3. Results and Discussion

The results of sixteen parameters of fiber and yield quality were analyzed and mentioned in the (Table 1). Depending upon performance, the accessions including 705244, 705252, 705242, 705441, 705230, and 705482 of upland cotton were established as potential donors for future breeding programs, as they presented highest mean values for bundle strength, seed plant yield, 2.5% span length and number of bolls per plants. The reorganization of donor for particular character, the high performance of these specific parameters can be calculated. Among the accessions, 705441 (6.4 g of boll weight), 705368, 705398, 705441, (43.1% of ginning outturn percentage %) were explicit for largest specific characters. The accession 705244 (31 mm, 19.2g/tex) obtained the largest 2.5% span length. Hence these accessions may be used for crossing techniques to ameliorate that specific trait in crop improvement. Chen 2007 was found to be compact type which can be utilized in development of genotype desirable for high density planting. The analyses of variance demonstrate high significant differences between all the traits analyzed in the (Table 2) and deduce genetic diversity among the genotypes.

Table 2. Analysis of variance for the various characters between the germplasm accessions of *G. hirsutum L.*

Source of Variation	Accession	Error
Degree of Freedom	51.0	55.0
Days to 50% flowering	11.4**	2.5
Plant height (cm)	476.6**	222.6
Internode length (cm)	0.4***	0.3
No of sympodial branch/ plant	12.1**	2.5
No of bolls per plant	19.3**	4.0
Boll weight (g)	0.5*	0.3
No of Seeds per boll	11.8**	5.43
No of ovules per flower	16.1**	5.5
Seed setting (%)	92.4**	38.1
Single plant yield (g)	451.9**	2.2
Lint index	1.2**	0.6
Seed index	4.5**	1.6
Ginning out turn (GOT,%)	18.1**	11.9
2.5% span length (mm)	12.2**	0.3
Bundle strength (g/tex)	5.1**	0.4**
Micronaire value	0.2	0.2

Table 3. Analysis of variance for yield fiber quality traits of *G. hirsutum L.* accessions.

Parameter	Phenotypic Variance	Genotypic Variance	PCV (%)	GCV (%)	H2 (%)	A	GA (% of Mean)
Days to 50% flowering	5.6	3.6	4.9	3.7	62.5	3.0	7.0
Plant height (cm)	345.6	121.0	15.0	13.2	34.2	16.7	14.3
Internode length (cm)	0.4	0.2	12.5	6.5	24.5	0.4	8.4
No of sym; branch/ plant	9.5	5.3	13.8	11.1	63.9	4.1	23.2
No of bolls per plant	12.7	5.7	13.4	9.9	56.2	5.2	22.8
Boll weight (g)	0.3	0.2	14.3	7.3	27.9	0.6	13.2
No of seeds per boll	7.9	3.0	11.3	5.1	33.2	3.0	8.9
No of ovules per flower	13.8	4.9	10.9	6.8	43.4	3.9	12.7
Seed setting percentage	66.3	23.7	8.5	6.5	36.2	7.6	8.8
Single plant yield (g/plant)	220.0	218.6	24.8	27.3	90.1	40.1	26.3
Lint index	0.6	0.8	16.0	12.1	45.3	1.6	20.2
Seedindex	2.4	1.5	18.9	12.4	59.2	2.4	24.1
Ginning outturn (%)	17.1	4.1	11.5	7.1	29.5	3.4	8.0
2.5% span length (mm)	5.3	4.2	8.6	6.1	95.3	6.2	18.4

PCV-phenotypic coefficient of variation; GCV-genotypic coefficient of variation; H^2- heritability; GA-genetic advance.

Genotypic variance, phenotypic variance, GCV, PCV and heritability was calculated for sixteen parameters are described in (Table 3). Understanding the nature and magnitude of variability available in the genotypes for different characters is a crucial for selection of characteristics to bring remarkable improvement in cotton.

The heritable (genotypic) variation is usually masked by non-heritable variation creating difficulty in exercising selection. In our study accessions 705230, 705240, 705242, 705244 are the potential donors for the desired characters including days to 50% flowering, whereas accessions 705368, 705398, 705441, are the potential donors for plant height. Accessions such as 705482, 705542, 705242, and 705244 are the potential donors for numbers of sympodial branch per plant, and 705441, 705398, 705368, 705366 are the potential donor for boll weight. Accession 705441 showed promising results for the yield parameters including highest single plant yield as well as in plant height, internode length, number of ovules per flower, number of bolls per plant, ginning outturn % and fiber strength. Hence it becomes necessary to partition overall variability into heritable and non-heritable components to enable the breeders to plan for proper breeding programme. In the phenotypic variance plant height is obtained largest value (345.6) whereas single plant yield showed highest value (220.0).

Heritability estimate was high for days to 50 % flowering, plant height, boll weight, upper half mean length, bundle strength, micronaire value and seed cotton yield. This determination was similar with earlier finding (Santoshkumar et al., 2014). The fiber fineness values displays the lowest phenotypic variance (0.2) with parameters such as, boll weight, fiber fineness, and inter node length, value had obtained the lowest value (0.2). The co-efficient of genotypic and phenotypic variance were estimated for all the characters under study. The phenotypic coefficient of variation ranged from 4.9 (days to 50% flowering) to 24.8% (single plant yield) . The largest phenotypic coefficient of variation was complying by boll weight (14.3), lint index (16.0%) plant height (14.0%), and seed index (18.9%),

Genotypic co-efficient of variation had a similar trend as phenotypic coefficient of variation. The range varied from 3.7 (Days to 50% flowering) to 27.3 single plant yield per plant. The maximum GCV was observed for SPY (27.3) followed by seed index (12.4), number of sympodial branch per plant (11.1), lint index (12.1) and number of bolls per plant (9.9), plant height (13.2). The lowest phenotypic coefficient of variation (4.4%) and GCV (3.6) value was observed in days to 50 % flowering (Figure 1). In the present study, there was a close correspondence between genotypic and phenotypic variance for days to 50% flowering, single plant yield, 2.5% span length, boll weight, inter node length, lint index, and micronaire value indicating less environmental influence. But number of sympodial branch per plant, plant height, number of seeds per boll, seed setting percentage%, number of bolls per plant, ginning outturn percentage% showed higher variation indicating the influence of environment on these characters (Dhivya et al., 2014). Since the variations are influenced by the magnitude of the units of measurement of different traits. Moreover significant role of climatic conditions on manifestation of these parameters is evident from PCV values.

