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Genetic divergence in *arboreum* cotton (*Gossypium arboreum*)

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ABSTRACT

Fortyfive genotypes were grouped in seven, five and ten clusters in three subsequent years, i.e 2004, 2005 and 2006. The maximum number of ten clusters were formed during 2006, followed by seven and four during 2004 and 2005 respectively. Cluster I contains the maximum number of genotypes (37, 40 and 29 in 2004, 2005 and 2006 respectively), followed by cluster II. The genotypes forming single cluster were PA 405, MALJARI, KWA 227, HD 440, and PA 304 thus, they were most divergent genotypes. In general, clustering of genotypes was not related to geographic diversity. Genotypes, viz. J. Tapti, KWA 24, KWA 23, AH 65, CINA 223, and DLSA 24 were grouped together in different years thus exhibited real genetic diversity based on yield factors and quality parameters in cotton. In the year, Clusters III and V were most divergent, ie maximum inter-cluster distance in 2004, cluster II and IV in 2005 and clusters II and VI in 2006. Hence, selection of genotypes from the cluster exhibiting maximum genetic divergence would be more reliable for high heterotic response and spectrum of variation in segregating generation. The contribution of boll/plant, sympodia/plant, monopodia/plant, nodes/plant, short fibre index and oil percentage towards genetic divergence was noted in the present material. Hence, the selection of parents or donors should be based on *per se* performance of these characters in the form of selection indices.

Key words: Clusters, Genetic divergence, Genotypes, Selection

The genetic improvement in cotton (*Gossypium hirsutum* L.) in the state began in 1942 at Institute of Pant Industry, Indore that got momentum after sanction of several centrally sponsored projects. A number of varieties and hybrids have been developed and recommended for general cultivation. But majority of these belong to *G. hirsutum*. On the other hand, *G. arboreum*, an Indian native that bears the ability to withstand the drought and perform better under adverse agro- Indian-calamities, remained ignored of genetic amelioration for better yield and quality traits. Any breeding programme aimed at improvement in *G. arboreum* can definitely help in increasing the quality of cotton in the state as well as in the country.

So far, no systematic and planned efforts have been made to improve the productivity of *G. arboreum* for rainfed farming.

Existence of genetic diversity is an essential requirement for successful hybridization programme. Genetically diverse parents are known to produce transgressive segregates in later generations. Several methods such as D^2 analysis, metroglyph analysis, canonical analysis, Euclidean cluster analysis, and dendogram analysis are available for identification of genetically diverse genotypes. Among them, D^2 analysis also known as Mahalanobis' D^2 analysis has been found an effective tool for the grouping of genotypes into distinct clusters based on genetic distance. Rajarathinam *et al.* (1994) evaluated 40 genotypes for five yield-related characters and grouped the genotypes into six clusters on the basis of D^2 values in such a way that genotypes having least genetic divergence were grouped together and *vice versa.* Boll weight, number of bolls/plant and 2.5 span length contributed most to the total genetic divergence. Patil *et al.* (1999) distributed 45 genotypes in five clusters based on genetic divergence. The existence of ample genetic diversity among the genotypes was reflected from the inter-cluster distance that was adequate for improvement in seed cotton yield. Sial and Pattnaik (2003) evaluated 27 genotypes of upland cotton for lint yield and yield components, viz., number of days to flowering, number of days to maturity, cotton yield, boll weight, number of bolls/plant, and ginning percentage to estimate the genetic divergence and grouped genotypes into 11 clusters. Esmail *et al.* (2008) evaluated 21 genotypes in cotton and grouped into two main groups at 20 Euclidean distance with 11 and 10 genotypes in both groups,

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respectively. They identified that first group were similar in highest seed cotton yield/plant.

In the present study, an attempt was, therefore made to identify the genetically diverse genotypes among 45 newly bred lines for planned hybridization and selection programme in *G. arboreum* which is known to perform better in rainfed farming. Mahalonobis's D^2 statistics was adopted for identification of diverse genotypes.

