



Research Article

Evaluation of new germplasm of Egyptian cotton (*G. barbadense*) through multivariate genetic component analysis

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Abstract

Five new diversified *Gossypium barbadense* germplasm accessions NGB-555, NGB-556, NGB-557, NGB-558 and NGB-559 with a check variety Suvin were studied for correlation coefficients, genetic component and path analysis at CICR, Regional Station, Coimbatore during *Kharif* season 2015-16. Significant differences were observed for plant height, days to 50% flowering, number of monopodia, number of sympodia, number of boll per plant, single boll weight, 2.5% span length, fibre strength, ginning percentage and seed cotton yield. Analysis of variance (ANOVA) depicted highly considerable and widespread differences among the cotton germplasm lines for all the studied attributes ($P < 0.01$) except for GOT%. In Principal component analysis (PCA) four PCs with Eigen value > 1 contributed 60.423% of the variation amongst the investigated lines. Positive correlation between seed cotton yield and number of bolls, single boll weight, 2.5% span length, fibre strength, ginning percentage were found. Five yield components and 10 morphological traits of the five accessions were separated using ANOVA procedure and the Duncan's multiple range test. The relationships between them and lint yield were investigated using correlation analysis and stepwise regression analysis. The results showed that there was statistically significant difference in bolls per plant and lint percentage for the three types, which increased with increasing lint yield. The Pearson's correlation coefficients between them and lint yield were the highest. The direct path coefficient was the maximum for bolls per plant to lint yield. The direct path coefficient of number of sympodia per plant to lint yield was positive and significant at 0.05 levels. Considering diversity pattern and quantitative performance, the genotypes NGB-556 and NGB-558 were identified as promising accessions and could be utilized for efficient hybridization in cotton.

Key words

Egyptian cotton, principal component analysis, germplasm, correlation

Introduction

The Egyptian cotton species *Gossypium barbadense* L. known as extra long staple cotton is restricted in its cultivation in India to small pockets in the southern part of the country as the northern peninsular parts of the country are not favourable for cultivation of this particular cotton species. It is grown in about 10 % of the cotton area and supplies about 4% of the current world production. In Southern cotton growing zone, Tamil Nadu leads in production of extra long staple cotton (Gururajan and Sundar, 2004). State of Tamil Nadu has the pride of having more than 2500 textile mills and the demand of extra long staple cotton for them is around 0.9 million bales. The current production of extra long staple cotton in the country is only 0.5 million bales. To cater the requirement of the textile mills in this state, the balance has to be met through imports. As the consumption pattern in India is expected to increase with the expansion of spinning capacity of Indian textile mills and the international prices of cotton also firming up, substantial opportunity exists for the export of Indian cotton to other countries. Hence, research programmes

are taken up to identify high yielding, extra long staple genotypes from *G. barbadense* germplasm to increase its production in the country. Successful breeding requires genetic diversity to maximize improvement and to minimize the inherent field genetic vulnerability further, to initiate a viable breeding programme, better understanding about the nature and genetic potential of existing germplasm, and the extent of relationship and association of different morphological and yield contributing traits with the seed cotton yield is of vital importance (Dias *et al.*, 2015). Evaluation and maintenance of germplasm accessions has genetic integrity and vital role in evolutionary breeding process which provided way of improving diversified genotypes (Khan *et al.*, 2015). The narrow genetic base of elite germplasm has been a significant impediment to sustained progress in the development of cotton cultivars to meet the needs of growers and industry in recent years (Jinfa Zhang *et al.*, 2014 and Khan *et al.*, 2015).

Multivariate analyses can provide useful additional information as a supplement to normal univariate analyses. Among several different multivariate analyses, Principal component analysis (PCA) and cluster analyses are considered as an important tool to understand the relationships among variables (Vijaya Lakshmi *et al.*, 2009). PCA facilitates in depth analysis of genetic divergence between genotypes in terms of spatial distance. It scores as input variables for the clustering process thereby genetic variability are assuming considerable significance (Haritha and Lal Ahemed, 2013 and Thulasi *et al.*, 2014). Hierarchical cluster analysis highlights the nature of relationship between any types of samples described by descriptors. The present study was executed to explore genetically divergent germplasm accessions with desirable correlated agronomic attributes. The prime objective of the present study was to analyze the genetic diversity among the accessions of *G. barbadense* cotton and exploiting them in the breeding programmes for yield and quality traits improvement.