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

No.	Trait	Potential Donor Accessions
1	Days to 50% flowering	705230, 705240, 705242, 705244
2	Plant height (cm)	705368, 705398, 705441,
3	Internode length (cm)	705244, 705252, 705360, 705366, 705368, 705398, 705441,
4	No of sympodial branch/ plant	705482, 705542,705242, 705244,
5	No of ovules per flower	705441,705482,705542
6	No of bolls per plant	705360, 705441, 705482, 705230, 705244, 705252
7	Boll weight (g)	705441, 705398, , 705368, 705366,
8	No of Seeds per boll	705244, 705252, 705242,
9	Seed setting percentage%	705242, 705542, 705482,
10	Single plant yield (g)	705244, 705252, 705242, 705441, 705230, 705482,
11	Lint index	705252, 705360, 705366
12	Seed index	705398, 705482, 705542
13	Ginning outturn (GOT %)	705360, 705366, 705368, 705398, 705441,
14	2.5% span length (mm	705244, 705252,
15	Bundle strength (g/tex)	705542,705482, 705441, 705252, 705230,
16	Micronaire value	705360, 705366, 705368, 705398

The highest PCV and GCV estimates were recorded for single plant yield indicating the presence of significant genetic variability in this character. Similar genetic variability in cotton was reported by (Dheva and Potdukhe, 2002; Preetha and Raveendran, 2007; Hafiz et al., 2013). Moderate GCV and PCV estimates were noticed for the character such as number of sympodial branch per plant, seed index, plant height, lint index, and number of bolls per plant. Similar variations in the genotypic and phenotypic coefficients in cotton were reported (Girase and Mehetre, 2002; Harshal, 2010) these parameters can be improved for genotype selection program. Fiber quality parameters like as micronaire values, 2.5% span length, and days to 50% flowering, displays less GCV and PCV which indicates that the breeding induced improvement are consistent with the earlier reports (An et al., 2008; Kowsalya and Raveendran, 1996). In a population, the discovered variability is a combined measure of environment and genetic causes.

Genetic variability describes inter-generation heritability in plants. The parameters which indicate huge genetic progress and high heritability as percentage of mean values could be utilized 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 heritability ranged from 90.1% (single plant yield) to 24.5 (internode length. The highest value of heritability (95.3%) was obtained in 2.5% span length comply by SPY (90.1%) and the lowest value of heritability was estimated in internode length (24.5%). The high heritability was registered in the traits such as, number of sympodial branch per plant, seed index, bundle strength, 2.5% span length, and single plant yield. Whereas in case of inter node length displays short heritability in present probe. The combination of high heritability with high genetic advance will provide a clear base on the reliability of that particular character in selection of variable entities. The genotypic advance as percent of mean for sixteen traits ranged from 7.5% to 26.3%. The higher GA as percent of means was recorded by single plant yield (26.3%) followed by seed index (24.1%), number of sympodial branch (23.2 %), number of bolls per plant (22.8 %). The lowest value (7.0%) was observed in the trait days to 50% flowering. High heritability along with high genetic advance was observed in traits such as, number of sympodial branch per plant, seed index, micronaire value, and single plant yields, in upland cotton (An et al., 2008). These traits are highly reliable during selection. High heritability combined with moderate genetic advance was found in the 2.3% span length, it was in accordance with of (Muhammad et al., 2004). Among the study material 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 the earlier is the preferred attribute and early flowering was taken into consideration.

4. Conclusion

The conclusions of the present study can be described that the parameters which shows that high range of variation and high genetic variability. A significant genotypic coefficient of variation over phenotypic coefficient of variation for the parameters study indicates that atmospheric effects the manifestation of these parameters under examined. High genetic advance, genetic gain and heritability were recorded for number of sympodial branch per plant, seed index, micronaire value, 2.5 % span length and single plant yield, performance can be haunt for the improvement of these traits in the upcoming crop improvement. In the conclusion the genotypes 705441, 705398 have larger genetic potential and space for further enhancement of seed cotton yield and its attributes. So for perceptible results in yield and yield contributing traits, due consideration will potentially utilize promising genotypes in the future cotton breeding programs under environmental conditions for cotton growing.

List of Abbreviations: BS, bundle strength; BW, boll weight; ECV%, environmental coefficient of variation; GA, genetic advance; GCV, genetic coefficient of variation; GOT%, ginning outturn percentage; H2, heritability; IL, internode length; LI, lint index; MV, micronaire value; PCV, phenotypic coefficient of variation; PH, plant height; SCY, seed cotton yield; SI, seed index; SL, span length; SPY, single plant yield; Ve, environmental variability; Vg, genetic variance; Vp, phenotypic variance.

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Authors Contribution: FS, QM, AHJ planned and designed the experiment, AHJ, LW, XW, ZHJ planted, grew and harvested the material and analysed the data. AHJ, XW drafted the manuscript; AHJ wrote the manuscript. All authors read and approved the final manuscript for submission.

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