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Assessment of genetic variability in diverse genotypes of *Gossypium arboreum* L. for yield and related traits under north western plains

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Abstract: The present study was conducted on seventeen diverse genotypes of cotton belonging to different parts of India to analyze the parameters of genetic variability for seed cotton yield and its components at Cotton Research Area, Punjab Agricultural University, Ludhiana and Regional Station, Faridkot, Punjab. Analysis of variance revealed significant differences for all the traits at both locations indicating sufficient variability present in the material. The phenotypic coefficient of variation (PCV) ranged from 7.95 to 34.66 at Faridkot whereas at Ludhiana it varied from 6.47 to 26.45 for ginning out turn and lint yield, respectively. Heritability ranged from 24.18 to 94.91 at Faridkot and 45.71 to 91.38 at Ludhiana, for boll weight and lint yield respectively. High genetic advance (GA) was observed in only two traits seed cotton yield (31.41 & 26.87) and plant height (28.12 & 19.19). High heritability coupled with high genetic advance as percentage of mean (GAM) was recorded for seed cotton yield (59.86 & 41.39), boll number (25.62 & 33.93), lint yield (57.71 & 49.79) and number of sympods (51.75 & 41.15) at Faridkot and Ludhiana respectively. Hence simple selection based on phenotypic performance of these characters would be more effective.

Key words: *Gossypium arboreum*, Genetic variability, Heritability, Genetic advance

Introduction

Cotton belongs to genus *Gossypium,* family *Malvaceae* and is distributed throughout tropical and subtropical regions of the world. Although *Gossypium* has 50 species which include 45 diploid and 5 allopolyploid, only two species of diploid cotton (*G. arboreum* and *G. herbaceum)* are under cultivation. *G. arboreum* known as 'old world cotton' is native of India having AA genome with 2n=26 number of chromosomes. The Indian sub-continent has a long tradition of cultivation of the diploid species which extends back to at least 4,300 years (Iqbal *et al.,* 2001). Cotton is one of the most important source of fibre as well as oil seed hence it is called "White Gold". It is one of the few crops which are accessible to development of genotypes as varieties and at the same time amenable for commercial exploitation of heterosis. India is the first country to make pioneering effort to exploit the phenomenon of heterosis in the crop (Reddy and Sarma, 2014). *G. arboreum* once covered 16% of total cotton and occupies 3rd position in area after hybrids (40%) and *G. hirsutum* (36%) but with introduction of Bt cotton the area under *G. arboreum* has further decreased. Yet *G. arboreum* has an excellent agronomic traits viz., coarse fibre, early maturing and high fibre strength which are lacking in tetraploid cotton. In addition, *G. arboreum* has resistance to cotton leaf curl virus, diseases like black root rot and pests such as nematodes and aphids (Kumar *et al.,* 2008). The drought resistance character of *G. arboreum* makes it well adapted to dryland conditions and low input farming. Also to exploit the commercial importance of *G. arboreum* for coarse fibre, development of varieties with high productivity and ginning out turn (GOT) is of utmost importance.

Success of any breeding programme for the improvement of agronomic traits depends upon the genetic variability (Sidra *et al*., 2014; Laila *et al*., 2014). Genetic variability is the tendency of individual genotypes in a population to vary from one another in response to environmental and genetic influences (Ali *et al.,* 2009). Creating genetic variability is pre-requisite for plant breeders to exercise selection, as a part of continuous variation is due to heredity. The coefficient of variation indicates only the extent of variability existing for various traits, but does not give any information about its heritable portion (Neelam and Patdukhe, 2002). The magnitude of heritability is influenced by variability, the extent to which a particular character is affected by prevailing environmental conditions. This would be useful in indicating the ease or difficulty in attaining effective selection on the basis of phenotypic performance. Heritability in itself provides no indication about the genetic progress that would result from selection. However, at a fixed selection pressure, the amount of genetic advance varies with magnitude of heritability. Genetic advance in a population cannot be predicted from heritability alone, the genetic gain for specific selection pressure has to be worked out (Ranganatha *et al.,* 2013). The measurement of genetic variation and mode of inheritance of qualitative and quantitative traits are always of prime importance in planning the breeding programmes (Shah *et al*., 2015; Ullah *et al.,* 2015). Therefore, Information on genetic variability, heritability and genetic advance is helpful for planning and execution of breeding programme and selection of diverse parents to achieve heterotic combinations and to generate segregating population with an objective of isolating superior genotypes. Therefore, the present study was conducted with the objective to determine the genetic variability, heritability and genetic advance study for seed cotton yield and its component traits in diverse genotypes of *Gossypium arboreum.*

