GENETIC VARIABILITY AND DIVERSITY STUDIES IN THE PROGENIES DERIVED FROM IRRADIATION AND RECOMBINATION IN DESI COTTON

Bangaremma S. Wadeyar* and S. T. Kajjidoni

Department of Genetics and Plant Breeding, U. A. S., Dharwad - 580 005 (Karnataka), India.

Abstract

Estimations of genetic variability and genetic diversity are essential for improvement of desi cotton. Diploid cotton has wide adaptability under rainfed situation and also high degree of resistance to biotic and abiotic stresses. The extent of variability gives information regarding the relative amount of variability present in different progenies, which helps in identification of good progenies for future generation. The genetic variability and diversity analysis have been worked out using five phenotypically diverse genotypes of diploid cotton (*G. herbaceum* (3) and *G. arboreum* (2)), with the objective to study the genetic variability and diversity for seed cotton yield and its components for seven quantitative characters in 202 progenies of desi cotton. High variability was noticed for seed cotton yield and number of bolls per plant. Heritability observed was high for all the seven traits under study. Similarly, the diversity analysis was carried out for the set of 202 progenies interestingly it was noticed that majority of progenies were grouped in cluster I, it was due to selection of progenies was made earlier based on seed cotton yield. Another interesting thing is that when the contribution of trait was analyzed, seed index was the major contributing trait towards the divergence.

Key words : Cluster, desi cotton, genetic diversity, heritability, genetic variability.

Introduction

Cotton is one of the most important fiber crops in the world. Many successful cotton cultivars have been developed from closely related parents. Pressure for higher productivity in cotton farming has repeatedly stimulated the same gene pool and led to a narrow genetic base, which is hindering breeding programs worldwide. Global production of cotton is 26.14 million tonnes of which India contributes 8.5 million tonnes amounting to 32.5 per cent world share. India is the second highest producer of cotton (lint) next to china. In India, about 90 per cent area is covered by *hirsutum* hybrids, 8 per cent by sea island varieties and 2 per cent by diploid cultivars (Anon, 2014). The area under cotton during 2012-13 in India was 11.978 lakh hacter with production and productivity of 365 lakh bales and 518 kg lint per hacter respectively and in the same year in Karnataka, cotton was grown over an area of 4.85 lakh hacter with a production of 15.00 lakh bales and productivity of 526 kg/ha (Annon. 2014).

About 90 per cent of the world's commercially produced cotton is *G. hirsutum* followed by *G. barbadense* (8%) and rest 2 per cent belongs to old world cotton grown mainly in South and South-East Asia. In India diploid cotton constituted a predominant area (97%) at the time of partition. The quantitative and qualitative advantage of hybrids ushered in diverse changes in cotton species scenario with *G. herbaceum* area reducing drastically. Though the tetraploid cotton hybrids are stable in performance over a wide range of congenial growing situations, their potential performance is often challenged by rainfall aberration, pest and disease and cost of cultivation. Hence, tetraploid cotton has become more risky and non-remunerative, creating a socio-economic tension among the cotton cultivars. Of the several factors contributing to low yield and productivity of cotton, biotic and abiotic constraints appear to be very important and these constraints can be overcome by using desi cotton varieties since they are being grown under poor management. However, desi

*Author for correspondence: E-mail: bangarammawadeyar@gmail.com

cotton is well adopted to a wide range of climatic conditions, including hotter environments due to prolific tap root system. In the present global climate change scenario desi cotton seem to posses additional advantage for cultivation in terms of better tolerance to low rainfall and high temperature stress environments, as these situations may not favor tetraploid cottons that require better management practices. Keeping all these ideas an effort was made to extract the amount of variability generated and to know the extent of diversity noticed in the desi cotton progenies derived from irradiation and recombinational ways.

