Characterization of diverse genotypes of American cotton for yield and its components in South Western Punjab

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Abstract
The present investigation was carried out on 34 American cotton genotypes, which were evaluated at PAU, Regional Research Station, Faridkot during *kharif* 2017 for seed cotton yield and its various component traits. Result reveals presence of highly significance variation among the all studied genotypes for all the characters. Out of the thirty four studied genotypes thirteen genotypes outperform over the checks for seed cotton yield. RAH0604, RS2906, RB607, BS2-17 and H1508 39 are the best five performing genotypes for seed cotton yield per plant and lint yield per plant. Some genotypes have shown best performance for specific trait(s). The traits like Boll wt, Bolls per plants, Sympods per plants and Plant height showed high to moderate heritability in broad sense and highly significant positive genotypic association with seed cotton yield.

Introduction

The cotton, *Gossypium Spp.* is the most important source of natural fiber that has met the clothing needs of mankind for several millennia. This plant plays a major role in the economy and social structure of many countries, and in fact, has helped shape the history of some parts of the world (Ranganatha *et al.* 2013). Although many other natural and synthetic fibers have been available, advantages related to the cost of production, many unique features offered by cotton lint, and the growing world population will ensure a continued increase in the demand for seed cotton (Rajan *et al* 2018).

In India, cotton is being grown in varied agro-climatic situation across nine major states of three cotton zones of the country with area of 11.69 million hectares with production of 36.59 million bales and productivity of 532 kg lint/hac during 2016-17 (http://www.indiastat.com). In Punjab, cotton is consider as major kharif crop which is mainly grown in south western area of Punjab occupying nearly 2.78 lakh hectares area with an annual production of 12.43 lakh bales in 2016-17 (http://www.indiastat.com).

A long-term challenge, a cotton breeder facing is the continuously development of new hybrids/varieties with superior performance for seed cotton yield and fiber quality traits over the existing hybrids/varieties to meet the demands of cotton grower and cotton industries (Choudhary and Gaur 2015). But development of such improved cultivars largely depends upon magnitude and nature of genetic variation present in breeding population. Hence characterization of various genotypes for genetic variability through the estimation of different genetic parameters like components of variances, genotype and phenotype coefficients of variation heritability and genetic advance as percent of mean make significantly important (Pujer *et. al.,* 2014).

Since seed cotton yield is a complex trait and influenced by various environmental factors, selection directly depended on yield may not be rewarded, therefore association analysis between seed cotton yield and its component characters is essential to determine traits combinations on which selection can be made in breeding programs (Baloch *et al*. 2014).

Present study is carried out to characterize diverse genotypes of American cotton developed at different cotton breeding centre of India with objective to select superiorly performing genotypes and estimation of genetic variability present in studied genotypes for yield and its contributing characters.

Material and Methods

The experimental material for the present investigation was comprised of **34** American cotton genotypes developed at different cotton breeding

centers under All India Coordinated Research Project on cotton. List of studied genotypes along with its developing centers has been provided in **table no.1**. These genotypes were evaluated during *Kharif* 2017 at experimental area of Punjab Agricultural University (P.A.U), Regional Research Station, Faridkot in randomized complete block design with three replications with plant to plant spacing of 60 cm and row to row spacing of 67.5 cm. The observations were recorded on Seed cotton yield (kg/hac), Lint yield (kg/hac), GOT (%), Boll wt (gm), Seed index (g), Lint index (g), Boll per Plant, Plant ht (cm), Monopods per Plant, Sympods per plant as per standard procedures.

Analysis of variance was carried out as per procedure given by Panse and Sukhatme, 1961 and the estimates of range, variance, phenotypic and genotypic co-efficients of variation (PCV, GCV), heritability in broad sense, genetic advance as percent of mean and Phenotypic and genotypic correlations for 10 characters of thirty four genotypes of cotton were estimated using OPSTAT software. Further all the studied characters were classified in three category of variation as high (>20 %), moderate (10 to 20 %) or low (<10 %) according to method given by Sivasubramanian and Menon (1973).) Based on value of heritability all studied characters were categorized as high (>60 %), medium (31 to 60 %) and low (<30 %) as per suggested by Jhonson *et al.* (1955).