Materials and Methods

The experimental material comprised of 17 genotypes consisting of seven genotypes from Punjab LD327, LD866, LD902, LD210, LD575, LD733 and LD694; HD457 from Haryana; RG395 and RG8 from Rajasthan; KWA147 from Madhya Pradesh; MDL2643 from Andhra Pradesh and PA255, PA606, AH11, AH38 and DLSa1001 from Maharashtra which were evaluated during *Kharif* 2010 (Fig. 1). The performance trials of 17 cultivars selected from diverse origin were conducted at two testing sites one at Cotton Research Area, Punjab Agricultural University, Ludhiana (30°90'N; 75°82'E) and other at Regional Station, Faridkot (30°67'N; 74°74'E). The material was sown in randomized complete block design with three replications. Each entry was grown in a two-row plot 6.7m long with 96.5 cm spacing between rows. Recommended package practices were followed in raising the crop. Data for ten characters i.e. seed cotton yield per plant (g), number of bolls, boll weight (g), seed index (g), halo length (mm), ginning out turn (%), lint index (g), lint yield (g), Plant height (cm), number of sympods was recorded on 10 competitive plants at each location. Single plant data for seed cotton yield was recorded after all pickings. Boll weight was determined on average weight of 20 well opened bolls. Ginning out turn percentage was determined by dividing the weight of the lint sample after ginning by the weight of the lint sample before ginning. Halo length was recorded with halo disc scale. Seed index was 100 seed weight.

Lint index = (Seed index x GOT) / 100 x GOT

Lint yield = (Seed cotton yield - GOT) / 100

Statistical analysis: The recorded data was subjected to analysis of variance (Panse and Sukhatme, 1985).

Genetic variability: Genotypic coefficient of variance (GCV), Phenotypic coefficient of variance (PCV) and broad sense heritability (H^2), genetic advance (GA), genetic advance as percentage mean (GAM) were computed according to Burton and Devane (1953), Johnson *et al.* (1955) and Singh and Chaudhary (1985).

Genotypic coefficient of variation (GCV) = $\sqrt{V_g}/GM \times 100$

Phenotypic coefficient of variation (PCV) = $\sqrt{V_P}/GM \times 100$

Heretablity (H^2) = V_g/V_p x100

Genetic advance (GA) = $K \sigma p H^2$

Genetic advance as percentage of mean (GAM) = (GA/GM) x 100

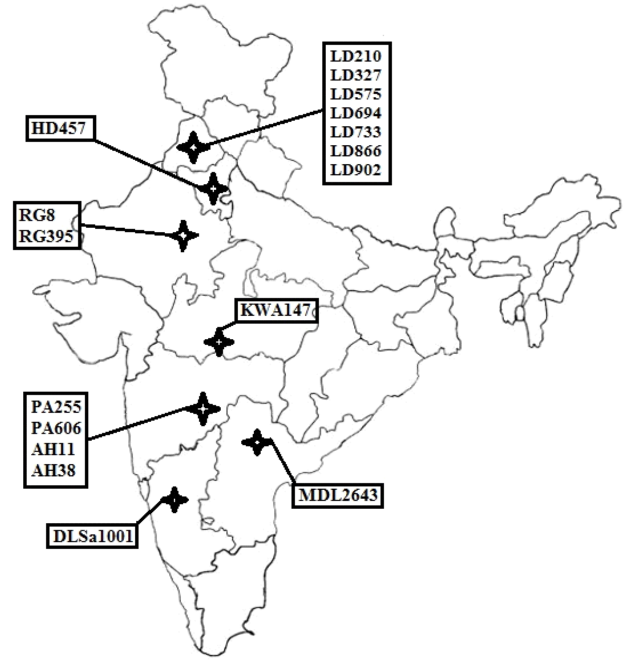

Fig. 1: Geographic origin of 17 *Gossypium arboreum* genotypes collected from seven different states of India

Where: V_g = Genotypic variance; V_P = Phenotypic variance; GM = Grand mean of the trait; H^2 = Broad sense heritability for a trait; K = 2.06 (selection differential at 5% selection intensity); σp = phenotypic standard deviation.