Materials and Methods

The total of two hundred and two progenies derived from irradiation and recombination, the single and double crosses were generated using 9749, RDC-88 and Jayadhar (*Gossypium herbaceum*) and MDL-2582 and DLSA-17 (*Gossypium arboreum*) parents taking Jayadhar as female in all crosses, since we were interested in obtaining the progenies similar to Jayadhar having high seed cotton yielding and good fiber quality properties and further single crosses were subjected for gamma irradiation to enhance genetic variability. These two hundred and two progenies were grown at University of Agricultural Sciences, Dharwad, ARS, Annigeri during 2012. The experiment was laid out in a randomized complete block design (RCBD) with three replications. Each plot consisted of 2 rows of 5m length with plant x row distance of 60 x 30 cm. Standard agronomic practices and plant protection measures were followed. The data were recorded on seed cotton yield and yield attributing traits. Five plants in each replication were used for recording all the morphological and yield traits. Mahalanobis's D^2 - statistics (1936) was used for assessing the genetic divergence was carried out for each character of the 202 progenies.

Results and Discussion

Variability parameters

In any sound plant breeding programme one should assess the phenotypic and genotypic coefficient of variability of the material under study as well as the heritability, genetic advance and genetic advance as per cent mean shown by the different traits. In this sense therefore, the heritability, genetic advance and genetic advance as per cent mean estimates in present study are applicable only to the material studied. However, estimates of these parameters in combination with phenotypic and genotypic coefficient of variability will be useful in genetic improvement of the character under consideration (table 1).

Seed cotton yield per plant

Seed cotton yield is a major factor governing economic worth and hence largely determines the agricultural values of a variety usually seed cotton yield is a major complex trait not readily amenable to genetic analysis since, it is governed by several yield contributing traits such as number of bolls per plant, boll weight etc, further number of bolls per plant and their size are the product of interaction between physiological process in development and morphological frame work of the plant.

High PCV, GCV, heritability, GA and GAM were recorded for all the above mentioned genetic parameters. The estimates of high heritability and GA suggest that simple phenotypic selection can be made to improve seed cotton yield *per se*. These results are also in accordance with the results obtained by other workers like Ashok *et al.* (2000) observed wide variability in treated Jayadhar for various quantitative characters. Similarly, Waghmore *et al.* (2000) noticed wide range of genetic variability in M_2 and M_3 population of *G. arboreum* for major yield contributing characters such as number of bolls per plant, number of fruiting branches and plant height, and also Talwar and Kajjidoni (2008, 2009 and 2010) reported high variability estimates of majority of traits in desi cotton. Similar trend of higher variability levels where noticed in urd bean by Kajjidoni *et al.* (2006 and 2008) (table 1).

Number of bolls per plant

Number of bolls per plant is one of the important yield related traits in cotton which is most targeted trait to improve the seed cotton yield. This trait bears closest relationship with seed cotton yield per plant, that a cotton plant bears at maturity is a component character of yield having the greatest bearing for increasing yield of seed cotton yield.

Higher magnitude of PCV, GCV, heritability, genetic gain and GAM estimates were recorded. Genetic gain can help to predict the extent of improvement that can be achieved for the trait. High heritability coupled with high genetic gain suggests that importance of additive genetic variability for genetic control of this trait so, simple phenotypic selection can be practiced to improve the final seed cotton yield in cotton. While, high heritability with low genetic gain indicates role of dominance of environmental factor. These results are in the line with the results of Waghmore *et al.* (2000) and Talwar and Kajjidoni (2008, 2009 and 2010) (table 1).