MATERIALS AND METHODS

The present investigation was carried out at All India Coordinated Cotton Improvement Project, Main Centre, J N Krishi Vishwa Vidyalaya, Regional Research Station, Khandwa, Madhya Pradesh during rainy (*kharif*) season of three subsequent years of 2004 to 2006. The climate of district Khandwa is subtropical moderate. The district is located in Nimar valley of Madhya Pradesh with average rainfall 725 mm. Soil of experimental site was shallow to medium black with loamy to clay texture and *p*H of 7.4. The topography is rolling to undulating with low water retention capacity. The available nitrogen, phosphorus and potassium is low, medium and high, respectively.

Fortyfive genotypes of cotton were selected for the present study on the basis of geographical diversity from genetic stock maintained under All India Coordinated Cotton Improvement Project. These genotypes varied in days to maturity from 100 to 170 and in seed yield from 1 000–1 200 to 2 000 – 2 200 kg/ha. Five competitive plants were randomly selected in each genotype, in each replication and each environment for recording observations on seed cotton yield/ plant and its component characters along with quality parameters. A total of 18 yield-attributing and quality parameters were considered for analysis.

Mahalanobis's (1936) D^2 statistic was used for assessing the genetic divergence between populations. Before calculating the D^2, the values of correlated traits were transformed to uncorrelated traits by the procedure suggested by Rao (1952).

RESULTS AND DISCUSSION

Genetic divergence among 45 genotypes was determined using seed cotton yield, its attributing characters and fibre quality traits. The significant estimates of 'V' statistics during 2004, 2005, and 2006 and in pooled analysis revealed significant differences among mean values of different correlated variables, thus analysis of genetic divergence among the tested cotton genotypes was considered to be most relevant. Progenies of diverse origin are known to give high heterotic response and release a broad spectrum of genetic variability for selection of transgressive segregates in advance generations. Mahalanobis's D^2 statistics has been found to be a powerful tool to quantify the degree of divergence. Very limited efforts have been made to quantify the degree of divergence among the genotypes based on yield attributes in *G. arboreum* (Rajarathinam *et al.* 1994. Patil and Raveendran 1999, Sial and Pattnaik 2003 and El-Adly *et al.* 2006). The practical utility of this technique to quantify the degree of divergence in cotton, based on fibre quality traits has been tested in the present investigation.

The divergence within the genotypes, tested by the Wilk's criteria was found significant and thus the genetic divergence for the present study was considered relevant in all the three sets of analyses. Fortyfive genotypes were grouped in seven, five and ten clusters in three subsequent years (Figs 1–3) in such a way that the genotypes within a cluster had smallest divergence than those in different clusters. The maximum number of ten clusters in 2006 revealed that the climatic conditions prevailing during the crop season were favourable for better expression of yield attributes together with quality parameters in comparison to rest of the two years. Cluster I contained the maximum number of genotypes (37, 40 and 29 in 2004, 2005 and 2006 respectively), followed by cluster II. The clusters III, IV, V and others were mono genotypic clusters. The genotypes forming single cluster were PA 405, MALJARI, KWA 227, HD 440, and PA 304 indicating that these are the most divergent genotypes. In general, clustering of genotypes was not related to geographic diversity. HD 440 grouped separately and formed mono-genotype cluster in each year revealing the stable genetic divergence from rest of the Indian genotypes. Genotypes, viz J Tapti, KWA 24, KWA 23, AH 65, CINA 223, and DLSA 24 were found to be grouped together in different years, thus, clearly indicating the existence of real genetic diversity based on yield factors and quality parameters in cotton. The clustering pattern in three years was not consistent and constituents of the cluster varied from year to year. It can be explained on the basis of gene expression that is universally known to depend on environmental conditions and would behave differently in different years. The ambient climatic conditions occurring prevalent in three subsequent years might have changed the phenotypic expression of the characters. The differential clustering pattern in three-year analyses was expected because each character is known to be governed by separate genetic system and would be determined by genotype-environment interaction. Thus, the genetic divergence would be different in varying environments (Table 1). These results are in conformity with the findings of Singh *et al.* (1990) and Jain and Yadav (2001) in cotton and Akotkar *et al.* (2010) in okra. The observations further indicate that such studies should be carried out under diverse environmental conditions for ful expression of various characters of a genotype for better classification of genetically diverse genotypes in cotton.