Results and Discussion

The analysis of variance revealed significant differences among the all genotypes for yield and related traits at both the locations i.e. Ludhiana and Faridkot indicating existence of variability in the present material selected for the study (Table-1). The material can be utilized for varietal improvement programme by selection of suitable genotypes for initial breeding. However, the absolute variability in different characters does not permit identification of the characters showing the highest degree of variability. Mean performance of most of the traits was better at Faridkot except for seed cotton yield (52.48g), lint yield (19.41g) and number of sympods (21.02) whereas at Ludhiana these traits having values of 64.91g, 23.67g and 25.53 respectively. Range for all the traits at both locations indicated sufficient variability in the genotypes under consideration (Table-2 and 3).

The partition of coefficient of variation into phenotypic and genotypic helps in better understanding of variability. The phenotypic coefficient of variation (PCV) ranged from 7.95 to 34.66 at Faridkot whereas at Ludhiana it varied from 6.47 to 26.45 for ginning out turn and lint yield, respectively. Similarly in genotypic coefficient of variation (GCV) range varied from 3.91 to 31.07 at Faridkot and 6.19 to 25.28 at Ludhiana for ginning out turn and lint yield respectively. The high PCV and GCV (more than 25%) was observed for three traits *i.e.* seed cotton yield (32.43 and 30.70) and number of sympods (26.47 & 25.79) at Faridkot only and lint yield (34.45 and 31.07) and (26.45 and 25.28) at Faridkot and Ludhiana respectively (Table-2 and 3). Concurrent results were reported by Jagtap and Mehetre

Table-1: Analysis of variance for yield and related traits

Traits	Mean Squares					
	Ludhiana			Faridkot		
	Replication	Treatment	Error	Replication	Treatment	Error
Df	2	16	32	2	16	32
Seed cotton yield	34.32	577.77**	12.08	96.43	808.54**	30.06
Boll number	37.04	77.82**	10.87	15.63	42.56**	8.19
Boll Weight	0.01	0.08*	0.02	0.02	0.18*	0.05
Halo Length	5.54	13.77**	1.82	0.13	13.79**	0.81
Seed Index	0.03	0.39**	0.07	0.23	0.48*	0.12
Ginning Out Turn	5.27	12.83**	1.82	2.27	12.72**	1.5
Lint Index	0.01	0.46**	0.02	0.04	0.38**	0.12
Lint Yield	3.37	110.81**	3.38	20.68	117.43**	8.36
Plant Height	120.79	466.29**	69.43	14.88	883.09**	102.87
Sympods number	5.47	88.50**	2.80	7.43	89.73**	3.58

*P e” 0.05;**Pe”0.01

Table-2: Genetic variability parameters in diverse genotypes of diploid cotton at Faridkot

Traits	Mean	Range	PCV	GCV	H^2	GA	GAM
Seed cotton yield	52.48	22.0-90.8	32.43	30.70	89.62	31.41	59.86
Boll Number	26.12	18.70-35.30	15.46	13.87	80.44	6.69	25.62
Boll Weight	2.53	1.86-3.17	12.19	8.06	43.71	0 .28	10.98
Halo Length	21.22	17.38-25.30	10.68	9.80	84.22	3.93	18.53
Seed Index	5.68	4.62-6.83	8.60	6.05	49.41	0.50	8.76
Ginning Out Turn	36.82	26.5-45.2	7.95	3.91	24.18	1.46	3.96
Lint Index	3.32	2.41-4.46	13.66	8.90	42.46	0.40	11.94
Lint Yield	19.41	7.4-33.6	34.45	31.07	81.31	11.20	57.71
Plant Height	195.40	166.7-233.0	9.75	8.25	71.66	28.12	14.39
Sympods	21.02	12-33	26.47	25.79	94.91	10.88	51.75

Table-3: Genetic variability parameters in diverse genotypes of diploid cotton at Ludhiana

Traits	Mean	Range	PCV	GCV	H^2	GA	GAM
Seed cotton yield	64.91	41.53-98.62	22.04	21.04	91.17	26.87	41.39
Boll Number	23.52	12.00-32.60	24.50	20.09	67.24	7.98	33.93
Boll Weight	2.10	1.51-2.60	9.53	6.45	45.71	0.19	8.98
Halo Length	20.52	15.53-26.53	11.74	9.73	68.69	3.41	16.61
Seed Index	5.22	4.47-6.01	8.08	6.19	58.67	0.51	9.76
Ginning Out Turn	36.22	30.56-42.85	6.47	5.29	66.91	3.23	8.91
Lint Index	3.01	2.26-4.28	13.70	12.69	85.88	0.73	24.23
Lint Yield	23.67	14.95-41.04	26.45	25.28	91.38	11.78	49.79
Plant Height	159.86	120-186	8.88	7.19	65.58	19.19	12.00
Sympods	25.53	16-37	21.94	20.94	91.06	10.51	41.15