Boll weight

Boll weight is another important and crucial trait in deciding final yield after the number of bolls per plant.
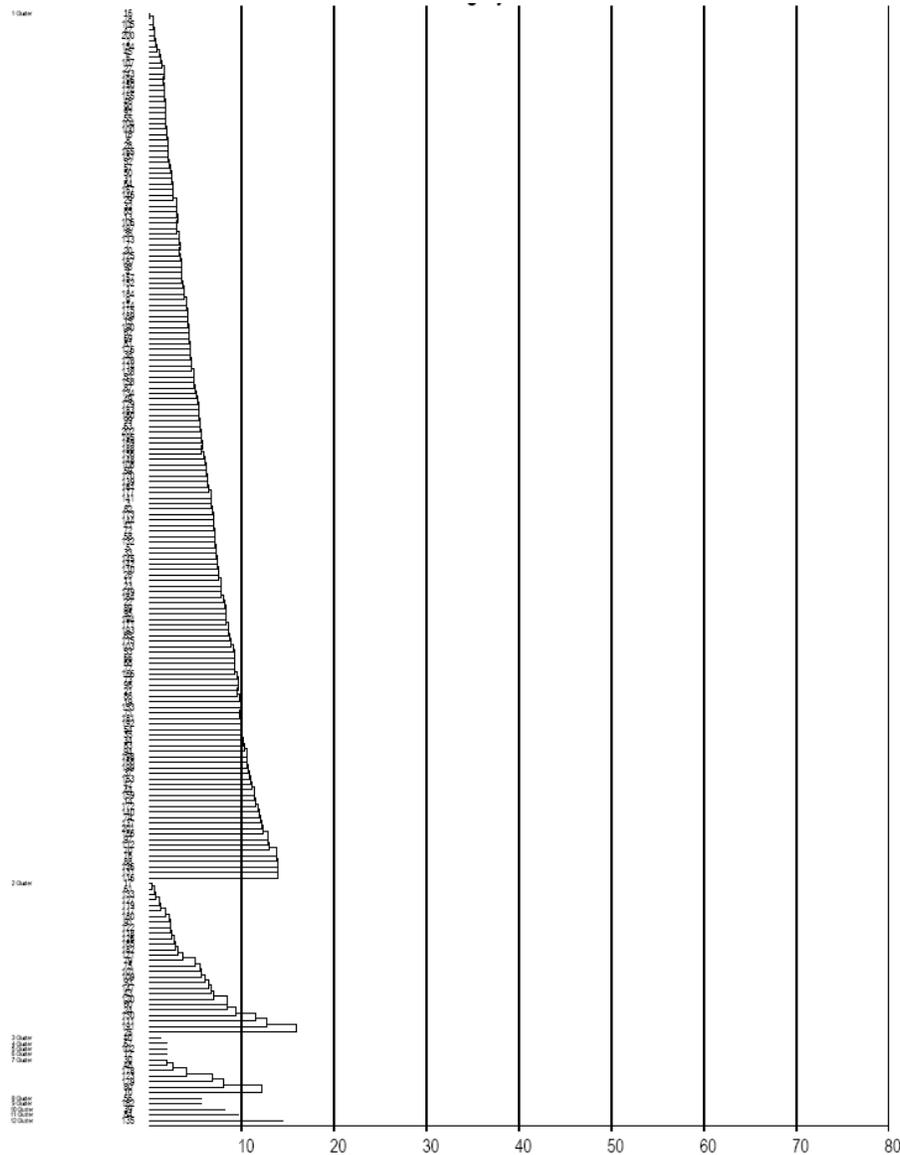
Fig. 1 : Dendogram representing different clusters.

This trait is a function of number of locules, seed weight and lint weight. The number of locules present in the boll can partly reflect the magnitude of boll weight. Since the desi cotton bear small bolls which will not be productive because harvesting or plucking of each individual small bolls need more time and work done will not be cost effective, so progenies bearing bigger boll size are preferred, we know that by increasing the boll size their will be reduction in number of boll per plant but still higher boll weight with optimum number of bolls per plant can make the desi cotton more productive.

Boll weight exhibited lower values of PCV, GCV and GA estimates indicate limited scope of selection for improvement of this trait. High values of heritability were recorded with moderate values of GAM indicating moderate response of trait for direct phenotypic selection. These results were in concurrent with the earlier findings made by Tommer *et al.* (1992) and they noticed moderate to high estimates of genetic variability, heritability and expected genetic advance for bolls per plant, seed cotton yield per plant, lint yield per plant and lint index in sixty F_1s along with 23 parents of desi cotton (table 1).

GOT, seed index and lint index

Ginning out turn is a character governed by seed weight and lint weight and it is first important trait where mechanical or manual processing activity that cotton undergoes on the way from field to textile mills, where it is spun and weaved into fabric. High seed index is mostly

Table 1 : Genetic variability parameters in F_5, F_5M_5, M_5 and double cross F_4 progenies for different traits in desi cotton (ARS Annigeri 2011-12).