The genotypes belonging to different regions of the country were grouped in same clusters, while genotypes developed at a particular centre were grouped in different clusters. These studies indicated no relation between genetic and geographic diversity as also reported by Arunachalm and Ram (1967), Sandhu and Boparai (1997), Candida *et al.*

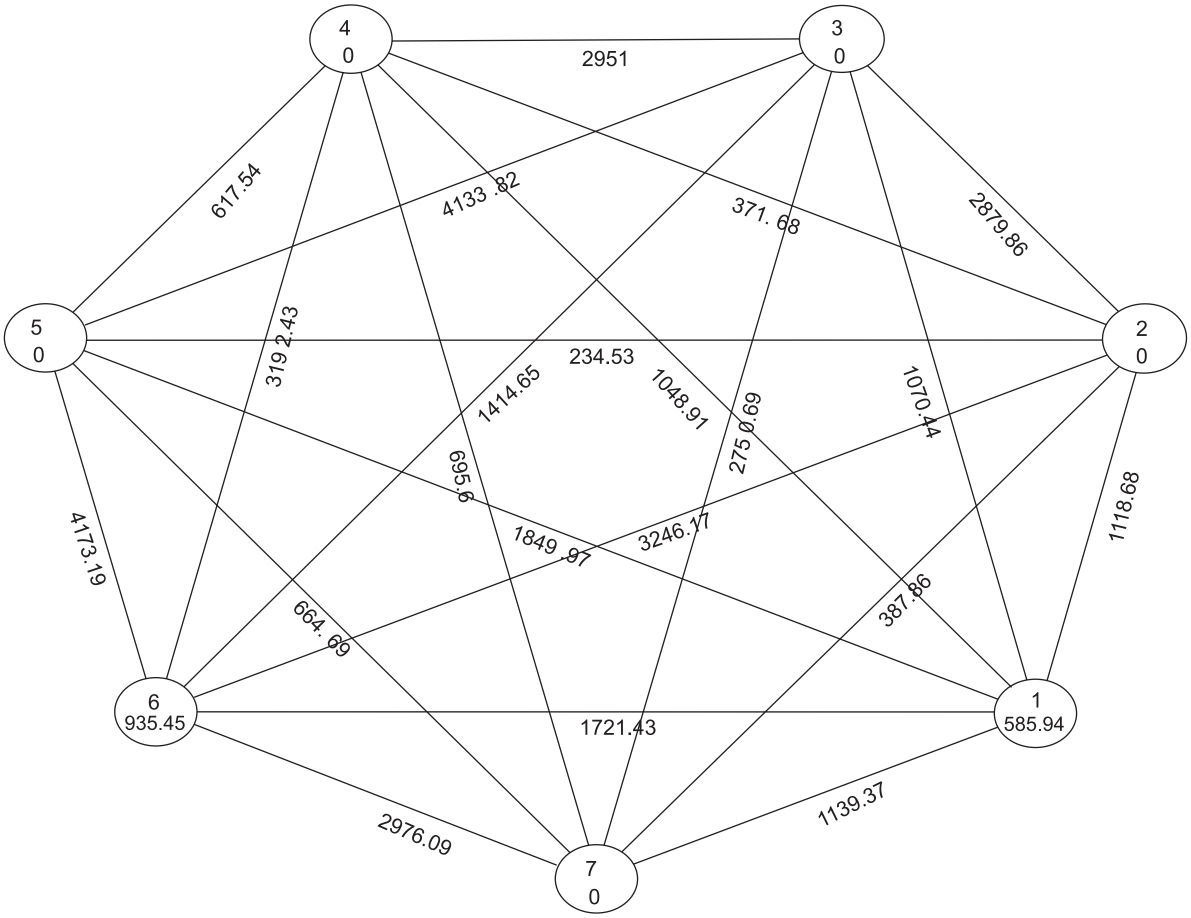

Fig 1 Intra- and inter- cluster distances among VII clusters during 2004

(2006) and Esmail *et al.* (2008) in cotton. Kulkarni and Nanda (2006) evaluated 29 upland cotton genotypes. The pattern of grouping of genotypes revealed that the genetic diversity is not fully related to the geographical diversity. Contrary to this, Khan *et al.* (2001) and Chaudhary *et al.* (2010) observed positive relation between genetic and geographic diversity in cotton. The genetic similarity obtained from the analysis could be used in selecting divergent parents for breeding and mapping purposes. The frequent exchange of segregating material, genetic drift and selection in different environments could cause greater genetic diversity between the