

## Original Research Article

# Genetic Diversity Studies in Genotypes of Cotton (*Gossypium hirsutum* and *Gossypium arboreum*)

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## ABSTRACT

### Keywords

D-square,  
Genetic  
divergence,  
Heterotic,  
Pubescence,  
Sucking pests,  
Tolerance

Cotton being one of the most important commercial crop and raw material for the textile industry faces serious problems of pest attack. Though *Bt* cotton turns out to be an effective way of controlling boll worms, shows susceptibility to sucking pests such as jassids and mirid bugs. The mechanisms imparting sucking pest tolerance include morphological barriers (pubescence traits, thickness of leaf lamina etc.) or an array of phytochemicals imparting resistance. So, the present study was conducted at Annigeri location with 86 genotypes including genotypes of *G. hirsutum* and *G. arboreum* were subjected to mahalanobis D square analysis considering 18 characters including four pubescence traits. The results indicated a clear cut divergence between genotypes of *G. hirsutum* and *G. arboreum* for the traits. Contribution of sucking pest tolerant traits was more pronouncing than the yield attributing traits towards divergence. This indicates the set of genotypes can be used for selecting better genotypes and improving them for sucking pest tolerance. Clusters I and VII show highest inter cluster diversity for the traits ensuring that the crossing programme involving genotypes form these two clusters intended to improve sucking pest tolerance can yield a heterotic genotype.

## Introduction

Cotton is one of the most important raw materials for the textile industry worldwide and known as the 'King of Fiber'. Having significant economic and social impact on Indian economy, cotton is commonly known as 'White Gold'. The major target of cotton breeding in the world has been to improve fibre yield and quality.

In the recent years, incidence of the sucking pest, leafhopper *Amrasca devastance* (Jassids) became one of the most serious production constraints of this crop not only in India but also in Pakistan, Bangladesh,

Thailand and other Southeast Asian countries. This outbreak of jassids or in broad sense sucking pests was mainly due to ignorance towards the IPM measures suggested after the introduction of *Bt* cotton. *Bt* cotton growers reduced or even stopped application of pesticides for bollworm complex which also used to keep in control the sucking pest to some extent, sufficient enough to keep them well below their ETL levels.

Defense mechanisms involve either morphological barriers or elaborative array

of phytochemicals, acting as repellents, phagodeterrents and oviposition deterrents, thus exhibiting resistance. Antixenosis and antibiosis were considered to be the mechanisms for sucking pest resistance. In cotton, various morphological traits are known to exhibit antixenosis, trichome density being one of the most important traits. Trichome density on the ventral surface of the leaves, hair length and hair density on mid-vein are the important and easily recognizable morphological traits which impart resistance against many sucking pests, mainly jassids, by interfering with oviposition of insect, attachment to the plant, feeding and ingestion.

Desi cotton (*G. arboreum*) has inbuilt resistance to sucking pests due to their peculiar leaf anatomy. Homopteran pests including jassids have preset target to reach phloem element and suck the sap by piercing stylet into lower epidermis. In *G. arboreum* distance of phloem from lower epidermis is relatively more and parenchyma cells are more compact compared to *G. hirsutum* (Kulkarni, 2002). Hence, a study on the morphological traits and the sucking pests in the two species may help in understanding the traits responsible for sucking pest tolerance such as pubescence in cotton.

Identifying genotypes which are diverse enough for the sucking pest tolerance traits, performing moderately well for yield attributing traits and improving them through suitable crossing programme to get heterotic genotypes may help in sustainably increasing tolerance to sucking pests with no penalty being imposed on yield levels.

In view of the aforementioned, present investigation was carried out to assess the genetic diversity of 86 genotypes at Annigeri for 11 yield attributing and 7 sucking pest tolerance traits.