Materials and Methods

The experiment was carried out during *kharif* season 2015-16 at CICR, Regional Station, Coimbatore. Five new diversified germplasm accessions *viz.*, NGB-555, NGB-556, NGB-557, NGB-558 and NGB-559 were evaluated for yield and other important agronomic traits. The experiment was planted in an RBD design with a spacing of 60 x 45cm spacing of four replications. Five tagged plants per accession in each replication were identified for collection of data and assessing analysis of variance, principal component analysis (PCA), correlation analysis, heritability % (h^2) and genetic advance (GA) in various morphological parameters such as plant height, total number of bolls, number of sympodial branches, number of monopodial branches, boll weight, ginning percentage and important fibre qualities such as 2.5% staple length, fiber strength and micronaire.

To estimate the extent of magnitude of variation among these traits, all data were subjected to analysis of variance. Broad sense heritability (h^2) and genetic advance (GA) were determined by following the method of Hanson *et al.*, 1956. Calculated mean data was subjected to Principal Component Analysis (PCA) using PAST software as suggested by Shoaib *et al.*, 2015.

Results and Discussion

The analysis of variance for each individual trait showed highly significant differences among the five new germplasm lines for all the ten traits. Analysis of variance (ANOVA) revealed highly significant

difference ($P < 0.01$) in five *G. barbadense* accessions (Table 1). Mean performance of yield contributing traits of five germplasm accessions were given in Table 2. There are considerable amount of variability observed among the accessions. In this study, out of five accessions, two principal components (PCs) extracted had Eigen value > 1 . Broad sense heritability (h^2) and genetic advance (%) of all attributes were studied. Range of broad sense heritability (h^2) was observed from 13.71 to 79.23%. Maximum broad sense heritability (h^2) was depicted by seed cotton yield (79.23) followed by 2.5% span length (57.03) number of sympodial branches (51.80) and number of bolls per plant (47.25). Maximum genetic advance was showed by number of sympodia per plant (34.62), followed by total number of bolls (38.21) and 2.5% span length and number of sympodial branches (21.17). These results were the evidence for the presence of considerable genetic variation in the experimental material. Outcome of this study were in agreement with findings of Haritha and Lal Ahemed, 2013, Tulasi *et al.*, 2014 and Shoaib Liaqat *et al.*, 2015 in upland cotton (*G. hirsutum*).

Genetic divergence existing in the population helps in the selection of suitable parents for utilization in any crop breeding programme leading to reduction in the number of crosses Diao *et al.*, (2015). Broad sense heritability (h^2) is vital and powerful technique in predicting the improvement of crop potential through selection procedure. Broad sense high heritability (h^2) coupled with high genetic advance provides the information about the specific attribute by additive gene effects and selection may be more reliable and effectual for those attributes (Rana Imtiaz *et al.*, 2015 and Shoaib Liaqat *et al.*, 2015).

The current production of extra long staple cotton in the country is only 0.5 million bales. To cater the requirement of the textile mills in this state, number of bolls, number of sympodial branches and boll weight (Table 1). These higher values of broad sense heritability and genetic advance suggested that these traits have additive gene action with less environmental effects and high potential for selection in cotton improvement. Parallel findings were reported by Venkateswarulu *et al.*, 2010.

The correlation analysis is very handy tool for plant breeder to examine the correlation among attributes which could be vital in breeding (Asha *et al.*, 2013). Correlation analysis of cotton accessions depicted positive and significant as well as non-significant relationship among different attributes (Table 2). In this study highly significant and positive association was

observed between seed cotton yield and days to first flowering. In the present investigation sympodial branches were positively correlated with number of bolls per plant and showed negative correlation with monopodial branches. Positive but non significant correlation was noted between 2.5% staple length and plant height indicating that increase in plant height result in higher staple length. Number of bolls per plant depicted considerably positive relationship with seed cotton yield. These results are parallel to the findings of Tulasi *et al.*, 2014 and Bayyapu Reddy *et al.*, 2015 in upland cotton (*G. hirsutum*).