Result and Discussions

Analysis of variance for all ten studied characters is presented in **Table no. 2**. Analysis of variance reveals presence of highly significance variation among the all studied genotypes for all the characters. Data on mean value of each character with respect to each genotype is given in **table no.1**. Out of the thirty four studied genotypes thirteen genotypes outperform over the checks for seed cotton yield. The seed cotton yield was ranged from 3387.7 kg/hac (RAH0604) to 401.6 kg/hac (PBH139) with total mean value of 1416.6 kg/hac. The lint yield was ranged from 1188.2 kg/hac (RAH0604) to 146 kg/hac (PBH139) with total mean value of 525.32 kg/hac. GOT was varied between 40.4 % (F2662) and 34 % (TSH332) with total mean of 37.01 %. The grand mean value of boll weight was 2.95 gm and it was varied from 3.8 gm (F2662) to 2.2 gm (RAH0603). The seed index was ranged between 8.3 gm (CSH1604) and 6.5 gm (F2596) with grand mean of 7.34 gm. The Lint index was ranged from 5.1 gm (F2662) to 3.7 gm (RAH0603) with total mean of 4.32 gm. The bolls/plant were varied from 56.6 (RAH0604) to 15.4 (TSH325) with grand mean of 31.27. The plant height was ranged between 152.5 cm

(RB607) to 60.8 cm (CPD1702) with total mean value of 112.77 cm. The grand mean value of monopods/plant was 1.35 and ranged from 2.7 (HS300) to 0 (TVH001). The sympods/plant was varied between 30.7 (TVH001) to 18.7 (CSH1604) with grand mean of 22.94. The genotype RAH0604 recorded the highest values for seed cotton yield (3387.7 kg/hac), lint yield (1188.2 kg/hac) and bolls/plant (56.6) whereas genotype F 2662 recorded the highest values for GOT (40.4 %) and boll weight (5.1 gm). These results indicate the presence of significant genetic variation in the studied genotypes. Result of this investigation was in concurrence with the findings of Tulasi *et al*, 2014 and Shoaib Liaqat *et al.*, 2015 in American cotton.

Overall, the best five genotypes which have outperformed the standard check for seed cotton yield per plant and lint yield per plant were RAH0604, RS2906, RB607, BS2-17 and H1508 39 whereas F2662, GSHV199, CSH 3129, SHJ23 and F2596 for ginning outturn, CSH1604, BGDS0607, RHC1346, GJHV520 and GJHV-523 for seed index, F2662, CSH1604, BGDS0607 and TVH001 for lint index, F2662, RS2906 and BGDS0607 for boll weight, RAH0604, H1508, RS2906, RB607 and CPD1701 for bolls per plant, RB607, BGDS0607, H1508, BS2-17 and TVH001 for plant height, HS300, RS2913, BS3-17, RB608 and F2662 for monopods per plant; TVH001, CPD1701, RB607, H1508, RAH0604 for sympods per plant.

The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) in broad sense and genetic advance as per cent mean of ten traits are presented in **Table 3**. Present results reveals that phenotypic coefficient of variation was ranged from 5.0 to 56.2 per cent whereas genotypic coefficient of variation was ranged from 2.9 to 55.4 per cent. Environmental impact was observed to be effective in all the studied traits because, PCV values were higher than GCV values in all studied traits. This finding is in agreement with the results obtained by Sakthi *et al.* (2007) and Pujer *et. al.,* (2014). High genotypic coefficient of variation was shown by Seed cotton yield, Lint yield, Boll per plant, Plant height, Monopods per plant, indicating that these characters were not much affected by the environment. So, selection based on these traits would be rewarded in successful isolation of desirable genotypes. Moderate phenotypic and genotypic coefficient of variation was revealed by Boll wt and Sympods per plant whereas low phenotypic and genotypic coefficient of variation was shown by traits like GOT, Seed index and Lint

index. Similar finding were obtained by Dinakaran *et al.* (2012), Usharani *et al.* (2014) and Reddy *et al.* (2015). Heritability gives the contribution of genetic causes to the phenotypic variance and predicts the extent to which it is transmitted to further generations. Traits like Seed cotton yield, Lint yield, Boll wt, Boll per Plant, Plant ht (cm), Monopods per Plant have shown high heritability in broad sense whereas GOT, Seed index, Lint index, Sympods per plant shown moderate high heritability in broad sense. These finding were also supported by the results obtained by Amir *et al.* (2012) and Abbas *et al.* (2013). In the present investigation high heritability coupled with high genetic advance was observed for Seed cotton yield (kg/hac), Lint yield (kg/hac), Boll wt (gm), Boll per Plant, Plant ht (cm) and Monopods per Plant indicating the preponderance of additive gene action in the inheritance of this trait.