## Materials and Methods

Present investigation was conducted at Agriculture Research Station, Annigeri, situated in the northern dry zone (Zone No. 3) of Karnataka with latitude of 15°8' N, longitude of 75°3' E and an altitude of 624.80 meters above mean sea level (MSL). Crop was grown under rainfed conditions and under unprotected conditions for the sucking pest incident. All other agronomic managements were followed according to recommended package of practices.

A total of 86 genotypes including 77 genotypes of *Gossypium hirsutum*, six genotypes of *Gossypium arboreum* and the checks, ARBH-813 and Sahana of *G. hirsutum* and DLSA-17 of *G. arboreum* have been sown in Randomized Block Design with each genotype in two lines replicated two times and in time observations were recorded. The data of 11 yield attributing traits, four pubescence traits and three entomological observations were run in Windostat, version 8.1 for the estimation of genetic divergence of the above mentioned genotypes for the 18 traits.

The observations were recorded for 11 yield attributing traits such as days to 50 per cent flowering, days to boll opening, plant height, number of bolls per plant, sympodial branches per plant, monopodial branches per plant, boll weight, seed cotton yield, lint index, seed index and ginning out turn and four pubescence traits. Observations on four pubescence traits such as abaxial leaf pubescence (AFLP) (Bourland *et al.*, 2003), bract marginal pubescence (BRMP), apical stem pubescence (APSP) and lower stem pubescence (LWSP) were recorded (Hornbeck and Bourland, 2007).

The data on leaf and stem pubescence were collected during August-September months using a hand lens (4X magnification). In

each entry five plants at random in each plot were chosen and labeled for recording observations and screened for pubescence based on rating system. The mean of five plants was used for statistical analysis.

The 0-9 point scale for pubescence as given by Bourland *et al.*, (2003) was used for screening in the present study (Plate 1). The proposed system includes a visual rating of trichomes on the abaxial surface of the leaf using a scale of 1 (smooth leaf), 3 (lightly hairy), 5 (hairy), 7 (very hairy) and 9 (pilose). Even numbered ratings were assigned to plants that appeared to be between the major rating classes.

Three entomological observations such as jassid nymphal count which was counted on five plants per genotype and five leaves in each of the five plants in each replication. The observations were recorded during mid of October during which jassid incidence was peak or at its ETL (2 nymphs/ leaf). Density of nymphs was counted by visual observations on abaxial surface of the leaf (5 leaves/ plant) Jassid score based on damage was recorded by visually rating the plants for evidence of hopper burn by adopting 1- 4 grade scale given by Indian Central Cotton Committee (ICCC). Based on grades entries were categorized as tolerant (Grade 1), moderately tolerant (Grade 2), susceptible (Grade 3) and highly susceptible (Grade 4) according to Sikka *et al.*, (1966) with slight modification. Mirid bug nymphal count was taken on five plants per genotype and ten squares in each of the five plants in each replication. The observations were recorded at the end of December during which mirid bug incidence was peak or at its ETL (2 nymphs/ leaf). Density of nymphs was counted by visually observing squares (10 leaves/ plant). The average value of ten squares on five plants in each entry was taken for the analysis

## Results and Discussion

### Contribution of characters towards divergence

Among yield attributing traits, lint index, days to boll opening, seed cotton yield, number of monopodia and days to 50 per cent flowering had major contribution. Similar results of substantial contribution of lint index to the diversity have been reported by Basavaraddi and Katageri (2011) and Abd El-Moghny *et al.*, (2015).

Whereas, among sucking pest tolerant traits, abaxila leaf pubescence, jassid nymphal count and jassid damage score put together have shown a very high per cent contribution (of around 43.20 per cent) under unprotected conditions, towards divergence of genotypes (Table 1). The overall contribution of sucking pest tolerant traits among yield attributing traits and sucking pest tolerant traits was more pronouncing. This indicates that the genotypes have a potential diversity for the sucking pest tolerant traits and also the yield attributing traits. So this diversity can be utilized efficiently in selecting genotypes with appreciable amount of yield and also the sucking pest tolerance, to combine them in one genotype with suitable crossing programmes.