Parameters	Plant height (cm)	No. of bolls/ plant	Boll weight (g)	Seed cotton yield/plant (g)	Ginning outturn (%)	Seed index (g)	Lint index (g)
PCV (%)	13.946	35.487	8.509	37.915	3.839	7.121	3.781
GCV (%)	12.152	33.140	7.685	35.152	3.536	7.030	3.267
h² (%)	75.900	87.200	81.600	86.000	84.800	97.500	74.600
GA	29.681	20.991	0.214	28.533	2.181	0.669	0.131
GAM (%)	21.815	63.753	14.300	67.134	6.708	14.295	5.814

Table 2 : Clustering of Progenies based on D^2 analysis in desi cotton.

Cluster	Total number of progenies	F_5	F_5M_5 and M_5	DC (F_4)
I	158	40	47	71
II	28	8	4	16
III	1	0	1	0
IV	1	1	0	0
V	1	1	0	0
VI	1	0	1	0
VII	7	1	3	3
VIII	1	1	0	0
IX	1	0	0	1
X	1	0	1	0
XI	1	0	1	0
XII	1	0	0	1
Total	**202**	**52**	**58**	**92**

Table 3 : Contribution of traits towards divergence in desi cotton (ARS Annigeri 2011-12).

Source	Times ranked (1st)	Contribution (%)
Plant height (cm)	1724	8.49
No. of bolls/plant	2705	13.32
Boll weight (g)	2085	10.27
Seed index (g)	12410	61.13
Lint index (g)	646	3.18
Ginning outturn (%)	384	1.89
Seed cotton yield/plant (g)	347	1.71

accompanied by boll weight and seed cotton yield per plant. Higher the seed index value reduces the ginning out turn values. Lint index is an important trait which indicates the weight of lint produced per seed and it is directly governed by ginning out turn so higher estimates of lint index is desirable. Lint index represents the absolute weight of the lint produced per seed and is highly correlated with lint yield. Lint index represents the absolute weight of the lint produced per seed. This trait can be considered as more important in breeding work than ginning percentage as it is highly correlated with lint yield. Lint index is the complementation of high seed index and high ginning out turn percentage (table 1).

Lower estimates of both PCV and GCV were recorded for the ginning out turn, seed index and lint index traits indicating the narrow range of variability for these traits and in turn it restricts the scope of selection. High heritability for these traits indicated that these traits are generally governed by the additive gene effects. But the dominance of environmental factors was evident as these traits exhibited low GA and moderate to low GAM (seed index). So, the improvement of yield through yield components should be based not on simple selection alone but also on progeny test as cotton is highly plastic as far as the expression of morphological traits are considered. Majority of earlier reported results explained that high estimates of PCV, GCV, heritability and GA were recorded here contrary results were recorded in present study for all the above mentioned genetic parameters except for heritability estimate (table 1).

Diversity

The precise information about the degree of relationship between different genotypes/progenies is very much essential for an effective breeding programme. The multivariate analysis helps in quantifying the magnitude of divergence between populations. The multivariate analysis has been demonstrated to classify genotypes/ progenies and to identify factors influencing their genetic divergence (Rao, 1952). Genetic diversity between genotype/progenies is the difference in the gene frequencies among them. A measure of genetic divergence must reflect these differences. In the absence of experimental techniques to measure the diversity with respect to genes affecting quantitative characters. Phenotypic diversity is usually considered to be an indication of underlying genetic differences.

In desi cotton the limited variability particularly for

Table 4 : Average intra and inter cluster distances in cotton (ARS Annigeri 2011-12).