genotypes developed at the same centre than between genotypes developed in different regions of the country (Jain and Yadav 2001). The free exchange of germplasm and their effective utilization in breeding programmes in the country have made the harmony in genetic diversity to certain extent. It alarms the identification of diverse sources of exotic germplasm and their introduction as per standard norms of Protection of Plant Varieties and Farmers Right (PPV and FR).

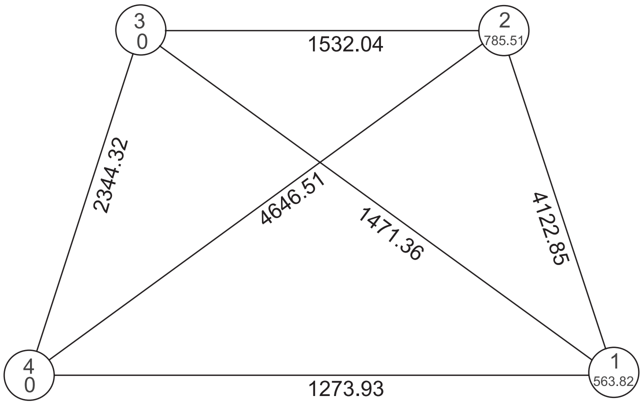

Fig 2 Intra- and inter- cluster distances among IV clusters during 2005

In 2004, cluster III and V were found most divergent, followed by cluster III and IV while, cluster II and V were the least divergent clusters. The maximum inter cluster distance of 4646.51 was recorded in between cluster II and IV, followed by cluster II and I in 2005. It indicates that these clusters contain the most divergent genotypes. In this year, cluster IV and I were found to be least divergent having the minimum inter- cluster distance of 1273.93. During 2006, clusters VI and IX, followed by clusters II and VI exhibited