In the present investigation, the principal components with eigen values more than one were retained and less than one were considered as non significant. Mean data matrix was arranged and subjected to Principal component analysis (PCA) to find out diversity of the accessions. Out of five principal components (PC's) four components were extracted which depicted more than 1 Eigen values. In this study, the PC analysis summarized the total variation into 5 PCs, out of which four PCs contributed 64.47% variation to the overall diversity among the accessions. The principal component 3 (PC3- 54.02%), PC4 (32.48%) and PC5 (22.23%) exhibited high variability than the PC1 and PC2 which have the total variability of 14.33 % and 10.48% respectively (Table 3). The PC1 was more related to seed cotton yield, where the PC2 and PC3 are more related to plant height and days to first flowering respectively. PC4 exhibits the numbers of bolls are more related while PC5 had more relation with 2.5% staple length. The biometrical multivariate technique, principal component analysis (PCA) is useful in accessing parental genotypes for successful future hybridization program (Islam Md Kamrul *et al.*, 2013; Rana Imtiaz Ahmad *et al.*, 2015 and Bayyapu Reddy *et al.*, 2015). A PC Biplot (Fig.1) showed that variables and accessions are super imposed on the plot as vectors. The distance of each variable with respect to PC-1 and PC-2 showed the contribution of these variables in the variation of accessions used. The Biplot showed that DRW, RD, CC and LT as a whole contributed maximum towards variability in five cotton germplasm.

The utilization of Biplot to find out most phenomenal and divergent genotypes has been done by many researchers Farias *et al.*, 2016 in cotton and Hafiz Saad Bin Mustafa *et al.*, 2015 in maize. The critical understanding about association among various attributes has ample scope for the initiation of any breeding program as it provides a chance for the selection having desirable characters at the same time. In this experiment the outcomes of this correlation analysis

depicted some important relationship among the accessions and its attributes. Positive relationship was found with number of bolls per plant, plant height, 2.5% staple length, tenacity and single boll weight in accessions NGB-556, NGB-557 and NGB-558 and these positive correlated traits could be contributing factors for higher yield. Similar findings were noticed in upland cotton by Shoaib Liaqat *et al.*, 2015. However, Rana Imtiaz Ahmad *et al.*, 2015 obtained contradictory results representing positive but significant association between plant yield via sympodial branches and monopodial branches parameters in *G. hirsutum* cotton. This difference may be due to presence of genetic diversity present in studied material. Boll weight is considered as vital selection criterion and yield contributing attribute having direct effect on cotton yield via number of bolls. During genotypes selection, considerable attention should be given to the boll weight. Similar outcome was observed by Venkateswarulu *et al.*, 2010, who also observed positive correlation between boll weight and number of bolls per plant in upland cotton (*G. hirsutum*).

The Unweighted Pair Group Method with Arithmetic Mean (UPGMA) cluster analysis was done to see the relationship of the accession. The accession NGB-559 and NGB-555 form a single cluster and NGB-556 and NGB-558 are form another cluster revealing that they are closely related with each other. While Suvin and CCB-557 form separate clusters and are distantly related with each other. Hence from this study, broad sense heritability and genetic advance with higher values exhibited that all the attributes have potential to be heritable in next generation. Results of cluster analysis based on PCA scores were compared with the results of the principal component analysis on a visual aid in desecrating clusters (Fig.1 & 2). Hierarchical cluster analysis gave an advantage of identifying sub-clusters of major groups at different levels so that each small group can be critically analyzed and exploited in the breeding programme for incorporation of desirable traits (Jinfa Zhang *et al.*, 2014). Utilization of principal component analysis combined with clustering of Ward's minimum variance method in genetic divergence studies in cotton was supported by Vijaya Lakshmi *et al.*, 2009; Haritha and Lal Ahamed, 2013; Tulasi *et al.*, 2014 and Bayyapu Reddy *et al.*, 2015.