Cluster distances	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	2.88	4.87	3.93	4.43	4.18	4.23	4.49	5.02	4.24	7.82	9.08	7.06
II		2.73	6.68	7.29	7.55	7.17	7.65	6.8	4.76	4.39	5.79	8.98
III			0	1.36	4.39	3.1	3.12	3.16	6.44	9.15	10.38	6.03
IV				0	4.55	2.94	2.89	4.25	6.75	9.67	10.62	6.91
V					0	3.92	3.33	5.81	6.47	10.88	12.11	6.37
VI						0	2.92	5.95	6.34	9.82	10.72	8.22
VII							3.04	5.32	6.86	10.47	11.45	7.02
VIII								0	7.52	9.17	10.75	3.79
IX									0	7.24	8.21	9.62
X										0	3.09	11.67
XI											0	13.38
XII												0

Diagonal values – Intra cluster distance.

Table 5 : Cluster mean values of quantitative traits in different clusters (ARS Annigeri 2011-12).

Cluster means	Plant height (cm)	Number of bolls/plant	Boll weight (g)	Seed index (g)	Lint index (g)	Ginning outturn (%)	Seed cotton yield/plant (g)
Cluster I	136.38	31.98	1.49	4.75	2.26	32.24	41.17
Cluster II	138.49	34.65	1.54	4.14	2.17	34.34	45.75
Cluster III	122.00	52.17	1.47	5.13	2.23	30.28	64.78
Cluster IV	109.50	43.50	1.36	5.22	2.27	30.33	50.55
Cluster V	148.50	28.06	1.59	5.14	2.56	33.21	38.44
Cluster VI	158.25	20.17	1.61	5.20	2.24	30.06	27.56
Cluster VII	135.69	33.06	1.47	5.24	2.40	31.45	41.38
Cluster VIII	126.25	86.17	1.45	4.92	2.25	31.41	110.85
Cluster IX	107.75	6.50	1.33	4.50	2.02	31.00	7.72
Cluster X	103.00	34.94	1.60	3.77	2.01	34.82	39.65
Cluster XI	110.00	22.00	1.34	3.65	2.01	35.53	25.36
Cluster XII	122.75	102.33	1.64	5.00	2.57	33.94	144.54

boll weight and fiber quality traits coupled with meager breeding efforts compared to tetraploids has lead to little success. In the present investigation, a systematic approach was made by careful selection of diverse donors and adopted parents. The study was taken up with a selection of two hundred and two advance breeding lines of desi cotton derived from irradiation and recombination involving these diverse and adopted parents to classify them on the basis of mahalnobis D^2 statistic and to identify the major components which contribute towards the divergence.

The multivariate analysis is utilized in quantifying the degree of divergence among the progenies to assess the relative contribution of different traits to the total divergence. The aim was to know that the trait which grouped these progenies into different clusters at Annigeri location, based on D^2 values, a total of two hundred and two progeny lines were grouped into twelve clusters indicating the presence of appreciable amount of genetic diversity among the progenies under study. The maximum number of progenies (158) were grouped in Cluster I, followed by Cluster II with 28 progenies and Cluster VII with seven progenies. The remaining clusters (III, IV, V, VI, VIII, IX, X, XI and XII) were solitary, each containing a single progeny. Maximum progenies were grouped in cluster I, this could be due to the progenies were preselected earlier based on seed cotton yield and boll weight traits from previous generation and further these progenies have attained F_6 generation indicating that progenies have stabilized and grouped into one cluster (table 2 and fig. 1).

The progenies were classified based on its origin within cluster, the maximum number of progenies were grouped in cluster I with 158 progenies, among these maximum number of progenies belonged to double cross (71) followed by 47 progenies belonged to single cross irradiated and irradiated Jayadhar and least number of progenies were belonging to single cross unirradiated. As many as 28 progenies were grouped in cluster II, among these again maximum progenies were from double cross progenies (table 2).

The analysis for estimating the contribution of various characters towards the expression of genetic divergence has indicated that seed index has accounted for 61.13 per cent was the single trait which has contributed most towards genetic divergence followed by number of bolls per plant (13.3%), boll weight (10.3%) and plant height (8.5%) as indicated in table 3. The remaining characters did not contribute significantly to the divergence. It is therefore, apparent that the seed index is the basic component of genetic divergence substituted by the characters mentioned above. There are no reports in literature indicating maximum contribution of seed index towards divergence, followed by boll weight and plant height traits, the results are in accordance with reports of earlier workers like Pusham *et al.* (2004), Gumber and Chahal (2006), Gopinath *et al.* (2009) and Kulkarni *et al.* (2011) in *G. hirsutum*. The study also revealed that the other traits like seed cotton yield had played relatively lesser role in causing genetic divergence between the progenies.