### Group constellation

A set of 86 genotypes was grouped into seven clusters based on  $D^2$  values (Table 2), indicating appreciable amount of diversity among the genotypes under study (Figure 1). The maximum numbers of genotypes were grouped into cluster II with 62 genotypes in it and the only one solitary cluster was cluster III with the genotype DHS-74. All *G. arboreum* genotypes were grouped in one cluster i.e. cluster I. The separate grouping

of genotypes of *G. arboreum* from genotypes of *G. hirsutum* might be due to the sucking pest tolerant traits, helping in clearly distinguishing the two species.

**Intra and inter-cluster distance**

The intra cluster D<sup>2</sup> value ranged from zero

in the solitary cluster (cluster III) to 53.84 in cluster VII. Out of seven clusters one and only solitary cluster has zero intra cluster D<sup>2</sup> value whereas, remaining all the clusters with more than one genotype in them have shown presence of some level of intra cluster diversity (Table 3).

**Table.1** Contribution of traits towards divergence in genotypes of *Gossypium hirsutum* L. and *Gossypium arboreum* L. at Annigeri location

Sl. No.	Source	Contribution (%)	Times ranked 1 <sup>st</sup>
1	Days to 50 per cent flowering	3.99%	146
2	Days to boll opening	14.17%	518
3	Plant height (cm)	0.66%	24
4	Number of bolls	1.15%	42
5	Number of sympodia	0.77%	28
6	Number of monopodia	4.05%	148
7	Boll weight (g)	0.71%	26
8	Seed cotton yield (t/ha)	4.98%	182
9	Seed Index (SI) (g)	0.49%	18
10	Lint Index (LI) (g)	19.26%	704
11	Ginning Out Turn (GOT) (%)	0.33%	12
12	Abaxila leaf pubescence	16.39%	599
13	Apical stem pubescence	4.21%	154
14	Lower stem pubescence	0.33%	12
15	Bract marginal pubescence	1.04%	38
16	Jassid nymphal count	16.22%	593
17	Jassid score based on damage	10.59%	387
18	Mirid bug nymphal count	0.66%	24

**Table.3** Intra and inter cluster distance between lines of *Gossypium hirsutum* L. and *Gossypium arboreum* L. at Annigeri location