Principal component analysis (PCA) in this investigation provided facilitation in assessment of genetic diversity among genotypes having better fiber quality and high yield potential. The positively significant correlations and the information obtained from correlation analysis and Principal component analysis (PCA) will be more



effective in planning of future breeding programs for identifying high yielding accessions with better fiber quality. It can be concluded from the above experiment that the new germplasm accessions in clusters II and IV hold good promise as best in seed cotton yield and fibre traits could be used in future breeding programmes for developing complex crosses in Egyptian cotton.

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Table 1. ANOVA for various traits of *G. barbadense* accessions

SOV	df	Plant ht (cm)	Daysto50% flowering	Noof monopodia	Noof Sympodia	Bolls/ plant	Boll wt	GP %	SCY	SL	ST
Replication	3	164.11	5.78	4.78	5.78	5.78	0.03	4.52	1008.77	4.25	0.44
Genotypes	5	3826.40	572.27	1.61	572.27	2060.90	1.39	13.71	25568.90	13.71	12.94
Error	15	667.80	52.88	1.89	52.89	42.89	0.46	9.59	7905.20	9.59	14.22
SEd	-	6.67	1.88	0.35	1.88	1.69	0.17	0.80	22.96	0.80	0.97
Heritability (%)		42.16	37.24	27.56	51.8	47.25	13.71	33.09	79.23	51.03	27.9
Genetic advance (%)		21.17	19.2	34.62	9.721	3.055	1.852	15.68	19.13	18.31	4.26
CD@5%	-	14.86	4.18	0.79	4.18	3.77	0.39	1.78	51.15	1.78	2.17
CV%	-	7.33	3.9	71.12	3.9	3.93	6.97	2.7	3.37	2.7	4.3

Table 2. Mean performance of yield contributing traits of germplasm accessions of *G. barbadense*

Accession	Plant ht (cm)	Days to 50% Flowering	No.of mono podia	No of sympodia	No. of bolls	Boll wt	2.5% Span length (mm)	Tenacity (g/tex)	GOT (%)	SCY kg/ha
NGB-555	132 ^{acb}	59.6 ^b	1.0 ^b	10.6 ^b	50.6 ^c	3.1 ^{ab}	37.2 ^a	26.6 ^c	31.6 ^a	779.3 ^c
NGB-556	115 ^{cb}	68.6 ^a	1.0 ^{bc}	9.3 ^{bc}	55.0 ^b	3.0 ^b	36.9 ^{ab}	28.00 ^{ab}	31.0 ^{ab}	853.3 ^b
NGB-557	125 ^{ab}	53.6 ^c	0.3 ^a	12.6 ^a	71.6 ^a	3.5 ^a	36.8 ^{ab}	29.3 ^a	28.6 ^c	1043.0 ^a
NGB-558	99 ^d	59.6 ^b	0.3 ^c	8.0 ^c	53.3 ^{bc}	2.6 ^c	34.9 ^c	27.6 ^{bc}	28.0 ^{cd}	886.0 ^b
NGB-559	105 ^{cd}	51.0 ^c	0.3 ^c	7.6 ^c	50.6 ^c	3.1 ^{ab}	35.2 ^{bc}	27.0 ^{bc}	29.6 ^{bc}	793.6 ^c
Suvin (c)	91 ^d	61.0 ^b	0.6 ^d	4.3 ^d	35.0 ^d	2.8 ^{bc}	36.2 ^{ab}	27.6 ^b	28.6 ^c	650.0 ^d

Table 3. Principal components (PCs) of various traits

Variables	PC1	PC2	PC3	PC4	PC5
Eigen values	1.72	2.00	3.62	1.36	0.67
Variability (%)	14.33	10.48	54.02	32.48	22.23
PH	0.061	0.974	-0.041	-0.165	0.032
DFF	-0.011	0.052	0.988	0.072	-0.023
NOM	-0.001	0.016	0.033	0.024	0.010
NOS	0.018	0.111	-0.015	-0.060	-0.047
NOB	0.088	0.137	-0.116	0.894	-0.015
BW	0.001	0.012	-0.019	0.121	0.133
SL	0.001	0.053	0.052	0.130	0.570
TEN	0.005	-0.019	0.028	0.126	0.659
GP	-0.002	0.090	0.052	0.335	-0.467
SCY	0.994	-0.073	0.024	-0.067	-0.005