The highest inter-cluster D² values were recorded between cluster XII and XI (13.38) which indicates the progeny belonging to these clusters are more diverse and these progenies can be target for further improvement of desired trait and this divergence is mainly based on the phenotype of the progeny. The lowest inter cluster was recorded between clusters III and IV (1.36). The intra-cluster D² values ranged from 0.00 to 3.04. The average intra-cluster distance between the members of Cluster VII was maximum followed by Clusters I and II suggesting that progenies in Cluster VII were relatively more diverse than progenies of the other clusters (table 4).

Analysis of cluster means indicated substantial variability among clusters grouped according to D² analysis. The variability observed in cluster means also points to the degree of variability. In the present investigation, mean values for seed cotton yield, number of bolls per plant, boll weight, ginning out turn and plant height was more in cluster II comparatively with other clusters, while seed index and lint index exhibited high mean values in cluster VII (table 5).

In the present investigation, it was observed that considerable amount of genetic diversity was present among the progenies with respect to seed cotton yield and its related traits. Cluster II can be considered as superior cluster with respect to seed cotton yield, number of bolls per plant, boll weight, GOT and plant height, while cluster VII for seed and lint index traits.

References

Anonymous (2014). Area production and yield of Cotton. <http: //www. cottoncorporationofindia. org. html> accessed on 20/06/2014.

Ashok, M. B., I. S. Katageri and B. M. Khadi (2000). Effect of gamma rays and EMS on quantitative characters in cotton (*Gossypium* spp.). *DAN BRNS Symposium*, Mumbai, pp. 230-236.

Gopinath, M., S. Rajamani, R. Krishnanaik and Mallikarjun Rao (2009). Genetic divergence for lint characters for upland cotton (*G. hirsutum*). *J. Cotton Res. Dev.*, **23 (1)** : 46-48.

Kulkarni, A. A., C. Nanda and S. G. Patil (2011). Studies on genetic diversity in plant cotton (*G. hirsutum* L.). *J. Cotton Res. Dev.*, **25 (1)** : 9-13.

Kajjidoni, S. T., K. Roopalakshmi, S. Immadi, R. Nagaral and I. Nagaral (2008). An innovative way of developing an improved variety utilizing both gamma rays induced and recombinational variability in blackgram (*Vigna mungo* (L.) Hepper). *FAO/IAEA Intl. Symp. on Induced Mutations in Plants* 12-15 August, 2008, Vienna, Austria IAEA-CN-167-064, p. 142.

Kajjidoni, S. T., Roopalaxmi and P. M. Salimath (2006). Comparison of induced and recombinational variability for improving productivity in urdbean. *Indian J. Pulses Res.,* **19 (1)** : 39-42.

Rao, C. R. (1952). *Advanced Statistical Methods in Biometrical Research*, John Willey and Sons. Inc., New York, pp. 357-363.

Tomar, S. K., S. P. Singh and S. R. S. Tomar (1992). Genetic variability of yield and its components over environments in desi cotton (*Gypsium arboreum* L.). *Crop Res.,* **5(2)** : 290-293.

Talwar, A. M. and S. T. Kajjidoni (2010). Frequency of superior segregants as influenced by hybridization (F_2) and hybridization followed by irradiation (F_2M_2) using selected parents for important component traits in desi cotton. *Electronic J. Plant Breed.*, **1(4)** : 675-679.

Talwar, A. M. and S. T. Kajjidoni (2009). Impact of induced mutation on genetic variability, association and frequency of superior segregants in desi cotton (*Gossypium herbaceum* L.)]. *Res. on Crops*, **10(3)** : 647-654.

Talwar, A. M. and S. T. Kajjidoni (2008). Induced Variability Studies on Productivity Related Traits in Desi Cotton. *Karnataka J. Agric. Sci.*, **21(4)** : pp 666.