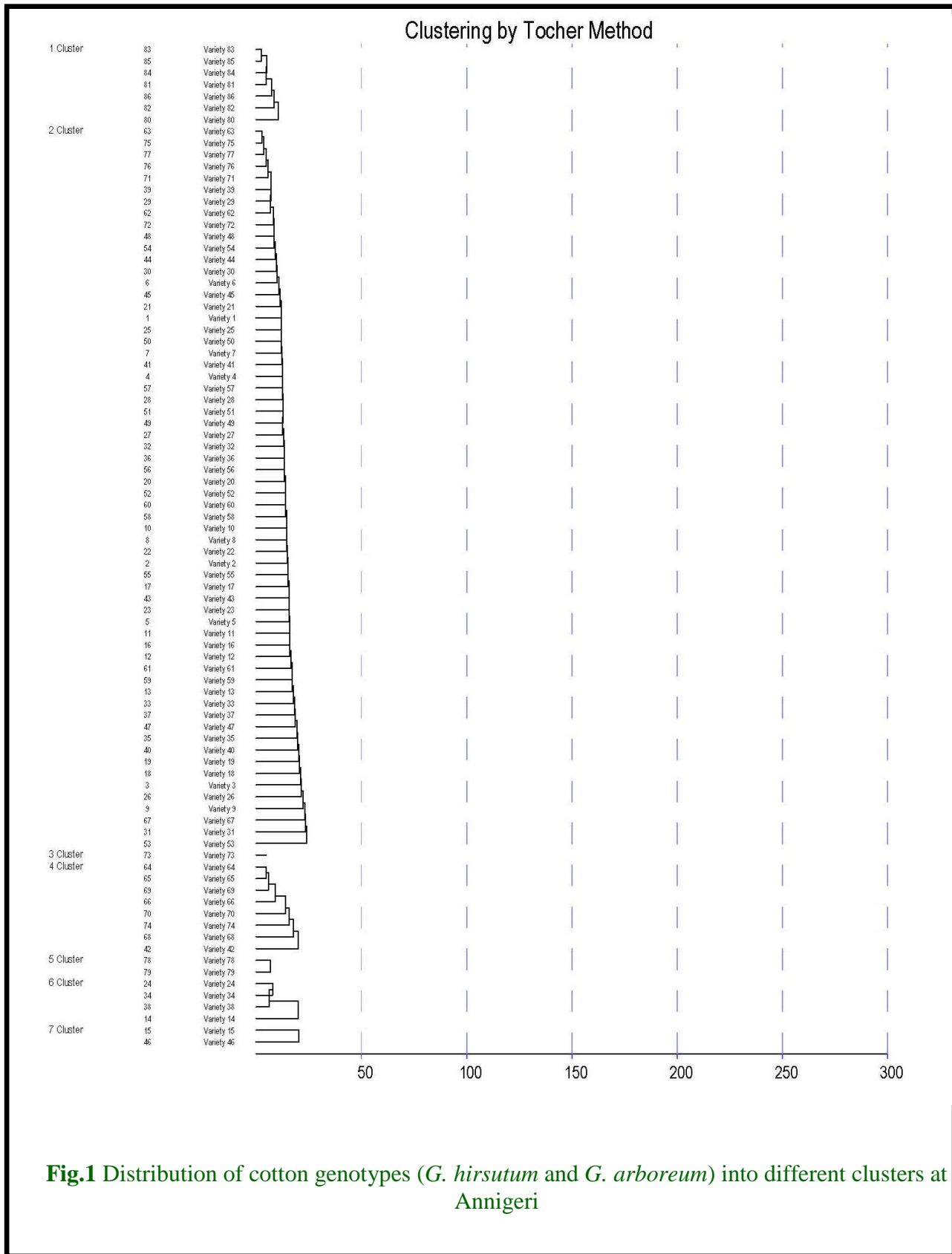
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	25.33	184.19	235.72	199.36	332.64	301.7	340.83
Cluster II		45.53	70.28	78.83	134.57	94.22	194.22
Cluster III			0	40.71	115.1	91.28	309.65
Cluster IV				48.17	143.5	140.59	319.4
Cluster V					18.2	156.18	237.29
Cluster VI						47.41	224.47
Cluster VII							53.84

**Table.2** Clustering of genotypes of *Gossypium hirsutum* L. and *Gossypium arboreum* L. at Annigeri location based on D<sup>2</sup> analysis