(1998); Reddy and Sarma (2014). High PCV and GCV indicating presence of high variability among these traits hence, selection can be effective. The Low PCV and GCV (less than 15%) was observed for most of the traits at both the locations. The moderate PCV and GCV (15% to 25%) was observed for seed cotton yield (22.04 and 21.04), number of sympods (21.94 and 20.94) and boll number (24.50 and 20.09) at Ludhiana. At Faridkot, for boll number moderate PCV (15.46) and Low GCV (13.87) was observed. Moderate PCV and GCV for boll number and boll weight were also reported by Neelima *et al.* (2008). The moderate to low coefficient of variation indicates that improvement for the traits is possible through intercrossing followed by recurrent selection to increase the gene flow and to fix favourable allele. The higher value of PCV than GCV in the present study for all the traits at both locations revealed environmental influence on the expression of the traits whereas, difference between PCV and GCV was observed to be less for all the characters at both locations (Neelam and Patdukhe, 2002). It indicates that traits were less influenced by environmental conditions hence could be improved by following different phenotypic selections i.e. directional, disruptive and stabilizing selection (Ranganatha *et al.,* 2013).

The heritability acts as predictive instrument in expressing the reliability of phenotypic value. It is an index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse population. In the present investigation, heritability ranged from 24.18 to 94.91 in ginning out turn and number of sympods respectively, at Faridkot and 45.71 to 91.38 in boll weight and lint yield respectively, at Ludhiana. High heritability (more than 60%) was observed for six traits viz., number of sympods (94.91), seed cotton yield (89.62), halo length (84.22), lint yield (81.31), boll number (80.44) and plant height (71.66) at Faridkot. At Ludhiana most of traits have high heritability except boll weight (45.71) and seed index (58.67) have moderate level of heritability (30 to 60%) (Table-2 and 3). The characters with high heritability indicate less influence of environment which ultimately helps the breeder to make the selections based on phenotypic expression by adopting simple selection methods. Selection for low heritability characters i.e. seed index (24.18) is not fruitful. Neelam and Patdukhe (2002) and Alkuddsi *et al.* (2013) also reported similar results.

The genetic advance is an indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.,* 1955). In present investigation, high genetic advance was observed in only two traits seed cotton yield (31.41 and 26.87) and Plant height (28.12 and 19.19) at Faridkot and Ludhiana respectively. Selection for these characters is more responsive (Table-2 and 3).

Heritability coupled with genetic advance as percentage mean (GAM) is more useful than heritability alone in predicting the resultant effect during selection of best individual genotype. Genetic advance is measure of genetic gain under selection and expression in percentage of mean (Johnson *et al.,* 1955). In present investigation high heritability and high GAM (more than 20) was recorded for seed cotton yield (59.86 and 41.39), boll number (25.62 and 33.93), lint yield (57.71 and 49.79) and number of sympods (51.75 and 41.15) at Faridkot and Ludhiana respectively, indicating predominance of additive gene action for these characters. Simple selection based on phenotypic performance of these traits would be effective. Alkuddsi *et al.* (2013) and Reddy and Sarma (2014) also reported high heritability accompanied by genetic advance and genetic advance as percentage mean for seed cotton yield. Moderate GAM (10-20) along with high heritability was observed for plant height (14.39 and 12.00) and halo length (18.53 and 16.61) at both locations indicating the influence of non-additive gene action along with environmental influence in the expression of these traits (Table-2 and 3). These traits can be exploited through manifestation of dominance and epistatic components through heterosis. Traits with low GAM (less than 10) don't have high heritability hence selection for such traits should be postponed for these traits or intermating can be exploited for creating segregation population using recombination breeding.

Conclusively, only heritable component of variability can be utilized, using suitable breeding methodologies to exploit both additive as well as non-additive gene effects. Use of multiple locations also helps in better understanding of genetic variability present in the genotypes to achieve main goal of varietal and hybrid development which will go a long way in the cotton improvement programme.

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