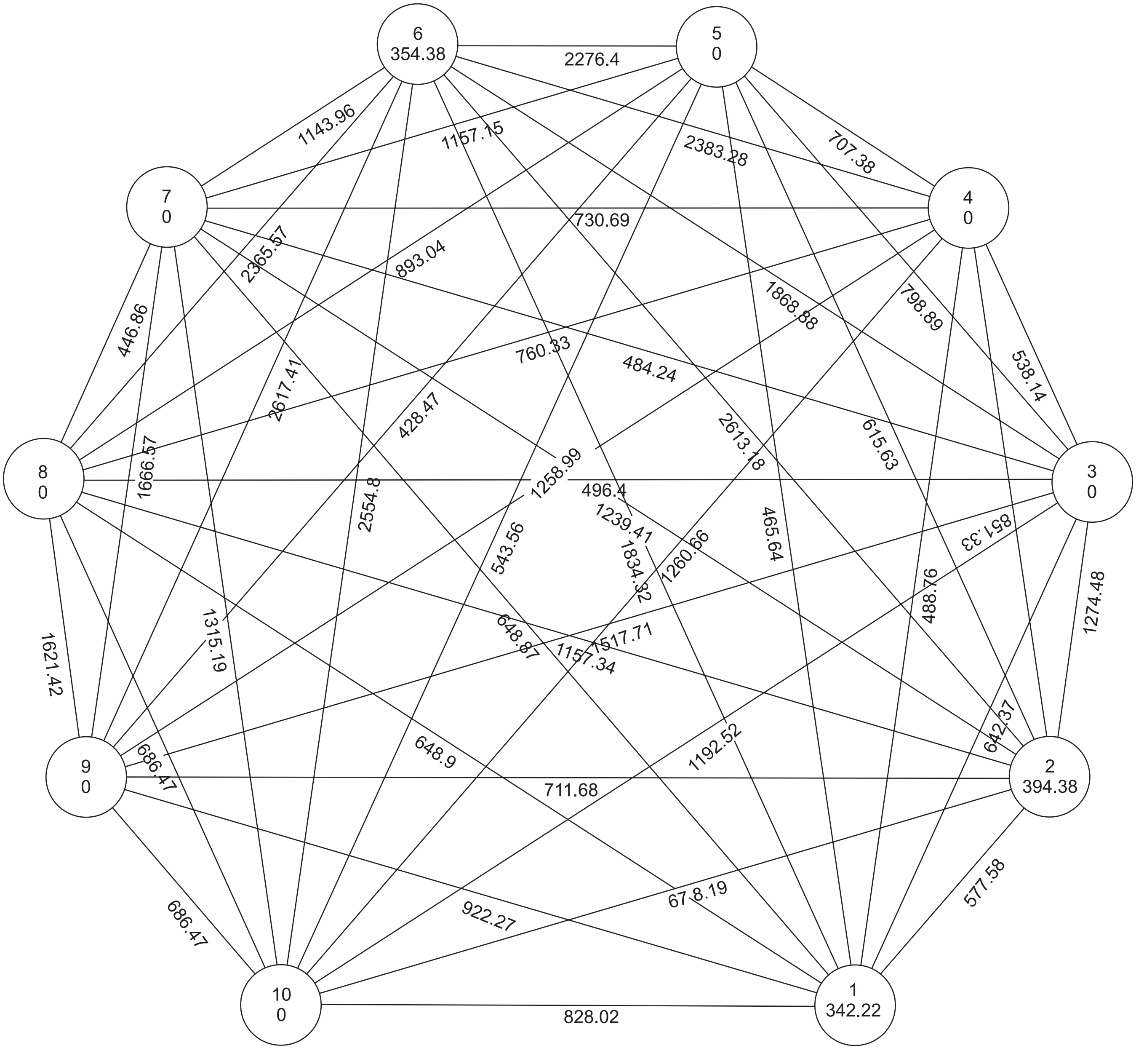

Fig 3 Intra- and inter- cluster distances among X clusters during 2006

the maximum inter-cluster distances in contrast to cluster V and IX having the minimum inter- cluster distance (Table 2). Thus, hybridization between genotypes under the highly divergent clusters should result in maximum hybrid vigour and highest numbers of useful segregants for the trait studied. Selection of genotypes from the cluster exhibiting maximum genetic divergence would be more reliable for obtaining high heterotic response that can give a wide range of variation in segregating generation for the search of desirable transgressive segregates in cotton.

The cluster means of various yield factors and fibre quality traits revealed the maximum contribution of seed cotton yield, followed by bolls/plant, sympodia/plant, monopodia/plant, nodes/plant, short fibre index and oil percentage towards genetic divergence in the present material. Higher contribution of seed cotton yield to total divergence was also reported by Sandhu and Boparai (1977), Amudha *et al.* (1997) and Pushpam *et al.* (2004) in upland cotton. Hence, the selection of parents or donors should be based on *per se* performance of these characters in the form of selection indices that will lead towards genetic improvement in seed cotton yield with better fibre quality characters in *G. arboreum.*

It is, thus, clear from the present study that genotypes, viz J Tapti, KWA 24, KWA 23, AH 65, CINA 223, and DLSA