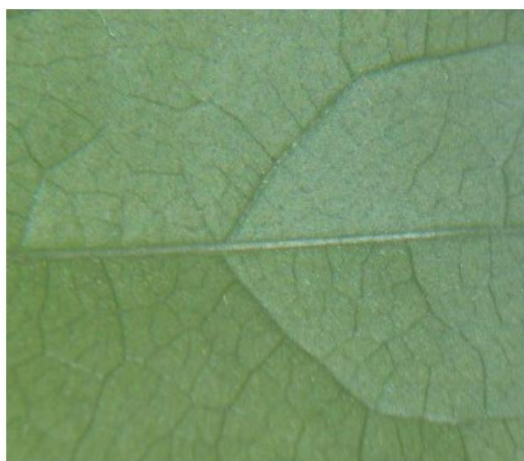
Cluster	Genotype in cluster	Number of genotype in cluster
Cluster I	Arb-1, Arb-5, Arb-6, Arb-7, Arb-8, Arb-9, DLSA-17	7
Cluster II	DHS-1, DHS-2, DHS-3, DHS-4, DHS-5, DHS-6, DHS-7, DHS-8, DHS-9, DHS-10, DHS-11, DHS-12, DHS-13, DHS-16, DHS-17, DHS-18, DHS-19, DHS-20, DHS-21, DHS-22, DHS-23, DHS-25, DHS-51, DHS-26, DHS-27, DHS-28, DHS-29, DHS-30, DHS-31, DHS-52, DHS-54, DHS-32, DHS-33, DHS-55, DHS-56, DHS-57, DHS-35, DHS-36, DHS-37, DHS-39, DHS-40, DHS-41, DHS-59, DHS-60, DHS-61, DHS-62, DHS-63, DHS-42, DHS-43, DHS-44, DHS-45, DHS-46, DHS-47, DHS-48, DHS-49, DHS-64, DHS-68, DHS-72, DHS-73, DHS-76, DHS-77, DHS-78	62
Cluster III	DHS-74	1
Cluster IV	DHS-58, DHS-65, DHS-66, DHS-67, DHS-69, DHS-70, DHS-71, DHS-75	8
Cluster V	Sahana, ARBH-813	2
Cluster VI	DHS-14, DHS-24, DHS-53, DHS-34	4
Cluster VII	DHS-15, DHS-38	2

**Table.4** Cluster mean of lines *Gossypium hirsutum* L. and *Gossypium arboreum* L. at Annigeri location

	Days to 50% flowering	Days to first boll opening	Plant height (cm)	Bolls per plant	Number of sympodia	Number of monopodia	Boll weight (g)	Seed cotton yield (q/ha)	Seed index (g)	Lint index (g)	Ginning outturn (%)	Abaxial leaf pubescence	Apical stem pubescence	Lower stem pubescence	Bract marginal pubescence	Jassid nymphal count	Jassid injury grade	Mirid bug nymphal count
Cluster I	74.79 (6)	124.64 (5)	134.21 (1)	22.4 (1)	18.5 (1)	1.17 (7)	2.82 (7)	18.54 (1)	7.4 (7)	3.84 (7)	34.44 (5)	4.43 (2)	4.49 (3)	3.88 (2)	3.73 (2)	0.47 (2)	0.31 (1)	0.34 (1)
Cluster II	72.46 (4)	114.8 (3)	68.04 (5)	11.81 (6)	10.23 (5)	1.45 (4)	3.8 (4)	9.84 (5)	9.1 (6)	4.64 (6)	33.62 (7)	2.89 (3)	3.19 (5)	2.61 (5)	2.74 (3)	3.38 (3)	2.37 (3)	0.91 (4)
Cluster III	71.5 (3)	121 (4)	84.6 (3)	20.3 (2)	11.7 (3)	3 (1)	3.05 (5)	3.38 (7)	9.57 (2)	5.66 (2)	37.2 (2)	1.4 (7)	2.3 (7)	2.2 (7)	1.9 (7)	4.8 (5)	2.9 (6)	1 (5)
Cluster IV	77.88 (7)	127.5 (6)	74.29 (4)	14.62 (4)	10.05 (6)	2.3 (2)	3.01 (6)	4.96 (6)	9.35 (4)	4.92 (5)	34.18 (6)	1.88 (6)	2.54 (6)	2.33 (6)	2.41 (5)	4.12 (4)	2.48 (5)	0.85 (2)
Cluster V	73.75 (5)	130.25 (7)	98 (2)	15.55 (3)	11.9 (2)	1.25 (6)	4.15 (2)	14.13 (2)	9.47 (3)	5.09 (4)	34.9 (4)	2.25 (5)	5.4 (2)	3.3 (3)	2.05 (6)	6.65 (6)	3.25 (7)	1.4 (6)
Cluster VI	71.38 (2)	109.5 (1)	61.93 (6)	13.63 (5)	10.48 (4)	1.35 (5)	3.87 (3)	12.94 (3)	10.38 (1)	7.13 (1)	40.72 (1)	2.63 (4)	3.4 (4)	2.63 (4)	2.6 (4)	3.25 (2)	2.3 (4)	0.9 (3)
Cluster VII	70.25 (1)	111.25 (2)	61.35 (7)	8.65 (7)	9.9 (7)	1.5 (3)	4.35 (1)	10.43 (4)	9.17 (5)	5.15 (3)	35.96 (3)	7.28 (1)	7.47 (1)	6.4 (1)	7.35 (1)	3.25 (2)	1.2 (2)	0.85 (2)