Correlation coefficient is a most important biometrical technique for formulating the best selection indices, as it identifies the strength and direction of relationship among the various studied traits. In present study, Lint yield, Boll wt, Lint index, Boll per Plant, Plant ht, Sympods per plant showed a highly significant positive phenotypic and genotypic association with seed cotton yield (Table 4). These traits can be collectively used for selection of superior genotypes for yield improvement in cotton. Boll weight and bolls per plant are taken as significant contributor in improvement of cotton seed yield since it is assumed that more number of bolls per plant with larger weight will result in higher seed cotton yield (Baloch *et al.* 2014). Haidar *et al.*(2014) and Thiyagu *et al.*(2010) also obtained similar positive association for boll weight, bolls per plant and sympods per plant with seed cotton yield.

On the contrary, monopods per plant exhibited a negative and significant correlation with seed cotton and lint yield whereas GOT did not show any positive or negative significant correlation with seed cotton and lint yield. Eswari *et al.,* (2017) also obtained the similar kind of result for monopods per plant. Highest value of positive and significant genotypic correlation was observed between seed cotton yield and lint yield (0.999) which is followed by boll wt and lint index (0.842), Plant ht and Sympods per plant (0.814), lint yield and Sympods per plant (0.801) whereas seed cotton yield and Monopods per Plant (0.487) exhibited highest value of negative and significant genotypic correlation followed by Boll per Plant and Monopods per Plant (0.481).

Present investigation reveals presence of significant variation among the various studied genotypes for seed cotton yield and its component traits. Genotypes namely, RAH0604, RS2906, RB607, BS2-17 and H1508 39 are the best five genotypes which have performed over the checks for seed cotton yield per plant and lint yield per plant. These genotypes can be release as a variety after evaluating in advanced trial and confirming their outperformance. Some genotypes have shown top performance for specific traits like F2662 for GOT, boll wt and lint index, RB607 and CPD1702 for higher and lower plant height respectively, PBH139 and TVH001 for lower monopods per plant, TVH001 for higher sympods per plant. These genotypes can be use as a parent according to objectives of various breeding procedures. The traits *viz.,*   Boll wt, Bolls per plants, Sympods per plants and Plant height were observed to be significant yield contributing traits since these traits showed high to moderate heritability in broad sense and highly significant positive genotypic association with seed cotton yield. So, selection based on these traits will reward genetic improvement of seed cotton yield.

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Table 1. List of cotton genotypes studied and mean value of each character with respect to each genotype.