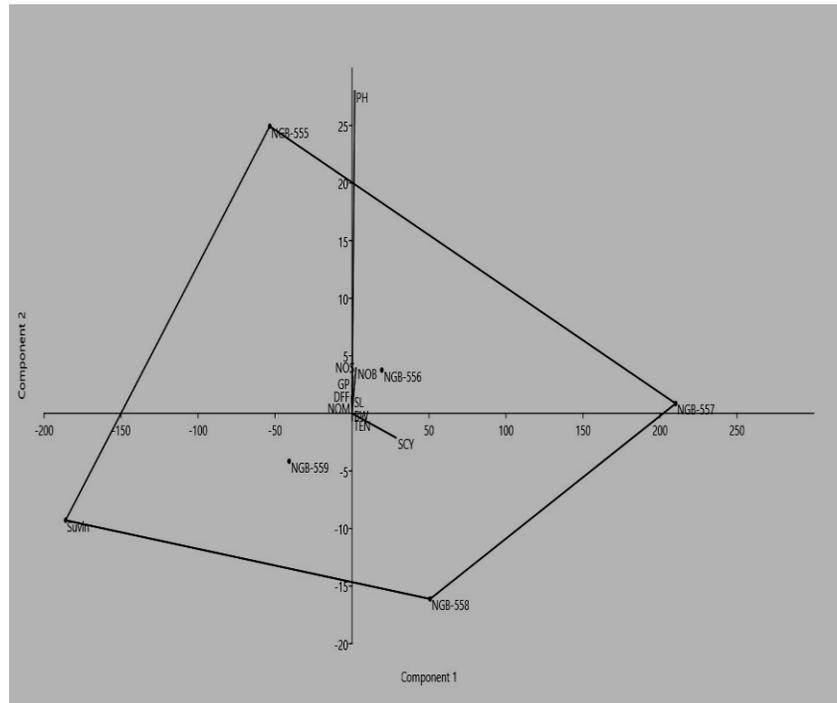


Fig. 1. Biplot based on Principal component analysis

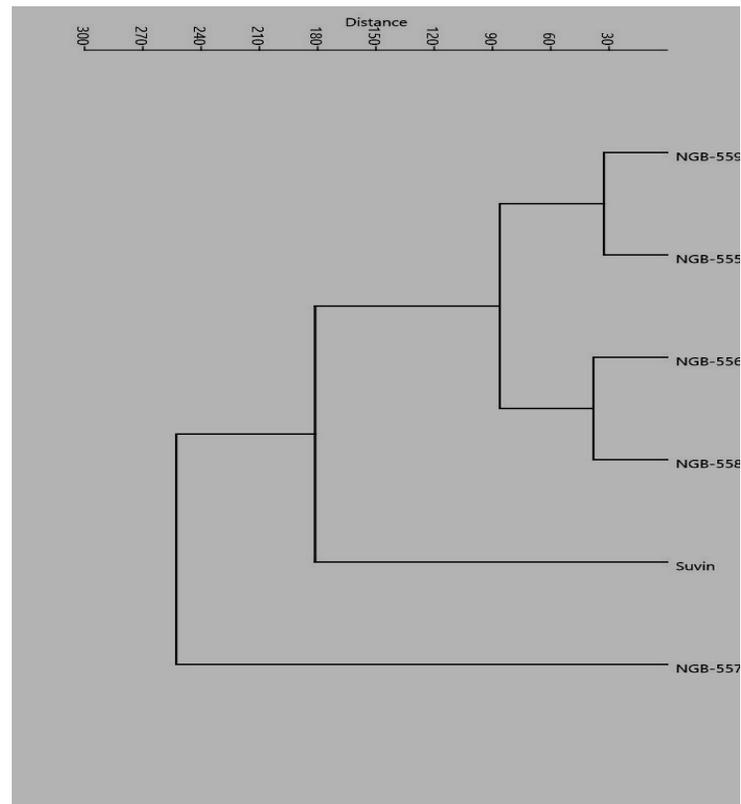


Fig. 2. Clustering pattern of germplasm accession of *G. barbadense*