Table 1 Clusters composition in cotton

Cluster	Season	Genotype	
		Number	Name
I	2004	37	PA 304, CINA 223, LD 713, DLSA 24, DLSA 17, PA 402, PAIG 29, PAIG 213, CINA 329, CINA 316, PAIG 8/3, PAIG 8/1, G.Cot 15, DLSA 202, AH 36, AH 10, PA 255, AKA 8401, PA 496, MDL 2601, MDL 2463, PAIG 210, PAIG 30, AH 65, PAIG 329, SARVOTTAM, PAIG 27, KWA 225, KWA 226, KWA 23, KWA 24, KWA 25, KWA 6, KWA 7, KWA 8, KWA 9, J Tapti
	2005	40	PAIG 213, G.Cot 15, DLSA 17, AH 10, AH 36, PAIG 210, PAIG 17, DLSA 24, AH 65, KWA 225, KWA 7, PA 304, CINA 223, LD 713, PA 405, PA 402, PAIG 29, CINA 329, LD 733, PAIG 8/1, DLSA 202, PA 225, AKA 8401, PA 496, MDL 2601, MDL 2463, PAIG 30, PAIG 329, SARVOTTAM, PAIG 27, KWA 226, KWA 227, KWA 23, KWA 24, KWA 25, KWA 6, KWA 8, KWA 9, J Tapti and MALJARI
	2006	29	CINA 223, DLSA 24, DLSA 17, PA 402, PA 405, PAIG 29, PAIG 213, CINA 329, DLSA 202, AH 36, AH 10, PA 255, AKA 8401, PA 496, MDL 2463, PAIG 210, PAIG 30, AH 65, SARVOTTAM, PAIG 27, KWA 27, KWA 225, KWA 226, KWA 227, KWA 23, KWA 24, KWA 25, KWA 6, KWA 7 and J.Tapti
II	2004	1	LD 733
	2005	3	KWA N-1, KWA N-2, KWA N-3
	2006	6	LD 713, LD 733, G.Cot 15, PAIG 329, KWA 8, KWA 9
III	2004	1	PA 405
	2005	1	PAIG 8/3
	2006	1	CINA 316
IV	2004	1	KWA 227
	2005	1	HD 440
	2006	1	MDL 2601
V	2004	1	MALJARI
	2005		
	2006	1	PA 304
VI	2004	3	KWA N-1, KWA N-2, KWA N-3
	2005		
	2006	3	KWA N-1, KWA N-2, KWA N-3
VII	2004	1	HD 440
	2005		
	2006	1	PAIG 8/1
VIII	2004		
	2005		
	2006	1	PAIG 8/3
IX	2004		
	2005		
	2006	1	HD 440
X	2004		
	2005		
	2006	1	MALJARI

24 showed real genetic diversity, while genotypes PA 405, MALJARI, KWA 227, HD 440 and PA 304, exhibited the true diversity. Among them, HD 440 exhibited stable diversity over the environments.

Hence, these genotypes can be utilized in systematic breeding programme aimed at genetic amelioration of seed cotton yield and fibre quality parameters in *G. arboreum.* The study further indicates that genetic diversity in the present material was independent to geographic origin of the genotypes in Indian subcontinent. Thus, geographic origin

Table 2 Inter- and intra- cluster distances in cotton for three seasons

Cluster	Season	I	II	III	IV	V	VI	VII	VIII	IX	X
I	2004	**585.94**	1118.68	1070.44	1048.91	1849.97	1721.43	1139.37			
	2005	**563.82**	4122.85	1471.36	1273.93						
	2006	**342.22**	577.58	642.37	488.76	465.64	1834.32	648.87	648.9	922.27	828.02
II	2004		**0.00**	2879.86	371.68	234.53	3246.17	387.86			
	2005		**785.51**	1532.04	4646.51						
	2006		**394.38**	1274.48	851.33	615.63	2613.18	1239.41	1157.34	711.68	678.19
III	2004			**0.00**	2951.00	4133.82	1414.65	2750.69			
	2005			**0.00**	2344.32						
	2006			**0.00**	538.14	798.89	1868.88	484.24	496.4	1517.71	1192.52
IV	2004				**0.00**	617.54	3192.43	695.6			
	2005				**0.00**						
	2006				**0.00**	707.38	2383.28	730.69	760.33	1258.99	1260.66
V	2004					**0.00**	4173.19	664.69			
	2005										
	2006					**0.00**	2276.4	1157.15	893.04	428.47	543.56
VI	2004						**935.45**	2976.09			
	2005										
	2006						**354.38**	1143.96	2365.57	2617.41	2554.80
VII	2004							**0.00**			
	2005										
	2006							**0.00**	446.86	1666.57	1315.19
VIII	2004										
	2005										
	2006								**0.00**	1621.42	989.6
IX	2004										
	2005										
	2006									**0.00**	686.47
X	2004										
	2005										
	2006										**0.00**

Bold figures denote the intra- cluster distances

cannot be considered as sole criteria for the selection of desirable donors for breeding programmes. The study again indicates the vigorous testing of exotic and indigenous genotypes over years and location for identification of stable genetic divergent genotypes in cotton.

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