S. No.	Name of Entry	Name of developing institute	Seed cotton Yield (kg/hac)	Lint (kg/hac)	GOT (%)	Boll wt (gm)	Seed index	Lint index (g)	Boll per Plant	Plant ht (cm)	Monopods per Plant	Sympods per Plant
1	PBH116	PAU, Bathinda	2135.8	798.2	37.4	3.1	7.0	4.2	33.2	132.2	1.7	25.6
2	F2662	PAU, Faridkot	1415.2	572.5	40.4	3.8	7.5	5.1	24.3	97.2	2.1	20.4
3	HS300	CCS HAU, Sirsa	491.4	168.1	34.2	2.6	7.1	3.7	27.2	90.8	2.7	18.7
4	F2596	PAU, Faridkot	907.0	347.1	38.3	2.9	6.5	4.0	38.2	76.1	1.5	20.5
5	PBH139	PAU, Bathinda	401.6	146.0	36.8	3.0	7.6	4.4	26.4	95.8	0.4	19.8
6	H1488	CCS HAU, Hisar	1802.5	681.5	37.7	2.9	7.2	4.4	33.7	87.5	1.9	21.4
7	F 2228	Zonal Check	868.7	321.9	37.3	3.4	7.7	4.6	23.5	98.6	1.9	21.3
8	H1508	CCS HAU, Hisar	2409.5	913.2	37.9	2.8	6.6	4.0	49.2	149.2	0.5	27.0
9	RS2906	ARS, Sriganganagar	2596.3	950.2	36.6	3.7	7.7	4.4	42.2	136.9	0.5	26.2
10	TSH325	TNAU, Srivilliputhur	620.6	235.8	38.0	2.7	7.1	4.4	15.4	82.2	1.5	20.2
11	CSH3419	CICR, Sirsa	1253.9	468.4	37.4	3.1	7.5	4.5	18.0	90.8	1.6	19.5
12	BGDS0607	UAS, B' Gudi	2353.5	858.9	36.5	3.7	8.2	4.8	34.3	150.8	0.9	24.5
13	LH 2108	Local Check	1694.3	624.6	37.0	3.0	6.8	4.0	31.4	123.3	0.8	25.5
14	RS2913	ARS, Sriganganagar	660.5	247.4	37.4	2.6	6.7	4.0	23.5	104.2	2.4	19.2
15	CSH 3129	Quality check	1908.6	736.9	38.6	2.8	7.0	4.4	35.9	124.7	1.3	26.2
16	BS2-17	OUAT, Bhawanipatna	2429.6	915.3	37.6	3.0	7.1	4.3	34.5	145.3	1.0	26.3
17	RB607	ARS, Banswara	2431.3	917.6	37.8	2.9	7.2	4.4	40.6	152.5	1.0	27.6
18	TVH001	TNAU, Veppanthattai	1786.8	675.4	37.9	3.0	7.7	4.7	37.4	143.6	0.0	30.7
19	RB608	ARS, Banswara	546.5	196.6	36.0	2.4	7.1	4.0	21.9	103.3	2.2	20.2
20	ARBH1701	UAS Arabhavi	964.6	359.2	37.1	2.9	7.3	4.3	34.7	105.6	1.2	23.4
21	TCH1828	TNAU, Coimbatore	678.2	247.2	36.4	2.5	6.9	4.0	25.9	88.0	1.2	19.1
22	RHC1346	MPKV, Rahuri	1989.3	730.0	36.7	3.3	8.0	4.6	38.0	119.7	1.8	24.5
23	CPD1701	UAS Dharwad	2386.4	912.2	38.2	3.0	6.7	4.2	40.3	137.2	0.9	27.7
24	GSHV199	NAU-Surat	884.0	343.1	38.9	2.7	7.0	4.4	38.1	130.0	1.1	26.6
25	BS3-17	OUAT, Bhawanipatna	683.1	259.4	38.2	3.1	7.5	4.6	32.4	122.5	2.4	19.4
26	RAH0604	UAS, Raichur	3387.7	1188.2	35.1	3.3	7.5	4.1	56.6	133.6	0.6	26.8
27	GJHV-523	JAU - Junagadh	1484.8	533.9	35.9	3.2	7.9	4.5	29.0	116.4	1.9	22.7
28	TSH332	TNAU, Srivilliputhur	904.1	306.3	34.0	2.7	7.7	4.0	26.9	127.0	1.9	19.8
29	GISV319	NAU-Surat	1031.3	368.9	35.8	2.8	7.6	4.2	21.8	104.2	1.0	23.4
30	CPD1702	UAS Dharwad	894.3	316.4	35.4	2.7	7.9	4.3	20.6	60.8	0.9	20.1
31	CSH1604	CICR, Sirsa	2151.8	790.7	36.8	3.1	8.3	4.9	31.0	110.8	0.8	18.7
32	SHJ23	SIMA CDRA	740.7	281.4	38.5	2.5	7.1	4.4	27.3	86.1	1.9	21.7
33	GJHV520	JAU - Junagadh	607.4	211.7	34.8	3.0	8.0	4.3	24.5	113.3	1.4	24.1
34	RAH0603	UAS, Raichur	664.6	236.6	35.6	2.2	6.7	3.7	25.3	93.9	0.9	21.1
	C.D.(5%)		206.6	90.8	2.5	0.3	0.6	0.5	6.1	17.7	0.4	4.5
	CV(%)		9.0	10.7	4.1	5.4	5.2	7.6	12.0	9.7	17.7	12.1