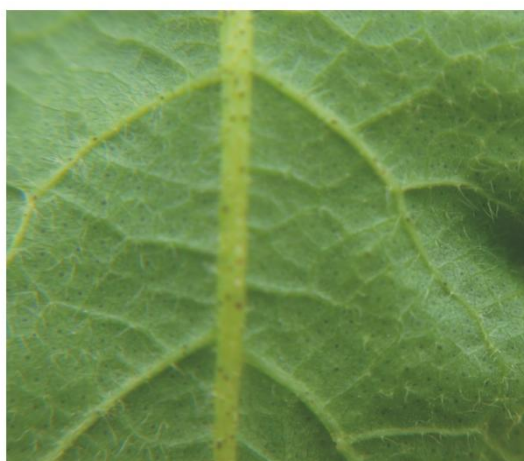
**Fig.1** Distribution of cotton genotypes (*G. hirsutum* and *G. arboreum*) into different clusters at Annigeri



**a. Glabrous**



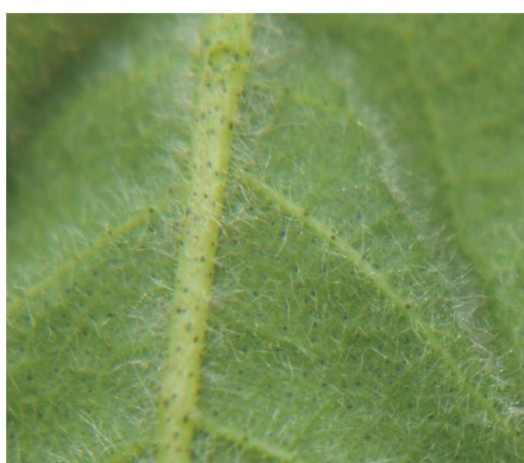
**b. Grade 1**



**c. Grade 3**



**d. Grade 5**



**e. Grade 7**



**f. Grade 9**

**Plate 1. 9-point scale for field evaluation of pubescence in cotton**

The inter cluster distance was observed to be highest between cluster I and VII (340.83), indicating that the two clusters are diverse for the characters under study. The lowest inter cluster distance was recorded for the clusters III and IV indicating low diversity between genotypes of these two clusters. Therefore, selection of genotypes falling under the clusters I and VII for further breeding programme may give better results with higher yields and other important contributing traits. Genotypes occurring in cluster I are *arboreum* genotypes and those occurring in cluster VII are the *hirsutum* genotypes with highest pubescence grades with moderate yield levels. So, there are maximum chances of getting a heterotic inter-specific genotype for the sucking pest tolerance.

#### **Analysis of cluster means**

Analysis of cluster means revealed the relative contribution of different traits to the total divergence through different clusters. Based on range of means, it is possible to know the characters influencing divergence. The genotypes under cluster VII ranked first (53 - score) with 13 characters in desirable direction (1-3), followed by cluster VI (57 - score) with nine traits and cluster I (60 - score) with 11 traits. The genotypes under the cluster IV ranked last (90 - score), with 16 traits in negative direction (Table 4).

Therefore selection of genotypes accommodated in clusters VII, VI and I

would be more beneficial in generating a desirable genetic resource through suitable crossing programmes, to be improved upon.

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