Table 2. Analysis of variance of RBD for different characters in Cotton

Source of Variation	d.f.	Seed cotton Yield (kg/hac)	Lint (kg/hac)	GOT (%)	Boll wt (gm)	Seed index	Lint index (g)	Boll per Plant	Plant ht (cm)	Monopods per Plant	Sympods per Plant
							Mean Sum Squares				
Replication	2	224028.31**	17764.99**	20.98*	0.22**	0.33	0.27	42.34*	34.34	0.14	7.91
Genotypes	33	1863593.3**	255554.65**	5.79**	0.41**	0.70**	0.28**	233.78**	1685.36**	1.25**	32.37**
Error	66	16334.03	3151.16	2.32	0.02	0.14	0.10	14.12	120.21	0.05	7.61

*Significant at P=0.05 level   **Significant at P=0.01 level

Table 3. Estimates of genetic parameters for different traits in cotton genotypes

Name Of Character	GM	Range		PCV	GCV	h^2 (%)	GAM
		Min	Max				
Seed cotton Yield (kg/hac)	1416.64	401.6	3387.7	56.1	55.4	97.4	112.6
Lint (kg/hac)	525.32	146	1188.2	56.2	55.2	96.4	111.6
GOT (%)	37.01	34	40.4	5.0	2.9	33.3	3.5
Boll wt (gm)	2.95	2.2	3.8	13.2	12.2	84.4	23.0
Seed index	7.34	6.5	8.3	7.9	5.9	55.9	9.1
Lint index (g)	4.32	3.7	5.1	9.5	5.7	35.7	7.0
Boll per Plant	31.27	15.4	56.6	29.9	27.4	83.8	51.6
Plant ht (cm)	112.77	60.8	152.5	22.5	20.3	81.3	37.6
Monopods per Plant	1.35	0	2.7	50.4	47.2	87.6	90.9
Sympods per Plant	22.94	18.7	30.7	17.3	12.5	52.0	18.6

GM= Grand Mean   PCV= Phenotypic Coefficients of Variation   GCV= Genotypic Coefficients of Variation h^2= Heritability (broad sense) GAM= Genetic advance as percent of mean (%)

Table 4. Genotypic and phenotypic correlation coefficients among various traits of cotton genotypes

		Seed cotton Yield (kg/hac)	Lint (kg/hac)	GOT (%)	Boll wt (gm)	Seed index	Lint index (g)	Boll per Plant	Plant ht (cm)	Monopods per Plant
Lint Yield (kg/hac)	G	0.999**								
	P	0.996**								
GOT (%)	G	0.174^{NS}	0.219*							
	P	0.104^{NS}	0.178^{NS}							
Boll wt (gm)	G	0.559**	0.560**	0.291**						
	P	0.513**	0.515**	0.152^{NS}						
Seed index	G	0.146^{NS}	0.118^{NS}	-0.425**	0.581**					
	P	0.097^{NS}	0.072^{NS}	-0.297**	0.476**					
Lint index (g)	G	0.281**	0.289**	0.368**	0.842**	0.685**				
	P	0.162^{NS}	0.204*	0.598**	0.526**	0.586**				
Boll per Plant	G	0.790**	0.787**	0.184^{NS}	0.327**	-0.139^{NS}	-0.012^{NS}			
	P	0.720**	0.715**	0.093^{NS}	0.275**	-0.113^{NS}	-0.023^{NS}			
Plant ht (cm)	G	0.731**	0.733**	0.047^{NS}	0.394**	0.087^{NS}	0.111^{NS}	0.693**		
	P	0.650**	0.656**	0.138^{NS}	0.346**	0.077^{NS}	0.174^{NS}	0.627**		
Monopods per Plant	G	-0.487**	-0.482**	0.004^{NS}	-0.169^{NS}	-0.108^{NS}	-0.090^{NS}	-0.481**	-0.413**	
	P	-0.458**	-0.452**	-0.021^{NS}	-0.153^{NS}	-0.086^{NS}	-0.078^{NS}	-0.384**	-0.336**	
Sympods per Plant	G	0.789**	0.801**	0.272**	0.319**	-0.083^{NS}	0.110^{NS}	0.793**	0.814**	-0.705**
	P	0.559**	0.567**	0.176^{NS}	0.182^{NS}	-0.069^{NS}	0.083^{NS}	0.583**	0.733**	-0.456**

G= Genotypic correlation   P= Phenotypic correlation